

Result No.	Query			DB	ID	Description
	Score	Match	Length			
1	5961	100.0	1132	3	US-08-951-843A-225	Sequence 225, App
2	5961	100.0	1132	3	US-08-974-549A-2	Sequence 2, App
3	5961	100.0	1132	3	US-08-854-050-225	Sequence 225, App
4	5961	100.0	1132	3	US-09-430-323-225	Sequence 225, App
5	5961	100.0	1132	3	US-09-128-354-2	Sequence 2, App
6	5961	100.0	1132	4	US-09-675-321-2	Sequence 2, App
7	5961	100.0	1132	4	US-09-052-919-2	Sequence 2, App
8	5961	100.0	1132	4	US-08-912-951-2	Sequence 2, App
9	5961	100.0	1132	4	US-09-402-181B-2	Sequence 2, App
10	5961	100.0	1132	4	US-09-721-456-2	Sequence 2, App
11	5961	100.0	1132	4	US-09-953-052-2	Sequence 2, App
12	5961	100.0	1132	4	US-09-042-460-3	Sequence 3, App
13	5961	100.0	1132	4	US-09-949-016-6326	Sequence 6326, App
14	5961	100.0	1154	3	US-08-974-549A-611	Sequence 611, App
15	5961	100.0	1154	4	US-08-912-951-323	Sequence 323, App
16	5961	100.0	1154	4	US-09-402-181B-611	Sequence 611, App
17	5961	100.0	1154	4	US-09-721-456-611	Sequence 611, App
18	5961	100.0	1189	3	US-08-974-549A-613	Sequence 613, App
19	5961	100.0	1189	4	US-08-912-951-325	Sequence 325, App
20	5961	100.0	1189	4	US-09-402-181B-613	Sequence 613, App
21	5961	100.0	1189	4	US-09-721-456-613	Sequence 613, App
22	5961	100.0	1200	3	US-08-974-549A-612	Sequence 612, App
23	5961	100.0	1200	4	US-08-912-951-324	Sequence 324, App
24	5961	100.0	1200	4	US-09-402-181B-612	Sequence 612, App
25	5961	100.0	1200	4	US-09-721-456-612	Sequence 612, App
26	5961	100.0	1285	3	US-08-974-549A-600	Sequence 600, App
27	5961	100.0	1285	4	US-08-912-951-314	Sequence 314, App

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; SEQUENCE CHARACTERISTICS:
; LENGTH: 1132 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-851-843A-225

Query Match 100.0%; Score 5961; DB 3; Length 1132;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MPRAPCRAVSLARSHREVLPVPLATFVRRVLPQGWRLVQRGDPAARALVAQCCLVCPW 60
Db 1 MPRAPCRAVSLARSHREVLPVPLATFVRRVLPQGWRLVQRGDPAARALVAQCCLVCPW 60

Qy 61 DARPPPAAPSPQVSCLEKELVARVQLRCERGAKNVLAFFGALLDGGAGGPPPEAFTTSVR 120
Db 61 DARPPPAAPSPQVSCLEKELVARVQLRCERGAKNVLAFFGALLDGGAGGPPPEAFTTSVR 120

Qy 121 SYLNTVTDALRGSGAWGLLRVGGDDVLLHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180
Db 121 SYLNTVTDALRGSGAWGLLRVGGDDVLLHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180

Qy 181 ATOARPPHAGSPRRRLGCERAWNHSVREAGVPLGLPAPGARRRGGASRLPLPKRPRR 240
Db 181 ATOARPPHAGSPRRRLGCERAWNHSVREAGVPLGLPAPGARRRGGASRLPLPKRPRR 240

Qy 241 GAAPEPERTVQGGSWAHGRTGRPSDRGFCVSPARPAEATSLGALSCTRSHSPSVG 300
Db 241 GAAPEPERTVQGGSWAHGRTGRPSDRGFCVSPARPAEATSLGALSCTRSHSPSVG 300

Qy 301 QOHAGPSTSRPRPMDTPCPVVAETKHPFLYSSGDKQLRPSFLSSRLPSLTGARRL 360
Db 301 QOHAGPSTSRPRPMDTPCPVVAETKHPFLYSSGDKQLRPSFLSSRLPSLTGARRL 360

Qy 361 VETFLGSRPMWGTRELPLPORYWOMRPLFLELLGNHAOCYPGVLLKTHCPRAAVT 420
Db 361 VETFLGSRPMWGTRELPLPORYWOMRPLFLELLGNHAOCYPGVLLKTHCPRAAVT 420

Qy 421 PAAGVCAREKPGQSVAAPEEDTPRRLVQLLRQHSPPWQVYGFVRACLRLVPPGLWGS 480
Db 421 PAAGVCAREKPGQSVAAPEEDTPRRLVQLLRQHSPPWQVYGFVRACLRLVPPGLWGS 480

Qy 481 RHNERFLRNTKXFTISLGKHAKLSIQELTWKMSVRDCAWLRSPGVGCVPAAEHRLREEI 540
Db 481 RHNERFLRNTKXFTISLGKHAKLSIQELTWKMSVRDCAWLRSPGVGCVPAAEHRLREEI 540

Qy 541 LAKFLHLMMSVYVVELLRSFFVVTETTPQKNRLFYRKSVMSKLSQIGIROHLKRVOLRE 600
Db 541 LAKFLHLMMSVYVVELLRSFFVVTETTPQKNRLFYRKSVMSKLSQIGIROHLKRVOLRE 600

Qy 601 LSEAEVROHREARPAALLTSRLRFPKPDGLRPIVNMDDYVVGARTFRREKRAERLTSRVKA 660
Db 601 LSEAEVROHREARPAALLTSRLRFPKPDGLRPIVNMDDYVVGARTFRREKRAERLTSRVKA 660

Qy 661 LFSVLNTERARRPGLLGASVULGLDDIHRAWTFVLRVAQDPPPELFFVKVDVTGAVDTI 720
Db 661 LFSVLNTERARRPGLLGASVULGLDDIHRAWTFVLRVAQDPPPELFFVKVDVTGAVDTI 720

Qy 721 PQDLRLTEVIASIIKPONTYCVRRVAVQKAAGHVRKAFKSHVSTLTDLQPYMQFVAHL 780
Db 721 PQDLRLTEVIASIIKPONTYCVRRVAVQKAAGHVRKAFKSHVSTLTDLQPYMQFVAHL 780

Qy 781 QETSPRLDAVIEQSSSLNEASSGLFDVFLRFMCHAVIRGKSVVQCQGIPOGSIILSTL 840
Db 781 QETSPRLDAVIEQSSSLNEASSGLFDVFLRFMCHAVIRGKSVVQCQGIPOGSIILSTL 840

Qy 841 LCSICYGDMENKLFAGIRRDGLLRVDDFLVLTPLTHAKTFTLTVRGVPEYGCVVNL 900
Db 841 LCSICYGDMENKLFAGIRRDGLLRVDDFLVLTPLTHAKTFTLTVRGVPEYGCVVNL 900

Qy 901 RKTVMNPFVEALGGTAVQMPAHGLFPWCGLLDTRTLEVSQSDYSYARTSIRASLTFF 960
Db 901 RKTVMNPFVEALGGTAVQMPAHGLFPWCGLLDTRTLEVSQSDYSYARTSIRASLTFF 960

; Sequence 2, Application US/08974549A
; Patent No. 6166178
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; APPLICANT: Lingner, Joachim
; APPLICANT: Nakamura, Toru
; APPLICANT: Chapman, Karen B.
; APPLICANT: Morin, Gregg B.
; APPLICANT: Harley, Calvin B.
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: Human Telomerase Catalytic Subunit
; NUMBER OF SEQUENCES: 727
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/974,549A
; FILING DATE: 19-NOV-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/851,843
; FILING DATE: 06-MAY-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/854,050
; FILING DATE: 09-MAY-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/911,312
; FILING DATE: 14-AUG-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/912,951
; FILING DATE: 14-AUG-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/915,503
; FILING DATE: 14-AUG-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/US97/17618
; FILING DATE: 01-OCT-1997
; PRIOR APPLICATION DATA:
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QY	781	QETSPLRD	AVVIEQSSS	INEASGL	PDVFLR	FMCHAVR	IRGKSYV	QCOG	IPOG	SIL	STL	840
Db	781	QETSPLRD	AVVIEQSSS	INEASGL	PDVFLR	FMCHAVR	IRGKSYV	QCOG	IPOG	SIL	STL	840
QY	841	LCSLCYG	DMENK	L	FAGIR	RDGL	LLRLV	DDFL	LVTPHL	THAKT	PLRTL	VRGVPEYGC
Db	841	LCSLCYG	DMENK	L	FAGIR	RDGL	LLRLV	DDFL	LVTPHL	THAKT	PLRTL	VRGVPEYGC
QY	901	RKTVMN	FPVEDE	ALGCTA	FVQMP	AHGL	FPWC	GILL	DDTR	LTLE	VQSDY	SSYARTS
Db	901	RKTVMN	FPVEDE	ALGCTA	FVQMP	AHGL	FPWC	GILL	DDTR	LTLE	VQSDY	SSYARTS
QY	961	NRGFKAG	RNRMR	KL	FGVBL	KCHSL	PLD	LQVNS	LQTVCT	NIYK	ILLQAYR	FHACVLQ
Db	961	NRGFKAG	RNRMR	KL	FGVBL	KCHSL	PLD	LQVNS	LQTVCT	NIYK	ILLQAYR	FHACVLQ
QY	1021	FHQQVW	KNPTFF	LURV	ISDTAS	LCYS	TLKAKN	AGMS	LGAKG	AGPLP	SEAVQW	LCHQAFLL
Db	1021	FHQQVW	KNPTFF	LURV	ISDTAS	LCYS	TLKAKN	AGMS	LGAKG	AGPLP	SEAVQW	LCHQAFLL
QY	1081	KLUTRHR	VTVP	LLGSL	RTAQT	QLSR	KLP	GTTLT	AL	EAAN	PAL	PSDFK
Db	1081	KLUTRHR	VTVP	LLGSL	RTAQT	QLSR	KLP	GTTLT	AL	EAAN	PAL	PSDFK

RESULT 3
 US-08-854-050-225
 ; Sequence 225, Application US/08854050
 ; Patent No. 6261836
 ; GENERAL INFORMATION:
 ; APPLICANT: Cech, Thomas R.
 ; APPLICANT: Lingner, Joachim
 ; APPLICANT: Nakamura, Toru
 ; APPLICANT: Chapman, Karen B.
 ; APPLICANT: Morin, Gregg B.
 ; APPLICANT: Harley, Calvin
 ; APPLICANT: Andrews, William H.
 ; TITLE OF INVENTION: No. 6261836el Telomerase
 ; NUMBER OF SEQUENCES: 225
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Townsend and Townsend and Crew LLP
 ; STREET: Two Embarcadero Center, 8th Floor
 ; CITY: San Francisco
 ; STATE: California
 ; COUNTRY: United States of America
 ; ZIP: 94111
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/854,050
 ; FILING DATE: 09-MAY-1997
 ; CLASSIFICATION: 536
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/851,843
 ; FILING DATE: 06-MAY-1997
 ; CLASSIFICATION: 536
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/844,419
 ; FILING DATE: 18-APR-1997
 ; CLASSIFICATION: 536
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/724,643
 ; FILING DATE: 01-OCT-1996
 ; CLASSIFICATION: 536
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Apple, Randolph T.

REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002930US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 225:
SEQUENCE CHARACTERISTICS:
LENGTH: 1132 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-854-050-225

Query Match 100.0%; Score 5961; DB 3; Length 1132;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 MPAPRCRAVRLSHRYREVLEPLATFVRRLLGPOGWRLLVQRGDPAAPRALVAQCLVCPW 60
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DB 61 DARPPAAPSPQVSLKELVARVLQRLCERGAKNVLAFGFALLDGAAGGPEAFTTSVR 120
QY 121 SYLNTVNTDALRGSGAWGLLRRVGDVLLVHLLARCALFVLVAPSCAYVQCGPLYQLGA 180
DB 121 SYLNTVNTDALRGSGAWGLLRRVGDVLLVHLLARCALFVLVAPSCAYVQCGPLYQLGA 180
QY 181 ATQAPPPHAGSPRRRLCERAWNHSVREAGVPLGLPAPGARRRGGSASRLPLPKPRR 240
DB 181 ATQAPPPHAGSPRRRLCERAWNHSVREAGVPLGLPAPGARRRGGSASRLPLPKPRR 240
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QY 361 VETIFLGSRPWMPGTPRLPRLPQRYQWMLPFLLELGNHAQCPVGVLLKTHCPRAAVT 420
DB 361 VETIFLGSRPWMPGTPRLPRLPQRYQWMLPFLLELGNHAQCPVGVLLKTHCPRAAVT 420
QY 421 PAAGVCAREKPGQSVAAPEEDTPRRLVQLLRQHSSEWQVYGFVRACLRRLVPPGLWGS 480
DB 421 PAAGVCAREKPGQSVAAPEEDTPRRLVQLLRQHSSEWQVYGFVRACLRRLVPPGLWGS 480
QY 481 RHNERFLNRTKFTSLGKHAKLSLOELTWKMSVRDCAWLRSPGVCVPAEHLREEI 540
DB 481 RHNERFLNRTKFTSLGKHAKLSLOELTWKMSVRDCAWLRSPGVCVPAEHLREEI 540
QY 541 LAKFLHLMWSVYVELLARSFFVYVETTFQKNRLFFYKSVMSKLSQSIGIRQHLKRVOLRE 600
DB 541 LAKFLHLMWSVYVELLARSFFVYVETTFQKNRLFFYKSVMSKLSQSIGIRQHLKRVOLRE 600
QY 601 LSEAEVROHREARPAALLTSRLRFPKPDGLRPIVNMMDYVVGARTFRREKRAERLTSRVKA 660
DB 601 LSEAEVROHREARPAALLTSRLRFPKPDGLRPIVNMMDYVVGARTFRREKRAERLTSRVKA 660
QY 661 LPSVLNTERARRPGLLGSVLGLDDIHRAWETFLVRPAQDPPPELYFVKVDVTGAYDTI 720
DB 661 LPSVLNTERARRPGLLGSVLGLDDIHRAWETFLVRPAQDPPPELYFVKVDVTGAYDTI 720
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QY 781 QETSPRLDAVIEQSSSLNEASSGLFDVFLRFMCHHAVIRKGSYVQCQGIPOQSILSTL 840
DB 781 QETSPRLDAVIEQSSSLNEASSGLFDVFLRFMCHHAVIRKGSYVQCQGIPOQSILSTL 840

QY 841 LCSLCYGDMEKLFAGIRRDGLLLRLVDDFLVTPHLLTHAKTFLRTLVRGVPEYGCVVNL 900
DB 841 LCSLCYGDMEKLFAGIRRDGLLLRLVDDFLVTPHLLTHAKTFLRTLVRGVPEYGCVVNL 900
QY 901 RKTVVPFVEDEALGGTAFVQMPAHGLFPMCGLLDTRTLEVSQSDYSYARTSIRASLTF 960
DB 901 RKTVVPFVEDEALGGTAFVQMPAHGLFPMCGLLDTRTLEVSQSDYSYARTSIRASLTF 960
QY 961 NRGFKAGRNMRRLFGVLRKCHSLFLDLQVNSLQTVCTNIYKILLLOAFRHACVLOLP 1020
DB 961 NRGFKAGRNMRRLFGVLRKCHSLFLDLQVNSLQTVCTNIYKILLLOAFRHACVLOLP 1020
QY 1021 FHOQVKNPTEFRLVSDTASLCVSIILKAKNAGSLGAKGAAGPLPSEAVOMLCHOAFLL 1080
DB 1021 FHOQVKNPTEFRLVSDTASLCVSIILKAKNAGSLGAKGAAGPLPSEAVOMLCHOAFLL 1080
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DB 1081 KLTRHRYVYVPLGSLRTAQTLRSKLPGTTLTALEAAANPALPSDFKTILD 1132
RESULT 4
US-09-430-323-225
Sequence 225, Application US/09430323
Patent No. 6309867
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin
Andrews, William H.
TITLE OF INVENTION: No. 6309867el Telomerase
NUMBER OF SEQUENCES: 225
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: United States of America
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/430,323
FILING DATE: 29-Oct-1999
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002930US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 225:
SEQUENCE CHARACTERISTICS:
LENGTH: 1132 amino acids
TYPE: amino acid

Db 241 GAAPEPRTVQGSWAHPGTRGSDRGFCVSPARPAEATSEGLSTRSHPSVG 300
Qy 301 ROHAGPSTSRPRPMDTPCPVYAEKHFYSSGDKQLRPSFLSSLPSTGARRL 360
Db 301 ROHAGPSTSRPRPMDTPCPVYAEKHFYSSGDKQLRPSFLSSLPSTGARRL 360
Qy 361 VETIFLGSRPMPGTPRRLPRLPQRYWQMRPLFLELLGNHAQCPYGVLLKTHCPRAAVT 420
Db 361 VETIFLGSRPMPGTPRRLPRLPQRYWQMRPLFLELLGNHAQCPYGVLLKTHCPRAAVT 420
Qy 421 PAAGVCAREKPGQSVAAPEEEDTPRRLVQLLRHSSPWQYGFVRACLRLVPGLWGS 480
Db 421 PAAGVCAREKPGQSVAAPEEEDTPRRLVQLLRHSSPWQYGFVRACLRLVPGLWGS 480
Qy 481 RHNERRFLRNTKFIISLGKHAKLSLQELTWKMSVRDCAWLRSPGVCPVAAEHLRBEI 540
Db 481 RHNERRFLRNTKFIISLGKHAKLSLQELTWKMSVRDCAWLRSPGVCPVAAEHLRBEI 540
Qy 541 LAKFLHLMVSVYVVELLRSPFYVTETTFQKNRLFYRKSVMSKLSQIGIRHKLKVQRE 600
Db 541 LAKFLHLMVSVYVVELLRSPFYVTETTFQKNRLFYRKSVMSKLSQIGIRHKLKVQRE 600
Qy 601 LSEAEVRQHREARPAALTSRLRFIPKPDGLRPIVNM DYVVGARTFRREKRAERLTSRKA 660
Db 601 LSEAEVRQHREARPAALTSRLRFIPKPDGLRPIVNM DYVVGARTFRREKRAERLTSRKA 660
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Db 661 LFSVLNVERARRPGLLGASVLGLDDIHRAWRTFVLRVRAQDPPPELVKVDVTGAYDTI 720
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Db 781 QETSPURDAVIEQSSSLNEASSGLFDVLRFMCHHVRIRGKSVYVOCQIPQGSII STL 840
Qy 841 LCSLCYGD MENKLFAGIRRDGLLRLVDDFLVTPH LTHAKTFLRLTVRGVPEYGC VVNL 900
Db 841 LCSLCYGD MENKLFAGIRRDGLLRLVDDFLVTPH LTHAKTFLRLTVRGVPEYGC VVNL 900
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Qy 961 NRGFKAGNMRRKLFGLVRLKCHSLFLDLQVNSLQTVCTNIYKILLQAYRFHACVLQLP 1020
Db 961 NRGFKAGNMRRKLFGLVRLKCHSLFLDLQVNSLQTVCTNIYKILLQAYRFHACVLQLP 1020
Qy 1021 FHQQWKNPTFRLVISTASLCYSILKAKNAGMSLGAKGAAGPLPSEAVOWLCHQAPLL 1080
Db 1021 FHQQWKNPTFRLVISTASLCYSILKAKNAGMSLGAKGAAGPLPSEAVOWLCHQAPLL 1080
Qy 1081 KLTHRRVTYVPLGLSLRFAOTQLSRKLGPTLTAL EAAANPALPSDFKTILD 1132
Db 1081 KLTHRRVTYVPLGLSLRFAOTQLSRKLGPTLTAL EAAANPALPSDFKTILD 1132

RESULT 6

US-09-675-321-2
; Sequence 2, Application US/09675321
; Patent No. 6440735
; GENERAL INFORMATION:
; APPLICANT: Gaeta, Federico C.A.
; APPLICANT: Geron Corporation
; TITLE OF INVENTION: Methods and Compositions for Eliciting an Immune
; TITLE OF INVENTION: Response to a Telomerase Antigen
; FILE REFERENCE: 015389-003500PC
; CURRENT APPLICATION NUMBER: US/09/675.321
; CURRENT FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: US 60/112,006

; PRIOR FILING DATE: 1998-03-31
; PRIOR APPLICATION NUMBER: WO PCT/US99/06898
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 1132
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-675-321-2
Query Match 100.0%; Score 5961; DB 4; Length 1132;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MPRAPRCRAVRSLLRSHYREVLP LPLATFVRRLGPGQWRLVQRGDPAAFRALVAQCLVCVPW 60
Db 1 MPRAPRCRAVRSLLRSHYREVLP LPLATFVRRLGPGQWRLVQRGDPAAFRALVAQCLVCVPW 60
Qy 61 DARPPPAAPSPROVSCIKELVARVLQRLCERGAKNVLAFCGALLDGDGAGGPPAFTTSVR 120
Db 61 DARPPPAAPSPROVSCIKELVARVLQRLCERGAKNVLAFCGALLDGDGAGGPPAFTTSVR 120
Qy 121 SYLPTVTVDALRGSGAWGLLLRRVDDVLLHLLARCALFVLVAPSCAYQVCGPPLYOLGA 180
Db 121 SYLPTVTVDALRGSGAWGLLLRRVDDVLLHLLARCALFVLVAPSCAYQVCGPPLYOLGA 180
Qy 181 ATQARPPHAGSPRRRLGRCERAWNHSVREAGVPLGLPAPGARRRGGASRSLSLPKPRR 240
Db 181 ATQARPPHAGSPRRRLGRCERAWNHSVREAGVPLGLPAPGARRRGGASRSLSLPKPRR 240
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Db 301 ROHAGPSTSRPRPMDTPCPVYAEKHFYSSGDKQLRPSFLSSLPSTGARRL 360
Qy 361 VETIFLGSRPMPGTPRRLPRLPQRYWQMRPLFLELLGNHAQCPYGVLLKTHCPRAAVT 420
Db 361 VETIFLGSRPMPGTPRRLPRLPQRYWQMRPLFLELLGNHAQCPYGVLLKTHCPRAAVT 420
Qy 421 PAAGVCAREKPGQSVAAPEEEDTPRRLVQLLRHSSPWQYGFVRACLRLVPGLWGS 480
Db 421 PAAGVCAREKPGQSVAAPEEEDTPRRLVQLLRHSSPWQYGFVRACLRLVPGLWGS 480
Qy 481 RHNERRFLRNTKFIISLGKHAKLSLQELTWKMSVRDCAWLRSPGVCPVAAEHLRBEI 540
Db 481 RHNERRFLRNTKFIISLGKHAKLSLQELTWKMSVRDCAWLRSPGVCPVAAEHLRBEI 540
Qy 541 LAKFLHLMVSVYVVELLRSPFYVTETTFQKNRLFYRKSVMSKLSQIGIRHKLKVQRE 600
Db 541 LAKFLHLMVSVYVVELLRSPFYVTETTFQKNRLFYRKSVMSKLSQIGIRHKLKVQRE 600
Qy 601 LSEAEVRQHREARPAALTSRLRFIPKPDGLRPIVNM DYVVGARTFRREKRAERLTSRKA 660
Db 601 LSEAEVRQHREARPAALTSRLRFIPKPDGLRPIVNM DYVVGARTFRREKRAERLTSRKA 660
Qy 661 LFSVLNVERARRPGLLGASVLGLDDIHRAWRTFVLRVRAQDPPPELVKVDVTGAYDTI 720
Db 661 LFSVLNVERARRPGLLGASVLGLDDIHRAWRTFVLRVRAQDPPPELVKVDVTGAYDTI 720
Qy 721 PODRLTEVIASIIKPQNTYCVRRYAVVQKAAHGHVRKAFKSHVSTLTDLPYMRQFVAHL 780
Db 721 PODRLTEVIASIIKPQNTYCVRRYAVVQKAAHGHVRKAFKSHVSTLTDLPYMRQFVAHL 780
Qy 781 QETSPURDAVIEQSSSLNEASSGLFDVLRFMCHHVRIRGKSVYVOCQIPQGSII STL 840
Db 781 QETSPURDAVIEQSSSLNEASSGLFDVLRFMCHHVRIRGKSVYVOCQIPQGSII STL 840
Qy 841 LCSLCYGD MENKLFAGIRRDGLLRLVDDFLVTPH LTHAKTFLRLTVRGVPEYGC VVNL 900
Db 841 LCSLCYGD MENKLFAGIRRDGLLRLVDDFLVTPH LTHAKTFLRLTVRGVPEYGC VVNL 900

Db 841 LCSLCYGMENKLFAGIRDRGDLRLVDDFLVTPHLTHAKTFRLTVRGVPEYGCVMNL 900
QY 901 RKTUVNFPVEDEALGTAQVQMPAHLGFWCGLLDTRTLEVOQSDYSSVARTSIRASLTF 960
Db 901 RKTUVNFPVEDEALGTAQVQMPAHLGFWCGLLDTRTLEVOQSDYSSVARTSIRASLTF 960
QY 961 NRGFKAGNRMRKLGVLRLKCHSLFLLDQVNSLOTVCNTIYKILLQAYRPHACVQLP 1020
Db 961 NRGFKAGNRMRKLGVLRLKCHSLFLLDQVNSLOTVCNTIYKILLQAYRPHACVQLP 1020
QY 1021 FHOQWKNPTFFLRVISTASLCYILKAKNAGMSLGAKGAGPLPSEAVOMLCHOAFLL 1080
Db 1021 FHOQWKNPTFFLRVISTASLCYILKAKNAGMSLGAKGAGPLPSEAVOMLCHOAFLL 1080
QY 1081 KLTRHRVTYVPLGSLRTAQTLRSKLPFGTTLTALEAAANPALPSDFKTILD 1132
Db 1081 KLTRHRVTYVPLGSLRTAQTLRSKLPFGTTLTALEAAANPALPSDFKTILD 1132

RESULT 7

US-09-052-919-2
; Sequence 2, Application US/09052919
; Patent No. 6444650
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; APPLICANT: Lingner, Joachim
; APPLICANT: Nakamura, Toru
; APPLICANT: Chapman, Karen B.
; APPLICANT: Morin, Gregg B.
; APPLICANT: Harley, Calvin B.
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: Antisense Compositions for Detecting and
; TITLE OF INVENTION: Inhibiting Telomerase Reverse Transcriptase
; NUMBER OF SEQUENCES: 72
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/052,919
; FILING DATE: 31-MAR-1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/851,843
; FILING DATE: 06-MAY-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/854,050
; FILING DATE: 09-MAY-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/911,312
; FILING DATE: 14-AUG-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/912,951
; FILING DATE: 14-AUG-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/915,503

; FILING DATE: 14-AUG-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/974,549
; FILING DATE: 19-NOV-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/974,584
; FILING DATE: 19-NOV-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/US97/17618
; FILING DATE: 01-OCT-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/US97/17885
; FILING DATE: 01-OCT-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Parent, Annette S.
; REGISTRATION NUMBER: 42,058
; REFERENCE/DOCKET NUMBER: 015389-003600US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1132 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-052-919-2

Query Match 100.0%; Score 5961; DB 4; Length 1132;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 MPRAPRCRAVRSLLRSHYREVLPLATFVRRLLGPOQWRVLRVQGDPAAPRALVAOCLVCPW 60
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Db 61 DARPPPAAPSPQVSCLEKELVARVLQRLCERGAKNVLAFGFALLDARGGPPFAFTTSVR 120
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Db 121 SYLENTVTDALRGSGAWGLLLRRVGGDVLVHLLARCALFVLVAPSCAYVQCGPPLYQLGA 180
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Db 781 QETSLRDAVIEQSSSINEASSGLFDVFLRFMCHAVIRGKSVQCGIPQGSII STL 840
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Db 1021 FHQQWKNTFFLRVISDTASLCYSILKAKNAGSLGAKGAAGPLPSEAVQWLCHQAFLL 1080
Qy 1081 KLTHRVTVYVPLLSRLTAQQLSRKLPGLTTLTALEAANPALPSDFKTI LD 1132
Db 1081 KLTHRVTVYVPLLSRLTAQQLSRKLPGLTTLTALEAANPALPSDFKTI LD 1132

RESULT 8

US-08-912-951-2
; Sequence 2, Application US/08912951
; Patent No. 6475789
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; APPLICANT: Lingner, Joachim
; APPLICANT: Nakamura, Toru
; APPLICANT: Chapman, Karen B.
; APPLICANT: Morin, Gregg B.
; APPLICANT: Harley, Calvin
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: HUMAN TELOMERASE CATALYTIC SUBUNIT: DIAGNOSTIC AND
; TITLE OF INVENTION: THERAPEUTIC METHODS
; NUMBER OF SEQUENCES: 335
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/912,951
; FILING DATE: 14-AUG-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/854,050
; FILING DATE: 09-MAY-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/851,843

; FILING DATE: 06-MAY-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph T.
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-002600US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1132 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-912-951-2
Query Match 100.0%; Score 5961; DB 4; Length 1132;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 1 MPAPRCRAVRSLLRSHYREVLPATFVRLRPGQWRLVQRGDPAAFRALVAQCLVCVPW 60
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Qy 481 RHNERFLRNTKKFISLGKHAQLSLOELTWKMSVRDCAWLRRSPGVCVPAAEHRLREEI 540
Db 481 RHNERFLRNTKKFISLGKHAQLSLOELTWKMSVRDCAWLRRSPGVCVPAAEHRLREEI 540
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Db 661 LFSVLNTERARRPGLLGASVLGDDIHRAWRTFVLKRAQDPPPELYFKVVDVTCAYDTI 720
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QY 781 QSTPLRDVAVTEQSSLINEASGLFDVPLRPMCHHAVIRKSVYQCGIPIQSGSILSTL 840
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Db 841 LCSLCYGDMEKLFAGIRDDGLLRLLVDDFLVTLTHAKTFLRTLVGRVPEYGCNVNL 900
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Db 1081 KLTRHRVTYVPLGLSLRTAQTQLSRKLPCTTTLTALEAAANPALPSDFKTILD 1132

RESULT 9
US-09-402-181B-2
; Sequence 2, Application US/09402181B
; Patent No. 6610839
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; Lingner, Joachim
; Nakamura, Toru
; Chapman, Karen B.
; Morin, Gregg B.
; Harley, Calvin B.
; Andrews, William H.
; TITLE OF INVENTION: Human Telomerase Catalytic Subunit
; NUMBER OF SEQUENCES: 633
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/402,181B
; FILING DATE: 29-Sep-1997
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; APPLICATION NUMBER: US 08/846,017
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; FILING DATE: 25-APR-1997
; APPLICATION NUMBER: US 08/851,843
; FILING DATE: 06-MAY-1997
; APPLICATION NUMBER: US 08/854,050
; FILING DATE: 09-MAY-1997
; APPLICATION NUMBER: US 08/911,312
; FILING DATE: 14-AUG-1997
; APPLICATION NUMBER: US 08/912,951
; FILING DATE: 14-AUG-1997
; APPLICATION NUMBER: US 08/915,503
; FILING DATE: 14-AUG-1997
; APPLICATION NUMBER: WO PCT/US97/17885
; FILING DATE: 01-OCT-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Ausenhus, Scott L.
; REGISTRATION NUMBER: 42,271
; REFERENCE/DOCKET NUMBER: 015389-002620US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1132 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-402-181B-2

Query Match 100.0%; Score 5961; DB 4; Length 1132;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 61 DARPPPAAPSPQVSCSKLKVRLQRCERGAKNVLAFFGALLDGAAGGPPPEAFTTSVR 120
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QY 181 ATQARPPPHASGPRRLRCERAWNHSVREAGVPLGLPAPGARRRGGSSASRLPLPKRRR 240
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QY 241 GAAPEPERTVQGSWAHPGTRGPDGFCVVSAPARAEATSLGALSGRHSHPSVG 300
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Db 1021 FHQQVWKNPFTFLRVISDTASLCYSILKAKNAGSLGAKGAGPLPSEAVQWLCHQAFLL 1080
Qy 1081 KLTHRVTVVPLGLSLRTAQQLSKPLPGTTLTALAAAANPALPSDFKTLID 1132
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RESULT 10

US-09-721-456-2
Sequence 2, Application US/09721456
Patent No. 6617110

GENERAL INFORMATION:

APPLICANT: Cech, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin B.
Andrews, William H.
TITLE OF INVENTION: Human Telomerase Catalytic Subunit
NUMBER OF SEQUENCES: 727
CORRESPONDENCE ADDRESS:
ADDRESS: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/721,456

FILING DATE: 22-NOV-2000

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/974,549A

FILING DATE: 19-NOV-1997

APPLICATION NUMBER: US 08/724,643

FILING DATE: 01-OCT-1996

APPLICATION NUMBER: US 08/844,419

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; FILING DATE: 18-APR-1997
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; APPLICATION NUMBER: US 08/851,843
; FILING DATE: 06-MAY-1997
; APPLICATION NUMBER: US 08/854,050
; FILING DATE: 09-MAY-1997
; APPLICATION NUMBER: US 08/911,312
; FILING DATE: 14-AUG-1997
; APPLICATION NUMBER: US 08/912,951
; FILING DATE: 14-AUG-1997
; APPLICATION NUMBER: US 08/915,503
; FILING DATE: 14-AUG-1997
; APPLICATION NUMBER: WO PCT/US97/17618
; FILING DATE: 01-OCT-1997
; APPLICATION NUMBER: WO PCT/US97/17885
; FILING DATE: 01-OCT-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph Ted
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-002610US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1132 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-721-456-2

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Query Match 100.0%; Score 5961; DB 4; Length 1132;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 361 VETIFLGSRPWMPGTPRRLPRLPQRYWQMRPLFLELLGNHACQPYGVLLKTHCPLRAAVT 420
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Qy 481 RHNERFLRNTKFKFISLGKHAJSLQBLTWKMSVRDCAWLRRSPGVGCVPAAEHRLREEI 540
Db 481 RHNERFLRNTKFKFISLGKHAJSLQBLTWKMSVRDCAWLRRSPGVGCVPAAEHRLREEI 540

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Db 661 LPSVLNYERARPGILGASVLGLDDIHRARWTFVLKRAQDPPPELYFKVDVDTGAYDTI 720
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Db 781 QETSPLRDAVIEQSSSINEASSGLFDVFLRMCHAVIRKSVVQCGIPOGSIILSTL 840
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Db 841 LCSLCYGDMEKFLFAGIRDGLLRLVDDFLVTPHLTHAKTFLRLVRGVPYGCNVNL 900
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Db 1021 FHQVWKNTFFLRVISDTASICYILKAKNAGMSLGAKGAGPLPSEAVQWLCHQAFLL 1080
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Db 1081 KLTHRVTVYVLLGLSLRTAQTLRSKLPCTTLTALAAAANPALPSDFKTILD 1132

RESULT 11

US-09-953-052-2
; Sequence 2, Application US/09953052
; Patent No. 6627619
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; Lingner, Joachim
; Nakamura, Toru
; Chapman, Karen B.
; Morin, Gregg B.
; Harley, Calvin B.
; Andrews, William H.
; TITLE OF INVENTION: Antisense Compositions for Detecting and
; Inhibiting Telomerase Reverse Transcriptase
; NUMBER OF SEQUENCES: 72
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/953,052
; FILING DATE: 14-Sep-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/052,919
FILING DATE: <Unknown>
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/911,312
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/974,549
FILING DATE: 19-NOV-1997
APPLICATION NUMBER: US 08/974,584
FILING DATE: 19-NOV-1997
APPLICATION NUMBER: WO PCT/US97/17618
FILING DATE: 01-OCT-1997
APPLICATION NUMBER: WO PCT/US97/17885
FILING DATE: 01-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Parent, Annette S.
REGISTRATION NUMBER: 42,058
REFERENCE/DOCKET NUMBER: 015389-00360005
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1132 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-953-052-2

Query Match 100.0%; Score 5961; DB 4; Length 1132;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 361 VETIFLGSRRPMPGTPRRLLPRLPQRYQWQMRPLFLELGNHAQCYPYGVLLKTHCPLRAAVT 420
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Qy 481 RHNERFURNTKFTSLGKHAKLSLOELTWKMSVRDCAWLRRSPGVCVPAAEHRLREI 540
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Db 841 LCSLCYGMENKLFAGIRRDGLLRLVDDFLVTPHLLTHAKTFLRTLVRGVPYGCVVNL 900
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Db 1021 FHQWKNPTFLRVLSTASLCYSILKAKNAGMSLGAKGAGPLPSEAVQWLCHQAPLL 1080
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Db 1081 KLTHRVTVVPLGLSLRTAQTLSKLPCTTLTALAAANPALPSDFKTILD 1132

RESULT 12

US-09-042-460-3

; Sequence 3, Application US/09042460

; Patent No. 6767719

; GENERAL INFORMATION:

; APPLICANT: Morin, Gregg B.

; APPLICANT: Allsopp, Richard

; APPLICANT: Depinho, Ronald

; APPLICANT: Greenberg, Roger

; TITLE OF INVENTION: Mouse Telomerase Reverse Transcriptase

; NUMBER OF SEQUENCES: 101

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Townsend and Townsend and Crew LLP

; CITY: San Francisco

; STATE: California

; COUNTRY: USA

; ZIP: 94111-3834

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/042,460

; FILING DATE: 16-MAR-1998
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/851,843
; FILING DATE: 06-MAY-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/854,050
; FILING DATE: 09-MAY-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/911,312
; FILING DATE: 14-AUG-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/912,951
; FILING DATE: 14-AUG-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/915,503
; FILING DATE: 14-AUG-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/US97/17618
; FILING DATE: 01-OCT-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/US97/17885
; FILING DATE: 01-OCT-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/974,549
; FILING DATE: 19-NOV-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/974,584
; FILING DATE: 19-NOV-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/979,742
; FILING DATE: 26-NOV-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Einhorn, Gregory P.
; REGISTRATION NUMBER: 38,440
; REFERENCE/DOCKET NUMBER: 015389-003110US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1132 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..1132
; OTHER INFORMATION: /note="human telomerase reverse
; OTHER INFORMATION: transcriptase (hTERT)"
; US-09-042-460-3

Query Match 100.0%; Score 5961; DB 4; Length 1132;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MPRAPRCRAVRSLLRSHYREVLPVPLATFVRRLGPOGWLVRGDDPAAPRALVAQCCLVCVCPW 60

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DB 181 ATQARPPPHASGPRRLGGERAWNSVREAGVPLGLPAGARRRGGSASRSIPLPKRPR 240
QY 241 GAAPPERTPVQGSWAHPGRTGRGSDRGFCVVSAPARPAEATSLEGALSGRHSHPSVG 300
DB 241 GAAPPERTPVQGSWAHPGRTGRGSDRGFCVVSAPARPAEATSLEGALSGRHSHPSVG 300
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DB 361 VETIFLGSPPMPGTPRRLPRLPQRYWQMRPLFLELLGNHQAQCPYGVLLKTHCPRAAVT 420
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DB 421 PAAGVCAREKPGQSVAAPEEEDTDPRRLVOLLROHSSPMQVYGFVRACLRRLVPPGLWGS 480
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DB 481 RHNERFLRNTKFTISLGKHAHLSLQELTWKMSVRDCAWLRRSPGVGCVPAAEHLRBEI 540
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DB 541 LAKFLHLMMSVYVELLSRFFYVTTTQKNRLLFFYRKSVWSKLSQSIGIRQHLKRVQRE 600
QY 601 LSEAEVROHREARPAALLTSRLRFIPKPDGLRPIVNM DYVVGARTFRREKRAERLTSRVA 660
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RESULT 13
 US-09-949-016-6326
 ; Sequence 6326, Application US/09949016

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; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6326
; LENGTH: 1132
; TYPE: PRN
; ORGANISM: Human
; US-09-949-016-6326

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Query Match 100.0%; Score 5961; DB 4; Length 1132;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 181 ATQARPPPHASGPRRLGGERAWNSVREAGVPLGLPAGARRRGGSASRSIPLPKRPR 240
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QY 241 GAAPPERTPVQGSWAHPGRTGRGSDRGFCVVSAPARPAEATSLEGALSGRHSHPSVG 300
DB 241 GAAPPERTPVQGSWAHPGRTGRGSDRGFCVVSAPARPAEATSLEGALSGRHSHPSVG 300
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DB 301 ROHAGPSTSRPPRPPMDTPCPVVAETKHFYSSGDKQLRPSFLLSLRSLTGARRL 360
QY 361 VETIFLGSPPMPGTPRRLPRLPQRYWQMRPLFLELLGNHQAQCPYGVLLKTHCPRAAVT 420
DB 361 VETIFLGSPPMPGTPRRLPRLPQRYWQMRPLFLELLGNHQAQCPYGVLLKTHCPRAAVT 420
QY 421 PAAGVCAREKPGQSVAAPEEEDTDPRRLVOLLROHSSPMQVYGFVRACLRRLVPPGLWGS 480
DB 421 PAAGVCAREKPGQSVAAPEEEDTDPRRLVOLLROHSSPMQVYGFVRACLRRLVPPGLWGS 480
QY 481 RHNERFLRNTKFTISLGKHAHLSLQELTWKMSVRDCAWLRRSPGVGCVPAAEHLRBEI 540
DB 481 RHNERFLRNTKFTISLGKHAHLSLQELTWKMSVRDCAWLRRSPGVGCVPAAEHLRBEI 540
QY 541 LAKFLHLMMSVYVELLSRFFYVTTTQKNRLLFFYRKSVWSKLSQSIGIRQHLKRVQRE 600
DB 541 LAKFLHLMMSVYVELLSRFFYVTTTQKNRLLFFYRKSVWSKLSQSIGIRQHLKRVQRE 600
QY 601 LSEAEVROHREARPAALLTSRLRFIPKPDGLRPIVNM DYVVGARTFRREKRAERLTSRVA 660
DB 601 LSEAEVROHREARPAALLTSRLRFIPKPDGLRPIVNM DYVVGARTFRREKRAERLTSRVA 660
QY 720 LFSVLNVERARRPGLLGASVLGLDDIHRWRTFVLVRAQDPPPELVKVDVTGAYDTI 720
DB 720 LFSVLNVERARRPGLLGASVLGLDDIHRWRTFVLVRAQDPPPELVKVDVTGAYDTI 720

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Db 721 PODRLTEVIAIIKPNQYCVRRYAVVQAAHGHVRKAFKSHVSTLTDLQPMRQFVAHL 780
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Db 781 QETSLRDAVIEQSSSLEASSGLFDVFLRFMCHHAVIRGKSVVQCGIPQGSILSTL 840
Qy 841 LCSLCYGMENKLFAGIRRDGLLRLLVDDFLVTPHLLTHAKTFLRTLVGRVPEYGCVVNL 900
Db 841 LCSLCYGMENKLFAGIRRDGLLRLLVDDFLVTPHLLTHAKTFLRTLVGRVPEYGCVVNL 900
Qy 901 RKTVPNPFVEALGGTAFVOMPAGHLPWGLLLDTRTLEVSQSDYSYARTSIRASLTF 960
Db 901 RKTVPNPFVEALGGTAFVOMPAGHLPWGLLLDTRTLEVSQSDYSYARTSIRASLTF 960
Qy 961 NRGFKAGNRMRKLFGLVLRKCHSLFLDLQNSLQTVCTNIYKILLQAYRFHACVQLP 1020
Db 961 NRGFKAGNRMRKLFGLVLRKCHSLFLDLQNSLQTVCTNIYKILLQAYRFHACVQLP 1020
Qy 1021 FHQQVWKNPFTFLRVIDSTASLCYSILKAKNAGMSLGAKGAGPLPSEAVQMLCHQAFLL 1080
Db 1021 FHQQVWKNPFTFLRVIDSTASLCYSILKAKNAGMSLGAKGAGPLPSEAVQMLCHQAFLL 1080
Qy 1081 KLTHRVTVYVLLGSLRTAQTLQSLKPLGTTLTALAAANPALSPDFKTIILD 1132
Db 1081 KLTHRVTVYVLLGSLRTAQTLQSLKPLGTTLTALAAANPALSPDFKTIILD 1132
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RESULT 14

US-08-974-549A-611
Sequence 611, Application US/08974549A
Patent No. 6166178

GENERAL INFORMATION:

APPLICANT: Cech, Thomas R.
APPLICANT: Lingner, Joachim
APPLICANT: Nakamura, Toru
APPLICANT: Chapman, Karen B.
APPLICANT: Morin, Gregg B.
APPLICANT: Harley, Calvin B.
APPLICANT: Andrews, William H.
TITLE OF INVENTION: Human Telomerase Catalytic Subunit
NUMBER OF SEQUENCES: 727
CORRESPONDENCE ADDRESS:
ADDRESS: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/974,549A
FILING DATE: 19-NOV-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/911,312
FILING DATE: 14-AUG-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-AUG-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-AUG-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/17618
FILING DATE: 01-OCT-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/17885
FILING DATE: 01-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph Ted
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002610US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 611:
SEQUENCE CHARACTERISTICS:
LENGTH: 1154 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
NAME/KEY: Protein
LOCATION: 1..1154
OTHER INFORMATION: /note="fusion protein composed of hTERT
protein sequence, vector sequences, the
OTHER INFORMATION: Myc epitope and His6 tag"
US-08-974-549A-611

Query Match 100.0%; Score 5961; DB 3; Length 1154;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MPRAPRCRAVRSLLRSHYREVLP	120
Db	1	MPRAPRCRAVRSLLRSHYREVLP	120
Qy	61	DAREPPAAPSFRQVSCLELVARV	120
Db	61	DAREPPAAPSFRQVSCLELVARV	120
Qy	121	SYLPTVTDALRGSGAWGLLLRR	180
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Qy	181	ATQARPPPHASGPRRLGCEAN	240
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Qy	241	GAAPEPRTVPGQSWAHPGTR	300
Db	241	GAAPEPRTVPGQSWAHPGTR	300
Qy	301	RQHHAGPSTSRPRPMDT	360
Db	301	RQHHAGPSTSRPRPMDT	360
Qy	361	VETIFLGSRRPMPCTPRRL	420
Db	361	VETIFLGSRRPMPCTPRRL	420
Qy	421	PAAGVCAREKFPQGSVAAP	480
Db	421	PAAGVCAREKFPQGSVAAP	480

Db 421 PAAGVCAREKPOGSAAPBEEDTDPRRLVQLLRQHSPPQVYGFVRACLRLRVLPPGLMGS 480
QY 481 RINERFLRNTKFTSLGKHAKLSLOELTWKMSVRDCAWLRSPGVCVPAAEHRLREI 540
Db 481 RINERFLRNTKFTSLGKHAKLSLOELTWKMSVRDCAWLRSPGVCVPAAEHRLREI 540
QY 541 LAKFLHMLSVVVELLRFFVYTTTFFQKNRLFFYKRSVMSKLSQSIGIRQHLKRVOLRE 600
Db 541 LAKFLHMLSVVVELLRFFVYTTTFFQKNRLFFYKRSVMSKLSQSIGIRQHLKRVOLRE 600
QY 601 LSEAEVROHREARPAALLTSLRBFIPKPDGLRPIVNDYVVGARTFRREKRAELTSRVKA 660
Db 601 LSEAEVROHREARPAALLTSLRBFIPKPDGLRPIVNDYVVGARTFRREKRAELTSRVKA 660
QY 661 LFSVLNRYEARPGLIGASVLGLDDIHRARWTFVLRAQDPPPELYFVKVDVTGAYDTI 720
Db 661 LFSVLNRYEARPGLIGASVLGLDDIHRARWTFVLRAQDPPPELYFVKVDVTGAYDTI 720
QY 721 PODRLTEVIASIIKQNTYCVRRYAVVQKAAGHVRKAFKSHVSTLTDLOPYMRQFVAHL 780
Db 721 PODRLTEVIASIIKQNTYCVRRYAVVQKAAGHVRKAFKSHVSTLTDLOPYMRQFVAHL 780
QY 781 QSTPLRDAVWIEQSSSLNEASSGLFDFELRWCHHVAIRKSYVQCOGIPQGSILSTL 840
Db 781 QSTPLRDAVWIEQSSSLNEASSGLFDFELRWCHHVAIRKSYVQCOGIPQGSILSTL 840
QY 841 LCSLCYGDMEKLFAGIRRDGLLLRLVDDFLVTPHLLTHAKTFLRLVGRVPEYGCNNL 900
Db 841 LCSLCYGDMEKLFAGIRRDGLLLRLVDDFLVTPHLLTHAKTFLRLVGRVPEYGCNNL 900
QY 901 RKTVMNFPVEDBALGTAFAVOMPANGLFPWCGLLDDTRTLEVSQSYSSYARTSIRASLTF 960
Db 901 RKTVMNFPVEDBALGTAFAVOMPANGLFPWCGLLDDTRTLEVSQSYSSYARTSIRASLTF 960
QY 961 NRGFKAGNRMRKLGVLRLKCHSLFDLOVNSLOTVCTNIYKILLQAYRHACVQLQP 1020
Db 961 NRGFKAGNRMRKLGVLRLKCHSLFDLOVNSLOTVCTNIYKILLQAYRHACVQLQP 1020
QY 1021 FHQQWKNTFFLRLVISTASLCYSILKAKNAGMSLGAKAAGPLPSEAVOMLCHQAFIL 1080
Db 1021 FHQQWKNTFFLRLVISTASLCYSILKAKNAGMSLGAKAAGPLPSEAVOMLCHQAFIL 1080
QY 1081 KLTRHRTVTVPLGLSLRTAQTLQSLRKLPGTTLTALAEAAANPALPSDFKTILD 1132
Db 1081 KLTRHRTVTVPLGLSLRTAQTLQSLRKLPGTTLTALAEAAANPALPSDFKTILD 1132

RESULT 15

US-08-912-951-323
; Sequence 323, Application US/08912951
; Patent No. 6475789
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; APPLICANT: Lingner, Joachim
; APPLICANT: Nakamura, Toru
; APPLICANT: Chapman, Karen B.
; APPLICANT: Morin, Gregg B.
; APPLICANT: Harley, Calvin
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: HUMAN TELOMERASE CATALYTIC SUBUNIT: DIAGNOSTIC AND
; THERAPEUTIC METHODS
; NUMBER OF SEQUENCES: 335
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/912,951

FILING DATE: 14-AUG-1997

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/854,050

FILING DATE: 09-MAY-1997

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/851,843

FILING DATE: 06-MAY-1997

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/846,017

FILING DATE: 25-APR-1997

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/844,419

FILING DATE: 18-APR-1997

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/724,643

FILING DATE: 01-OCT-1996

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Apple, Randolph T.

REGISTRATION NUMBER: 36,429

REFERENCE/DOCKET NUMBER: 015389-002600US

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 576-0200

TELEFAX: (415) 576-0300

INFORMATION FOR SEQ ID NO: 323:

SEQUENCE CHARACTERISTICS:

LENGTH: 1154 amino acids

TYPE: amino acid

STRANDEDNESS:

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-912-951-323

Query Match 100.0%; Score 5961; DB 4; Length 1154;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPAPRCRAVRSLLSHYREVLPATFVRRRLGPGQWRVLVQRGDPAAFRALVAQCLVCPW 60

Db 1 MPAPRCRAVRSLLSHYREVLPATFVRRRLGPGQWRVLVQRGDPAAFRALVAQCLVCPW 60

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Db 61 DARPPPAAPSPFQVSCLELVARVLQRLCERGAKNVLAFGFALLDGAAGGPPPEAFTTSVR 120

QY 121 SYLPNTVTDALRGSGAWGLLLRRVGGDDVLVHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180

Db 121 SYLPNTVTDALRGSGAWGLLLRRVGGDDVLVHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180

QY 181 ATQARPPPHASGPRRLGCERAWNHSVREAGVPLGLPAGARRRGGSSASRSLPLPKRPRR 240

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Db 241 GAAPEPERTVGGQSWAHPGTRGSDRGFCVVSAPAEATSLGALSGTGHSHPSVG 300

QY 301 RQHAGPPSTSRPRPMDTTPCPVVAETKHFYLSGDKQLRPSFLLSRLPSLTGARRL 360

Db 301 RQHAGPPSTSRPRPMDTTPCPVVAETKHFYLSGDKQLRPSFLLSRLPSLTGARRL 360

QY 361 VETIFLGSRPWMPGTTPRLPRLPQRYQWMLFLLELLGNHAQCYPYVLLKTHCPRAAAT 420

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481 RHNERFLRNTKFTISLGHAKLSIQELTWKMSVRDCAWLRRSPGVCPVAAEHLRLEEI 540
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RESULT 16
US-09-402-181B-611
; Sequence 611, Application US/09402181B
; Patent No. 6610839
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; Lingner, Joachim
; Nakamura, Toru
; Chapman, Karen B.
; Morin, Gregg B.
; Harley, Calvin B.
; Andrews, William H.
; TITLE OF INVENTION: Human Telomerase Catalytic Subunit
; NUMBER OF SEQUENCES: 633
; CORRESPONDENCE ADDRESS:
; ADDRESS: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/402.181B
; FILING DATE: 29-Sep-1997
; CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; APPLICATION NUMBER: US 08/851,843
; FILING DATE: 06-MAY-1997
; APPLICATION NUMBER: US 08/854,050
; FILING DATE: 09-MAY-1997
; APPLICATION NUMBER: US 08/911,312
; FILING DATE: 14-AUG-1997
; APPLICATION NUMBER: US 08/912,951
; FILING DATE: 14-AUG-1997
; APPLICATION NUMBER: US 08/915,503
; FILING DATE: 14-AUG-1997
; APPLICATION NUMBER: WO PCT/US97/17885
; FILING DATE: 01-OCT-1997
ATTORNEY/AGENT INFORMATION:
; NAME: Ausenhus, Scott L.
; REGISTRATION NUMBER: 42,271
; REFERENCE/DOCKET NUMBER: 015389-002620US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 611:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1154 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..1154
; OTHER INFORMATION: /note= "fusion protein composed of hTERT
; protein sequence, vector sequences, the
; Myc epitope and His6 tag"
; SEQUENCE DESCRIPTION: SEQ ID NO: 611:
US-09-402-181B-611
Query Match 100.0%; Score 5961; DB 4; Length 1154;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MPRAPRCRAVRLSLRSHYREVLPVPLATFVRRLPGQWRVLVQRGDPAAFRALVAQCILVCVPW 60
Db 1 MPRAPRCRAVRLSLRSHYREVLPVPLATFVRRLPGQWRVLVQRGDPAAFRALVAQCILVCVPW 60
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Db 61 DARPPPAAPSFQVSCVCLKELVARVLQRCERGANVLAFGFALLDARGGPEAFTTSVR 120
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Db 121 SYLPNTVTDALRGSGANGLLRLRRVDDVLVHLLARCALFVLVAPSCAYQVCGPPLYQUGA 180
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Db 181 ATQARPPPHASGPRRLRGCCERANVHVSREAGVPLGAPGARRRGGSASRLPLPKRPRR 240
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Db 241 GAPEPERTPVGQSWAHQRTGPGSDRGFCVSPARPAEAEATSLGALSCTRHSHPVSG 300
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Db 301 ROHAGPSTPRPFDWTPCPVVAETKHFYSGDKQLRPSFLLSLRSLTGARL 360
Qy 361 VETIFGSRPMPGTGPRRLPRLPQRYWQMRPLFLELLGNHAQCPYGVLLKTHCPRAAVT 420
Db 361 VETIFGSRPMPGTGPRRLPRLPQRYWQMRPLFLELLGNHAQCPYGVLLKTHCPRAAVT 420
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Db 421 PAAGVCAREKPGQSVAAPEEDTDPRLLVOLLRQHSPPQVYGVFRACLRRLVPPGLWGS 480
Qy 481 RINERREFLNTKFTISLGHAKLSLOELTWKMSVRDCAMLRSPGVCVPAEHLRREI 540
Db 481 RINERREFLNTKFTISLGHAKLSLOELTWKMSVRDCAMLRSPGVCVPAEHLRREI 540
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Db 541 LAKFLHMLSVVVELLSRFFVYTTTFOKNRLEFFYKRSVWSKLSIGIRQHLKRVQRE 600
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Db 601 LSEAEVRQREARPPALLTSRLRPIPKPDGLRPIVMNDYVVGARTFRREKRAERLTSRVKA 660
Qy 661 LFSVLNVERARPPGLGASVLGDDIHRARWTFVLRAQDPPPELYFYKVDVTGAYDTI 720
Db 661 LFSVLNVERARPPGLGASVLGDDIHRARWTFVLRAQDPPPELYFYKVDVTGAYDTI 720
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Db 721 PODRLTEVIASIIKQNTYCVRYAVVQKAAHGHVKAFKSHVSTLTDLPYMRQFVAHL 780
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Db 781 QTSPLRDADVIEQSSSNEASGLFDVFLRPMCHHVAIRGKSVYQCGIPQGSILSTL 840
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Db 841 LCSLCYGMENKLFAGIRDDGLLRLVDDPLVTHLTHAKTFLRLTVRGVPEYGCNVNL 900
Qy 901 RKTVNVFVEDEALGATFVOMPAGLFPWCGLLDTRLEQSDYSSVARTSIRASLTF 960
Db 901 RKTVNVFVEDEALGATFVOMPAGLFPWCGLLDTRLEQSDYSSVARTSIRASLTF 960
Qy 961 NRGFKAGNRMRKLFVGLRLKCHSLFDLQVNSLQTVCTNIYKILLQAYRFHACVLQLP 1020
Db 961 NRGFKAGNRMRKLFVGLRLKCHSLFDLQVNSLQTVCTNIYKILLQAYRFHACVLQLP 1020
Qy 1021 FHQQVWKNTFFLRVISDTASLCYSILKAKNAGMSLGAKAGPLPSEAVQWLCHQAFIL 1080
Db 1021 FHQQVWKNTFFLRVISDTASLCYSILKAKNAGMSLGAKAGPLPSEAVQWLCHQAFIL 1080
Qy 1081 KLTRHRTVYVPLGLSLRTAQTLSRLPGTTLTALAAANPALPSDFKTILD 1132
Db 1081 KLTRHRTVYVPLGLSLRTAQTLSRLPGTTLTALAAANPALPSDFKTILD 1132

RESULT 17

US-09-721-456-611

Sequence 611, Application US/09721456

Patent No. 6617110

GENERAL INFORMATION:

APPLICANT: Cech, Thomas R.

Lingner, Joachim

Nakamura, Toru

Chapman, Karen B.

Morin, Gregg B.

Harley, Calvin B.

Andrews, William H.

TITLE OF INVENTION: Human Telomerase Catalytic Subunit

NUMBER OF SEQUENCES: 727

CORRESPONDENCE ADDRESS:

ADDRESSEE: Townsend and Townsend and Crew LLP

STREET: Two Embarcadero Center, Eighth Floor

CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/721,456
FILING DATE: 22-Nov-1997
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/974,549A
FILING DATE: 19-NOV-1997
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/911,312
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: WO PCT/US97/17618
FILING DATE: 01-OCT-1997
APPLICATION NUMBER: WO PCT/US97/17885
FILING DATE: 01-OCT-1997

ATTORNEY/AGENT INFORMATION:

NAME: Apple, Randolph Ted

REGISTRATION NUMBER: 36,429

REFERENCE/DOCKET NUMBER: 015389-002610US

TELEPHONE: (415) 576-0200

TELEFAX: (415) 576-0300

INFORMATION FOR SEQ ID NO: 611:

SEQUENCE CHARACTERISTICS:

LENGTH: 1154 amino acids

TYPE: amino acid

STRANDEDNESS: <Unknown>

TOPOLOGY: linear

MOLECULE TYPE: protein

FEATURE:

NAME/KEY: Protein

LOCATION: 1..1154

OTHER INFORMATION: /note= "fusion protein composed of hTERT

protein sequence, vector sequences, the

Myc epitope and His6 tag"

SEQUENCE DESCRIPTION: SEQ ID NO: 611:

US-09-721-456-611

Query Match 100.0%; Score 5961; DB 4; Length 1154;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MPRAPRCVAVSLRSHYREVLPATFVRRLLGPGQWRVLRVQGRDPAAFRALVAQCLVCPW 60
Db 1 MPRAPRCVAVSLRSHYREVLPATFVRRLLGPGQWRVLRVQGRDPAAFRALVAQCLVCPW 60
Qy 61 DARPPAAPSPQVSCSLKELVARVLQRLCERGAKNVLAFFGALLDCAAGGPEAFTTSVR 120
Db 61 DARPPAAPSPQVSCSLKELVARVLQRLCERGAKNVLAFFGALLDCAAGGPEAFTTSVR 120
Qy 121 SYLPNTVTDALRGSGAWGLLRVDDVYLHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180

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Db 121 SYLNTVTVDALRGSGAWGLLRRVGDVVLVHLLARCALFVLVAPSCAVQVCGPPYQLGA 180
Qy 181 ATQARPPPHAGPPRRRLGECERAWNHVSREAGVPLGLPAPGARRRGGSASRSLPLPKPRR 240
Db 181 ATQARPPPHAGPPRRRLGECERAWNHVSREAGVPLGLPAPGARRRGGSASRSLPLPKPRR 240
Qy 241 GAAPEPERTVQOGSWAHPTGRPSDRGFCVSPARPAEATSLGALSCTRHSHPSVG 300
Db 241 GAAPEPERTVQOGSWAHPTGRPSDRGFCVSPARPAEATSLGALSCTRHSHPSVG 300
Qy 301 RQHAGPPSTSRPRPMDTPCPVVAETKFLYSKGDEQLRPSFLSSRLPSLTGARRL 360
Db 301 RQHAGPPSTSRPRPMDTPCPVVAETKFLYSKGDEQLRPSFLSSRLPSLTGARRL 360
Qy 361 VETIFLGRPMWPGTPRRLPLPORYQWMBPLFLELLGNHQAQCPYGVLLKTHCPIRAAT 420
Db 361 VETIFLGRPMWPGTPRRLPLPORYQWMBPLFLELLGNHQAQCPYGVLLKTHCPIRAAT 420
Qy 421 PAAGVCAREKPGQSVAAPEEDTDPRLVLQRLQHSPPQVYGVFVACRLRELVPGLWGS 480
Db 421 PAAGVCAREKPGQSVAAPEEDTDPRLVLQRLQHSPPQVYGVFVACRLRELVPGLWGS 480
Qy 481 RHNERRFLRNTKFTSLGKHAKLSLQELTWKMSVRDCAWLRSPGVCVPAEHLREEI 540
Db 481 RHNERRFLRNTKFTSLGKHAKLSLQELTWKMSVRDCAWLRSPGVCVPAEHLREEI 540
Qy 541 LAKFLHLMVSVVVELLRSFYVTTETTPQKRLFPYKSVMSKLSQSGIROLKRVQIRE 600
Db 541 LAKFLHLMVSVVVELLRSFYVTTETTPQKRLFPYKSVMSKLSQSGIROLKRVQIRE 600
Qy 601 LSEAVRORHREARPAALTSLRFLPKPDGLRPIVNMVYVVGARTFRKRAERLTSRVKA 660
Db 601 LSEAVRORHREARPAALTSLRFLPKPDGLRPIVNMVYVVGARTFRKRAERLTSRVKA 660
Qy 661 LFSVLNVERARRPGLLGASVLGLDDIHRARTFVLVRAQDPPPELYFVKVDVTGAYDTI 720
Db 661 LFSVLNVERARRPGLLGASVLGLDDIHRARTFVLVRAQDPPPELYFVKVDVTGAYDTI 720
Qy 721 PQDRLTEVIASIIKPQNTYCVRRYAVVQAAHGHVRKAFKSHVSTLTDLPYMQFVAHL 780
Db 721 PQDRLTEVIASIIKPQNTYCVRRYAVVQAAHGHVRKAFKSHVSTLTDLPYMQFVAHL 780
Qy 781 QETSLRDAVTEQSSSINEASSGIFDVLRFPMCHHVRIRGKSVQCGIPQGSILSTL 840
Db 781 QETSLRDAVTEQSSSINEASSGIFDVLRFPMCHHVRIRGKSVQCGIPQGSILSTL 840
Qy 841 LCSLCYGDMENKLFAGIRRDGILLRLVDDFLVTPHLLTHAKTFLRTLVRGVPEYGCVVNL 900
Db 841 LCSLCYGDMENKLFAGIRRDGILLRLVDDFLVTPHLLTHAKTFLRTLVRGVPEYGCVVNL 900
Qy 901 RKTVMNPFVEBALGGTAFVQMPAHGLFPWCGLLDTRTLEVQSDYSSYARTSIRASLTF 960
Db 901 RKTVMNPFVEBALGGTAFVQMPAHGLFPWCGLLDTRTLEVQSDYSSYARTSIRASLTF 960
Qy 961 NRGFKAGNMRKLFVGLRLKCHSLFDLOVNSLQTVCTNIYKILLQAYRPHACVLQLP 1020
Db 961 NRGFKAGNMRKLFVGLRLKCHSLFDLOVNSLQTVCTNIYKILLQAYRPHACVLQLP 1020
Qy 1021 FHQQWKNPTFFLRVISDTASLCYSILKAKNAGMSLGAKGAGPLPSEAVQWLCHQAFLL 1080
Db 1021 FHQQWKNPTFFLRVISDTASLCYSILKAKNAGMSLGAKGAGPLPSEAVQWLCHQAFLL 1080
Qy 1081 KLTHRVTVVPLGLSLRTAQOLSKLPGTTLTALEAAANPALPSDFKTIILD 1132
Db 1081 KLTHRVTVVPLGLSLRTAQOLSKLPGTTLTALEAAANPALPSDFKTIILD 1132

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RESULT 18

US-08-974-549A-613
; Sequence 613, Application US/08974549A
; Patent No. 6166178
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.

```

; APPLICANT: Lingner, Joachim
; APPLICANT: Nakamura, Toru
; APPLICANT: Chapman, Karen B.
; APPLICANT: Morin, Gregg B.
; APPLICANT: Harley, Calvin B.
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: Human Telomerase Catalytic Subunit
; NUMBER OF SEQUENCES: 727
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/974,549A
; FILING DATE: 19-NOV-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/851,843
; FILING DATE: 06-MAY-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/854,050
; FILING DATE: 09-MAY-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/911,312
; FILING DATE: 14-AUG-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/912,951
; FILING DATE: 14-AUG-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/915,503
; FILING DATE: 14-AUG-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/US97/17618
; FILING DATE: 01-OCT-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/US97/17885
; FILING DATE: 01-OCT-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph Ted
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-002610US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 613:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1189 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..1189
; OTHER INFORMATION: /note= "fusion protein composed of
; OTHER INFORMATION: melittin signal sequence and full length

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; TYPE: amino acid

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Db	1018	NRGFKAGNRNRKLFVGLRLKCHSLFLDLQVNSLQTVCTNIYKILLQAYRPHACVQLP	1077
Qy	1021	FHOQVKNPTFFFLRVISDTSASLCYSILKAKNAGWSLGAKGAGPLPSEAOWMLCHQAFLL	1080
Db	1078	FHOQVKNPTFFFLRVISDTSASLCYSILKAKNAGWSLGAKGAGPLPSEAOWMLCHQAFLL	1137
Qy	1081	KLTHRVTVVPLGLSIRTAQTQLSRKLPGTTLTALEAAANPALPSDFKTLTD	1132
Db	1138	KLTHRVTVVPLGLSLRTAQTLQSRKLPGTTLTALEAAANPALPSDFKTLTD	1189

RESULT 20
 US-09-402-181B-613
 ; Sequence 613, Application US/09402181B
 ; Patent No. 6610839
 ; GENERAL INFORMATION:
 ; APPLICANT: Cech, Thomas R.
 ; Lingner, Joachim
 ; Nakamura, Toru
 ; Chapman, Karen B.
 ; Morin, Gregg B.
 ; Harley, Calvin B.
 ; Andrews, William H.
 ; TITLE OF INVENTION: Human Telomerase Catalytic Subunit
 ; NUMBER OF SEQUENCES: 633
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Townsend and Townsend and Crew LLP
 ; STREET: Two Embarcadero Center, Eighth Floor
 ; CITY: San Francisco
 ; STATE: California
 ; COUNTRY: USA
 ; ZIP: 94111-3834
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/402,181B
 ; FILING DATE: 29-Sep-1997
 ; CLASSIFICATION: <Unknown>
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/724,643
 ; FILING DATE: 01-OCT-1996
 ; APPLICATION NUMBER: US 08/844,419
 ; FILING DATE: 18-APR-1997
 ; APPLICATION NUMBER: US 08/846,017
 ; FILING DATE: 25-APR-1997
 ; APPLICATION NUMBER: US 08/851,843
 ; FILING DATE: 06-MAY-1997
 ; APPLICATION NUMBER: US 08/854,050
 ; FILING DATE: 09-MAY-1997
 ; APPLICATION NUMBER: US 08/911,312
 ; FILING DATE: 14-AUG-1997
 ; APPLICATION NUMBER: US 08/912,951
 ; FILING DATE: 14-AUG-1997
 ; APPLICATION NUMBER: US 08/915,503
 ; FILING DATE: 14-AUG-1997
 ; APPLICATION NUMBER: WO PCT/US97/17885
 ; FILING DATE: 01-OCT-1997
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Ausenhus, Scott L.
 ; REGISTRATION NUMBER: 42,271
 ; REFERENCE/DOCKET NUMBER: 015389-002620US
 ; TELEPHONE: (415) 576-0200
 ; TELEFAX: (415) 576-0300
 ; INFORMATION FOR SEQ ID NO: 613:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 1189 amino acids
 ; TYPE: amino acid

STRANDEDNESS: <Unknown>

TOPOLOGY: linear

MOLECULE TYPE: protein

FEATURE:

NAME/KEY: protein

LOCATION: 1..1189

OTHER INFORMATION: /note="fusion.protein composed of
melittin signal sequence and full length
hTERT protein"

SEQUENCE DESCRIPTION: SEQ ID NO: 613:

US-09-402-181B-613

Query Match 100.0%; Score 5961; DB 4; Length 1189;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPRAPRCRAVSLRSHREVLPATFVRRLGPGQWRVQGDPAAFRALVAQCVCVPM 60
DB 58 MPRAPRCRAVSLRSHREVLPATFVRRLGPGQWRVQGDPAAFRALVAQCVCVPM 117
QY 61 DARPPAAPSPRQVSCLEKELVARVLQRCERGAKNVLAFFGALLDARGGPPPEAFTTSVR 120
DB 118 DARPPAAPSPRQVSCLEKELVARVLQRCERGAKNVLAFFGALLDARGGPPPEAFTTSVR 177
QY 121 SYLNTVTDALRGSGAWGALLRRVGDVVLVHLARCALFVLVAPSCAYQVCGPPYQLGA 180
DB 178 SYLNTVTDALRGSGAWGALLRRVGDVVLVHLARCALFVLVAPSCAYQVCGPPYQLGA 237
QY 181 ATOARPPHAGSPRRLCERAWNSVREAGVPLGLPARGARRRGSASRSILPKRPRR 240
DB 238 ATOARPPHAGSPRRLCERAWNSVREAGVPLGLPARGARRRGSASRSILPKRPRR 297
QY 241 GAAPEPERTVQGSWAHPGTRGSDRGFCVSPARPAEATSEGLSGALSGTRHSPVSG 300
DB 298 GAAPEPERTVQGSWAHPGTRGSDRGFCVSPARPAEATSEGLSGALSGTRHSPVSG 357
QY 301 ROHAGPSTSRPPRMDTPCPVVAETKHFYSSGDKQLRPSFLLSRPSLTGARRL 360
DB 358 ROHAGPSTSRPPRMDTPCPVVAETKHFYSSGDKQLRPSFLLSRPSLTGARRL 417
QY 361 VETIFLGRPMWPGTPRPLRPQRYWQWRPLFLELLGNHQAQCPYGVLLKTHCPLRAAVT 420
DB 418 VETIFLGRPMWPGTPRPLRPQRYWQWRPLFLELLGNHQAQCPYGVLLKTHCPLRAAVT 477
QY 421 PAAGVCAREKPGSVAAPPEEDTPRRLVOLLRQHSWPQVYGFVRACLRRLVPPGLWGS 480
DB 478 PAAGVCAREKPGSVAAPPEEDTPRRLVOLLRQHSWPQVYGFVRACLRRLVPPGLWGS 537
QY 481 RHNERFLRNTKCFISLGHAKLSLQELTWKMSVRDCAWLRSPGVCVPAAEHRLREEI 540
DB 538 RHNERFLRNTKCFISLGHAKLSLQELTWKMSVRDCAWLRSPGVCVPAAEHRLREEI 597
QY 541 LAKFLHLMVYVVELLSRFFVTETTKQKRLFPYKRSVMSKLOSIGIRHQLKRVQRE 600
DB 598 LAKFLHLMVYVVELLSRFFVTETTKQKRLFPYKRSVMSKLOSIGIRHQLKRVQRE 657
QY 601 LSEAVRQHRARPALLTSRLRFIPKPGLRPIVNMDSVVGARTFRERKRAERLTSRVKA 660
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DB 718 LFSVLNYERARRPGLLGASVLGLDDIHRAWRTFVLIRVRAQDPPPLFYKVDVTGAYDTI 777
QY 721 PODRTEVTIASIIKPNQYCVRRYAVQKAAGHVRKAFKSHVSTLTDLQPMRFVAHL 780
DB 778 PODRTEVTIASIIKPNQYCVRRYAVQKAAGHVRKAFKSHVSTLTDLQPMRFVAHL 837
QY 781 QETSLRDAVTEQSSSNEASSGLFDVFLRPMCHHVRIRKGSVVCQGIPOGSIILSTL 840
DB 838 QETSLRDAVTEQSSSNEASSGLFDVFLRPMCHHVRIRKGSVVCQGIPOGSIILSTL 897
QY 841 LCSLCYGMENKLFAGIRRDGLLLRLVDDFLVTPHLTHAKTFLRTLVRGVPYGCVVNL 900

RESULT 21

US-09-721-456-613

; Sequence 613, Application US/09721456

; Patent No. 6617110

; GENERAL INFORMATION:

; APPLICANT: Cech, Thomas R.

; ; Lingner, Joachim

; ; Nakamura, Toru

; ; Chapman, Karen B.

; ; Morin, Gregg B.

; ; Harley, Calvin B.

; ; Andrews, William H.

; TITLE OF INVENTION: Human Telomerase Catalytic Subunit

; NUMBER OF SEQUENCES: 727

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Townsend and Townsend and Crew LLP

; STREET: Two Embarcadero Center, Eighth Floor

; CITY: San Francisco

; STATE: California

; COUNTRY: USA

; ZIP: 94111-3834

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent In Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/721,456

; FILING DATE: 22-No. 6617110-2000

; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US/08/974,549A

; FILING DATE: 19-NOV-1997

; APPLICATION NUMBER: US 08/724,643

; FILING DATE: 01-OCT-1996

; APPLICATION NUMBER: US 08/844,419

; FILING DATE: 18-APR-1997

; APPLICATION NUMBER: US 08/846,017

; FILING DATE: 25-APR-1997

; APPLICATION NUMBER: US 08/851,843

; FILING DATE: 06-MAY-1997

; APPLICATION NUMBER: US 08/854,050

; FILING DATE: 09-MAY-1997

; APPLICATION NUMBER: US 08/911,312

; FILING DATE: 14-AUG-1997

; APPLICATION NUMBER: US 08/912,951

; FILING DATE: 14-AUG-1997

; APPLICATION NUMBER: US 08/915,503

; FILING DATE: 14-AUG-1997

; APPLICATION NUMBER: WO PCT/US97/17618

; FILING DATE: 01-OCT-1997

; APPLICATION NUMBER: WO PCT/US97/17885

; FILING DATE: 01-OCT-1997

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/911,312
FILING DATE: 14-AUG-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-AUG-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-AUG-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/17618
FILING DATE: 01-OCT-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/17885
FILING DATE: 01-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph Ted
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002610US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 612:
SEQUENCE CHARACTERISTICS:
LENGTH: 1200 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
NAME/KEY: Protein
LOCATION: 1..1200
OTHER INFORMATION: /note= "fusion protein composed of His6 and Anti-Xpress tags, enterokinase
OTHER INFORMATION: cleavage site and full length hprt
OTHER INFORMATION: protein"
US-08-974-549A-612
Query Match 100.0%; Score 5961; DB 3; Length 1200;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MPAPRCBAVRSLLRSHYREVLPATFVRRILGPGQWRVLVQRCDDPAAFALVAQCILVCPW 60
Db 69 MPAPRCBAVRSLLRSHYREVLPATFVRRILGPGQWRVLVQRCDDPAAFALVAQCILVCPW 128
Qy 61 DARPPAAPSPROVSKLKVRLVQLRCERGAKNVLAFFGALLDGGAGPPEAFTTSVR 120
Db 129 DARPPAAPSPROVSKLKVRLVQLRCERGAKNVLAFFGALLDGGAGPPEAFTTSVR 188
Qy 121 SYLPTNTVDALRGSGAWGLLRRVDDVLLHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180
Db 189 SYLPTNTVDALRGSGAWGLLRRVDDVLLHLLARCALFVLVAPSCAYQVCGPPLYQLGA 248
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Db 249 ATQARPPPHASGPRRLRCERAWNHSVREAGVPLGLPAGARRRGGASRSPLPKRPRR 308
Qy 241 GAAPPERTPVQGSWAHPGTRGSDRGFCVSPARPAEATSLGALSGTRHSHPSVG 300
Db 309 GAAPPERTPVQGSWAHPGTRGSDRGFCVSPARPAEATSLGALSGTRHSHPSVG 368
Qy 301 RQHAGPSTSRPPRPDTPCPVYAEKTHFLYSSGDKQLRPSPLSLRPSLTGARRL 360
Db 369 RQHAGPSTSRPPRPDTPCPVYAEKTHFLYSSGDKQLRPSPLSLRPSLTGARRL 428
Qy 361 VETIFLGRSPWPGTPRRLPRLPQRYWQMRPLFLELLGNHACQPGVLLKTHCPRAAVT 420
Db 429 VETIFLGRSPWPGTPRRLPRLPQRYWQMRPLFLELLGNHACQPGVLLKTHCPRAAVT 488
421 PAAGVCAREKPGQSVAAPEEDTDPRLVLQRLRHSSPMQVYGFVRACLRLVPPGLMGS 480
Db PAAGVCAREKPGQSVAAPEEDTDPRLVLQRLRHSSPMQVYGFVRACLRLVPPGLMGS 548
Qy RHNRERFLRNTKKTISLGKHAKLSLOELTWKMSVRDCAWLRSPGVCVPAAEHLRBEI 540
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Db RKTVNPPEVEDEALGGTAFVOMPAHGLFPWCGLLDTRTLEVSQDYSSYARTSIRASLTFF 1028
Qy NRGFKAGNMRERKLFGLVRLKCHSLFLDLQVNSLQTVCTNIYKILLQAYRFHACVQLP 1020
Db NRGFKAGNMRERKLFGLVRLKCHSLFLDLQVNSLQTVCTNIYKILLQAYRFHACVQLP 1088
Qy FHQVWKNTPTFFLRVSDTASLCYSILKAKNAGSLGAKGAAGPLPSEAVQWLCHQAFLL 1080
Db FHQVWKNTPTFFLRVSDTASLCYSILKAKNAGSLGAKGAAGPLPSEAVQWLCHQAFLL 1148
Qy KLTRHRTVTVPLLGSLRTAQTOLSKRLPGTTLTALAAAANPALPSDFKTILD 1132
Db KLTRHRTVTVPLLGSLRTAQTOLSKRLPGTTLTALAAAANPALPSDFKTILD 1200
RESULT 23
US-08-912-951-324
Sequence 324, Application US/08912951
Patent No. 6475789
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
APPLICANT: Lingner, Joachim
APPLICANT: Nakamura, Toru
APPLICANT: Chapman, Karen B.
APPLICANT: Morin, Gregg B.
APPLICANT: Harley, Calvin
APPLICANT: Andrews, William H.
TITLE OF INVENTION: HUMAN TELOMERASE CATALYTIC SUBUNIT: DIAGNOSTIC AND
THERAPEUTIC METHODS
NUMBER OF SEQUENCES: 335
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: United States of America
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk


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;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/912,951
;; FILING DATE: 14-AUG-1997
;; CLASSIFICATION: 435
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/854,050
;; FILING DATE: 09-MAY-1997
;; CLASSIFICATION: 435
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/851,843
;; FILING DATE: 06-MAY-1997
;; CLASSIFICATION: 435
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/846,017
;; FILING DATE: 25-APR-1997
;; CLASSIFICATION: 435
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/724,643
;; FILING DATE: 01-OCT-1996
;; CLASSIFICATION: 435
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Apple, Randolph T.
;; REGISTRATION NUMBER: 36,429
;; REFERENCE/DOCKET NUMBER: 015389-002600US
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (415) 576-0200
;; TELEFAX: (415) 576-0300
;; INFORMATION FOR SEQ ID NO: 324:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 1200 amino acids
;; TYPE: amino acid
;; STRANDEDNESS:
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
US-08-912-951-324

Query Match 100.0%; Score 5961; DB 4; Length 1200;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MPAPRCVAVSLRLSHRYEVLPLATFVRLGPGQWRLVQRGDPAAPRALVAQCLVCVPW 60
Db 69 MPAPRCVAVSLRLSHRYEVLPLATFVRLGPGQWRLVQRGDPAAPRALVAQCLVCVPW 128

Qy 61 DARPPPAAPSPQVSCLELVARVLQRLCERGAKNVLAFGPALLDGAAGGPEAFTTSVR 120
Db 129 DARPPPAAPSPQVSCLELVARVLQRLCERGAKNVLAFGPALLDGAAGGPEAFTTSVR 188

Qy 121 SYLNTVTTDALRGSGAWGLLRLRRVDDVLLVHLLARCALFVLVAPSCAYQVCGPELYQLGA 180
Db 189 SYLNTVTTDALRGSGAWGLLRLRRVDDVLLVHLLARCALFVLVAPSCAYQVCGPELYQLGA 248

Qy 181 ATQARPPPHAGPARRRLCERAMNHSVREAGVPLGLPAPGARRRGSGASRLPLPKRPRR 240
Db 249 ATQARPPPHAGPARRRLCERAMNHSVREAGVPLGLPAPGARRRGSGASRLPLPKRPRR 308

Qy 241 GAAPPERTPVQGSWAHPGRTGRPSDRGFCVSPAPAEATSLGALSCTRHSHPFSVG 300
Db 309 GAAPPERTPVQGSWAHPGRTGRPSDRGFCVSPAPAEATSLGALSCTRHSHPFSVG 368

Qy 301 ROHAGPSTSRPRPMDTPCPVVAETKHFLYSSGDKQLRPSFLSSLRPSLTGARRL 360
Db 369 ROHAGPSTSRPRPMDTPCPVVAETKHFLYSSGDKQLRPSFLSSLRPSLTGARRL 428

Qy 361 VETIFLAGSRPMPGTPRRLPRLPORYWQMRPLFLELLGNHAQCPYGVLLKTHCPLRAAVT 420
Db 429 VETIFLAGSRPMPGTPRRLPRLPORYWQMRPLFLELLGNHAQCPYGVLLKTHCPLRAAVT 488

Qy 421 PAAGVCAREKPOGSAVAPEEEDTDPRELVQLLRQHSSPQWYGVFVRACLRLVPPGLWGS 480
Db 489 PAAGVCAREKPOGSAVAPEEEDTDPRELVQLLRQHSSPQWYGVFVRACLRLVPPGLWGS 548

Qy 481 RHNERFLRNTKRFISLGKHAKLQSLQELTWKMSVRDCAWLRRSPGVCVPAAEHRLREEI 540
Db 549 RHNERFLRNTKRFISLGKHAKLQSLQELTWKMSVRDCAWLRRSPGVCVPAAEHRLREEI 608

Qy 541 LAKFLHLMMSVYVVELLSRFYVTTETTFQKNRLFFYRKSVMSKLSQSIGIRHKLKRVQURE 600
Db 609 LAKFLHLMMSVYVVELLSRFYVTTETTFQKNRLFFYRKSVMSKLSQSIGIRHKLKRVQURE 668

Qy 601 LSEAEVQHQREARPAALLTSRLRFIPKPDGLRPIVNMDDYVVGARTFRREKRAERLTSRKA 660
Db 669 LSEAEVQHQREARPAALLTSRLRFIPKPDGLRPIVNMDDYVVGARTFRREKRAERLTSRKA 728

Qy 661 LFSVLNYERARRPGLLGASVLGLDDIHRARWTFVLVRADQPPPELYFVKVDVTGAYDTI 720
Db 729 LFSVLNYERARRPGLLGASVLGLDDIHRARWTFVLVRADQPPPELYFVKVDVTGAYDTI 788

Qy 721 PQDLRLTEVIASIIKPQNTYCVRRYAVVQKAAHGHVRKAFKSHVSTLTDLOPYMQFVAHL 780
Db 789 PQDLRLTEVIASIIKPQNTYCVRRYAVVQKAAHGHVRKAFKSHVSTLTDLOPYMQFVAHL 848

Qy 781 QETSPLRDAVVIQSSSLNEASSGLFDVFLRFMCHHAVRIRGKSYVQCQGIPOGSIILSTL 840
Db 849 QETSPLRDAVVIQSSSLNEASSGLFDVFLRFMCHHAVRIRGKSYVQCQGIPOGSIILSTL 908

Qy 841 LCSLCYGDMMENKLFAGIRRDGLLLRLVDDFLLVTPHLLTHAKTFLRTLVRGVPYGCVVNL 900
Db 909 LCSLCYGDMMENKLFAGIRRDGLLLRLVDDFLLVTPHLLTHAKTFLRTLVRGVPYGCVVNL 968

Qy 901 RKTVMNFPVEDEALGGTAFVQMPAHGLFPWCGLLDTRTLEVOQSDYSYARTSIRASLTF 960
Db 969 RKTVMNFPVEDEALGGTAFVQMPAHGLFPWCGLLDTRTLEVOQSDYSYARTSIRASLTF 1028

Qy 961 NRGFKAGRNMRRLFGVLRKLKCHSLFDLQVNSLQTVCTNIYKILLQAVRFHACVQLP 1020
Db 1029 NRGFKAGRNMRRLFGVLRKLKCHSLFDLQVNSLQTVCTNIYKILLQAVRFHACVQLP 1088

Qy 1021 FHOQVKNPFFLRVSDTASLCYSILKAKNAGSLGAKGAGPLPSEAVOMLCHOAFLL 1080
Db 1089 FHOQVKNPFFLRVSDTASLCYSILKAKNAGSLGAKGAGPLPSEAVOMLCHOAFLL 1148

Qy 1081 KLTRHRYVYVPLGLSLRTAQTLRSRKLPGTTLTAAEAAAANPALPSDFKTILD 1132
Db 1149 KLTRHRYVYVPLGLSLRTAQTLRSRKLPGTTLTAAEAAAANPALPSDFKTILD 1200

RESULT 24
US-09-402-181B-612
; Sequence 612, Application US/09402181B
; Patent No. 6610839
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; Lingner, Joachim
; Nakamura, Toru
; Chapman, Karen B.
; Morin, Gregg B.
; Harley, Calvin B.
; Andrews, William H.
; TITLE OF INVENTION: Human Telomerase Catalytic Subunit
; NUMBER OF SEQUENCES: 633
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA: US 08/402,181B
FILING DATE: 29-Sep-1997
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/911,312
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: WO PCT/US97/17885
FILING DATE: 01-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Ausenhus, Scott L.
REGISTRATION NUMBER: 42,271
REFERENCE/DOCKET NUMBER: 015389-002620US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300

INFORMATION FOR SEQ ID NO: 612:
SEQUENCE CHARACTERISTICS:
LENGTH: 1200 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
NAME/KEY: Protein
LOCATION: 1..1200
OTHER INFORMATION: /note= "fusion protein composed of His6 and Anti-Xpress tags, enterokinase cleavage site and full length hrRT protein"

SEQUENCE DESCRIPTION: SEQ ID NO: 612:
US-09-402-181B-612

Query Match 100.0%; Score 5961; DB 4; Length 1200;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MPRAPRCRAVRLSHRYEVLPLATFVRRLLGPGQWRVLRGDPAAFRALVAQCLVCPW	60
DB	69	MPRAPRCRAVRLSHRYEVLPLATFVRRLLGPGQWRVLRGDPAAFRALVAQCLVCPW	128
QY	61	DARPPPAAPSPQVSCLEKELVARVLQRCERGAKNVLAFGFALLDCAAGGPPPEAFTTSVR	120
DB	129	DARPPPAAPSPQVSCLEKELVARVLQRCERGAKNVLAFGFALLDCAAGGPPPEAFTTSVR	188
QY	121	SYLNTVTDALRGSGAWGLLLRRVGDVLLVHLLARCALFVLVAPSCAYQVCGPPPLYQLGA	180
DB	189	SYLNTVTDALRGSGAWGLLLRRVGDVLLVHLLARCALFVLVAPSCAYQVCGPPPLYQLGA	248
QY	181	ATQARPPPHASGRRRLGCERAWNHVSREAGVPLGLPAPCARRRGGSASRSPLPKRPRR	240
DB	249	ATQARPPPHASGRRRLGCERAWNHVSREAGVPLGLPAPCARRRGGSASRSPLPKRPRR	308
QY	241	GAAPPERTPVQGSWAHPGRTGRGFCVVSPPARPAEATSLGALSGRTRHSHPSVG	300

DB	309	GAAPPERTPVQGSWAHPGRTGRGFCVVSPPARPAEATSLGALSGRTRHSHPSVG	368
QY	301	ROHAGAPSTSRPPRPWDTPCPVYAEATKHFYSSGDEQELRPSFLLSLSPSLTGARRL	360
DB	369	ROHAGAPSTSRPPRPWDTPCPVYAEATKHFYSSGDEQELRPSFLLSLSPSLTGARRL	428
QY	361	VETIFLAGSRPMPGTPRRLPRLPORYWQMRPLFLELLGNHAQCPYGVLLKTHCPRAAVT	420
DB	429	VETIFLAGSRPMPGTPRRLPRLPORYWQMRPLFLELLGNHAQCPYGVLLKTHCPRAAVT	488
QY	421	PAAGVCAREKPGQSVAAPEEEDTPRRLVQLLRHSSPMQVYGVRACTRLVLPPLGWS	480
DB	489	PAAGVCAREKPGQSVAAPEEEDTPRRLVQLLRHSSPMQVYGVRACTRLVLPPLGWS	548
QY	481	RHNERRFLRNTKFTISLGKHAQLSIQELTWMSVRDCAWLRRSPGVGCVPAAEHLRBEI	540
DB	549	RHNERRFLRNTKFTISLGKHAQLSIQELTWMSVRDCAWLRRSPGVGCVPAAEHLRBEI	608
QY	541	LAKFLHMLMSVYVVELLRSPFYVTETTPQKRLFPYRKSVMSKLSQSIGIRHLKRVQRE	600
DB	609	LAKFLHMLMSVYVVELLRSPFYVTETTPQKRLFPYRKSVMSKLSQSIGIRHLKRVQRE	668
QY	601	LSEAEVRQREARPAALLTSRLRFPKPDGLRPIVNMDDYVVGARTFRREKRAERLTSRYKA	660
DB	669	LSEAEVRQREARPAALLTSRLRFPKPDGLRPIVNMDDYVVGARTFRREKRAERLTSRYKA	728
QY	661	LFSVLNVERARRPGLIGASVLGLDDIHRAWTFVLVRQAQDPPPELYFVKVDVTGAYDTI	720
DB	729	LFSVLNVERARRPGLIGASVLGLDDIHRAWTFVLVRQAQDPPPELYFVKVDVTGAYDTI	788
QY	721	PDRLTEVIASIIKPONTYCVRRYAVVQKAAHGHVKAFAKSHVSTLTLDQPMRQFVAHL	780
DB	789	PDRLTEVIASIIKPONTYCVRRYAVVQKAAHGHVKAFAKSHVSTLTLDQPMRQFVAHL	848
QY	781	QETSPDRDAVIEQSSSLNEASSGLFDVFLRFMCHAVRIRKSVYQCGIPQGSILSTL	840
DB	849	QETSPDRDAVIEQSSSLNEASSGLFDVFLRFMCHAVRIRKSVYQCGIPQGSILSTL	908
QY	841	LCSLCYGMENKLFAGIRRDGLLLRLVDDFLLVTPHLTHAKTFLTLVRGVEYGCNVNL	900
DB	909	LCSLCYGMENKLFAGIRRDGLLLRLVDDFLLVTPHLTHAKTFLTLVRGVEYGCNVNL	968
QY	901	RKTVMNFEVEALGGTAFVQMPAHGLFPWCGLLDTLTLEVSQSYSSYARTSIRASLTF	960
DB	969	RKTVMNFEVEALGGTAFVQMPAHGLFPWCGLLDTLTLEVSQSYSSYARTSIRASLTF	1028
QY	961	NRGFKAGNRRKLFVGLRLKCHSLFLLDQVNSLOTCTNIYKILLQAYRPHACVQLP	1020
DB	1029	NRGFKAGNRRKLFVGLRLKCHSLFLLDQVNSLOTCTNIYKILLQAYRPHACVQLP	1088
QY	1021	FHQQWKNPTFFLRVISTASLCYSILKAKNAGSLGAKGAGPLPSEAVQWLCHQAFLL	1080
DB	1089	FHQQWKNPTFFLRVISTASLCYSILKAKNAGSLGAKGAGPLPSEAVQWLCHQAFLL	1148
QY	1081	KLTRHRTVTVPLLSLRTAQTQLSRKLPGLTTLTALAAANPALPSDFKTILD	1132
DB	1149	KLTRHRTVTVPLLSLRTAQTQLSRKLPGLTTLTALAAANPALPSDFKTILD	1200

RESULT 25
US-09-721-456-612
; Sequence 612, Application US/09721456
; Patent No. 6617110
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; ; Lingner, Joachim
; ; Nakamura, Toru
; ; Chapman, Karen B.
; ; Morin, Gregg B.
; ; Harley, Calvin B.
; ; Andrews, William H.
; TITLE OF INVENTION: Human Telomerase Catalytic Subunit
; NUMBER OF SEQUENCES: 727

CORRESPONDENCE ADDRESS:
 ADDRESSEE: Townsend and Townsend and Crew LLP
 STREET: Two Embarcadero Center, Eighth Floor
 CITY: San Francisco
 STATE: California
 COUNTRY: USA
 ZIP: 94111-3834
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/721,456
 FILING DATE: 22-NOV-2000
 CLASSIFICATION: <Unknown>
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/08/974,549A
 FILING DATE: 19-NOV-1997
 APPLICATION NUMBER: US/08/724,643
 FILING DATE: 01-OCT-1996
 APPLICATION NUMBER: US/08/844,419
 FILING DATE: 18-APR-1997
 APPLICATION NUMBER: US/08/846,017
 FILING DATE: 25-APR-1997
 APPLICATION NUMBER: US/08/851,843
 FILING DATE: 06-MAY-1997
 APPLICATION NUMBER: US/08/854,050
 FILING DATE: 09-MAY-1997
 APPLICATION NUMBER: US/08/911,312
 FILING DATE: 14-AUG-1997
 APPLICATION NUMBER: US/08/912,951
 FILING DATE: 14-AUG-1997
 APPLICATION NUMBER: US/08/915,503
 FILING DATE: 14-AUG-1997
 APPLICATION NUMBER: WO PCT/US97/17618
 FILING DATE: 01-OCT-1997
 APPLICATION NUMBER: WO PCT/US97/17885
 FILING DATE: 01-OCT-1997
 ATTORNEY/AGENT INFORMATION:
 NAME: Apple, Randolph Ted
 REGISTRATION NUMBER: 36,429
 REFERENCE/DOCKET NUMBER: 015389-002610US
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 576-0200
 TELEFAX: (415) 576-0300
 INFORMATION FOR SEQ ID NO: 612:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1200 amino acids
 TYPE: amino acid
 STRANDEDNESS: <Unknown>
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 FEATURE:
 NAME/KEY: Protein
 LOCATION: 1..1200
 OTHER INFORMATION: /note= "fusion protein composed of His6
 and Anti-Xpress tags, enterokinase
 cleavage site and full length hTERT
 protein"
 SEQUENCE DESCRIPTION: SEQ ID NO: 612:

Query Match 100.0%; Score 5961; DB 4; Length 1200;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 1 MPAPRCRAVSLRSHRYREVLPLATFVRRLLGPQGRVLRQGDPAAPRALVAQCILVCPW 60
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Db	189	SYLPTVTDALRGSGAWGLLLRRVGDVVLVHLLARCALFVLVAPSCAYQVCGPPLYLQGA	248
Qy	181	ATQARPPPHASGPRRLGRCERAWNHSVREAGVPLGLPAGARRRGGSASRSLPLPKRRR	240
Db	249	ATQARPPPHASGPRRLGRCERAWNHSVREAGVPLGLPAGARRRGGSASRSLPLPKRRR	308
Qy	241	GAAPERTPVGQSWAHGTRGTRGFCVSPARPABEATSLGALSSTRISHPSVG	300
Db	309	GAAPERTPVGQSWAHGTRGTRGFCVSPARPABEATSLGALSSTRISHPSVG	368
Qy	301	RQHHAGPSTSRPPRWDTPCPVYAEYKHFYSSGDKQLRPSFLLSSLPSTGARRL	360
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Db	429	VETIFLGSRPWMPGTPRRLPRLPORYQWMPRLFLELLGNHAOCYPVLLKTHCPLRAAVT	488
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Db	489	PAAGVCAREKPOGSVAAPBEEDTPRLLVOLLROHSSPWQVYGFVRACLRLVPPGLWGS	548
Qy	481	RHNERFLRNTKTFISLGKHAQLSLQBLTWKMSVRDCAWLRSPGVCVPAAEHRLREEI	540
Db	549	RHNERFLRNTKTFISLGKHAQLSLQBLTWKMSVRDCAWLRSPGVCVPAAEHRLREEI	608
Qy	541	LAKFLHLMSSVYVVELLRSFFYVTTTFOKRLFFYKSVWSKLOSGIROLKRVQURE	600
Db	609	LAKFLHLMSSVYVVELLRSFFYVTTTFOKRLFFYKSVWSKLOSGIROLKRVQURE	668
Qy	601	LSEAEVQHREARPAALLTSRLRFPKPDGLRPIVNMDDVVGARTFRREKRAERLTSRKA	660
Db	669	LSEAEVQHREARPAALLTSRLRFPKPDGLRPIVNMDDVVGARTFRREKRAERLTSRKA	728
Qy	661	LFSVLNERARRPGLLGASVLGLDDIHRAMRTFVLVRAQDPPPELVFKVVDVTGAYDTI	720
Db	729	LFSVLNERARRPGLLGASVLGLDDIHRAMRTFVLVRAQDPPPELVFKVVDVTGAYDTI	788
Qy	721	PODLTEVIASIIKPQNTYCVRRYAVVQKAHGHVRKAFKSHVSTLTDLPYMQFVAHL	780
Db	789	PODLTEVIASIIKPQNTYCVRRYAVVQKAHGHVRKAFKSHVSTLTDLPYMQFVAHL	848
Qy	781	QETSLRDAVVEQSSSINEASSGLFDVFLRFMCHAVRIRGKSVQCGIPQGSILSTL	840
Db	849	QETSLRDAVVEQSSSINEASSGLFDVFLRFMCHAVRIRGKSVQCGIPQGSILSTL	908
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Qy	901	RKTVNFPEDEALGGTAFVQMPAHGLFPWCGLLDTRTLEVSQSDYSYARTSIRASLTF	960
Db	969	RKTVNFPEDEALGGTAFVQMPAHGLFPWCGLLDTRTLEVSQSDYSYARTSIRASLTF	1028
Qy	961	NRGFKAGRNMRKLPGLVRLKCHSLFDLQVNSLQTVCTNIYKILLQAYRFHACVLQLP	1020
Db	1029	NRGFKAGRNMRKLPGLVRLKCHSLFDLQVNSLQTVCTNIYKILLQAYRFHACVLQLP	1088
Qy	1021	FHQQVWKNPTFFLRVISTASLCYSILKAKNAGMSLGAKGAAGLPSEAVQWLCHQAFLL	1080
Db	1089	FHQQVWKNPTFFLRVISTASLCYSILKAKNAGMSLGAKGAAGLPSEAVQWLCHQAFLL	1148
Qy	1081	KLTHRVYVPLLGSLRTAQTOLSRKLPGLTTLTALEAANPALSPDKFTILD 1132	
Db	1149	KLTHRVYVPLLGSLRTAQTOLSRKLPGLTTLTALEAANPALSPDKFTILD 1200	

Sequence 600, Application US/08974549A
Patent No. 6166178
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
APPLICANT: Lingner, Joachim
APPLICANT: Nakamura, Toru
APPLICANT: Chapman, Karen B.
APPLICANT: Morin, Gregg B.
APPLICANT: Harley, Calvin B.
APPLICANT: Andrews, William H.
TITLE OF INVENTION: Human Telomerase Catalytic Subunit
NUMBER OF SEQUENCES: 727
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/974,549A
FILING DATE: 19-NOV-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/911,312
FILING DATE: 14-AUG-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-AUG-1997
PRIOR APPLICATION DATA:
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FILING DATE: 14-AUG-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/17618
FILING DATE: 01-OCT-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/17885
FILING DATE: 01-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph Ted
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002610US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 600:
SEQUENCE CHARACTERISTICS:
LENGTH: 1285 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:

NAME/KEY: Protein
LOCATION: 1..1285
OTHER INFORMATION: /note= "fusion protein composed of
enteroxinase cleavable, His tagged
OTHER INFORMATION: thioerodoxin moiety and full length hTRI"
US-08-974-549A-600
Query Match 100.0%; Score 5961; DB 3; Length 1285;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MPRAPRCRAVRSLLRSHYREVLPATFVRRLGPGQWRLLVORCDPAAFRALVAQCLVCVPM 60
DB 154 MPRAPRCRAVRSLLRSHYREVLPATFVRRLGPGQWRLLVORCDPAAFRALVAQCLVCVPM 213
QY 61 DARPPPAAPSFRQVSKLKLVARLQRCERGAKNVLAFFGALLDGAAGGPPPEAFTTSVR 120
DB 214 DARPPPAAPSFRQVSKLKLVARLQRCERGAKNVLAFFGALLDGAAGGPPPEAFTTSVR 273
QY 121 SYLPNTVTDALRGSGAMGLLLRRVGGDDVLVHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180
DB 274 SYLPNTVTDALRGSGAMGLLLRRVGGDDVLVHLLARCALFVLVAPSCAYQVCGPPLYQLGA 333
QY 181 ATQARPPPHASGPRRRLOCERAWNHVSREAGVPLGLPAGARRRGGASRSRLPLKPRRR 240
DB 334 ATQARPPPHASGPRRRLOCERAWNHVSREAGVPLGLPAGARRRGGASRSRLPLKPRRR 393
QY 241 GAAPEPRTPVQGSWAHPGRTGRGSDRGFCVSPARPAEAEATSLEGALSGTRHSHPSVG 300
DB 394 GAAPEPRTPVQGSWAHPGRTGRGSDRGFCVSPARPAEAEATSLEGALSGTRHSHPSVG 453
QY 301 RQHAGPSTSRPPRPMDTPCPVYAEATKHFYSSGDKQLRPSFLLSSRLSGARL 360
DB 454 RQHAGPSTSRPPRPMDTPCPVYAEATKHFYSSGDKQLRPSFLLSSRLSGARL 513
QY 361 VETIFLGRPMWPGTPRRLPRLPQRYQWMLFLELLGNHQAQCPGVLLKTHCPRAAVT 420
DB 514 VETIFLGRPMWPGTPRRLPRLPQRYQWMLFLELLGNHQAQCPGVLLKTHCPRAAVT 573
QY 421 PAAGVCAREKPGQSVAAPEEDTDPRRLVOLLRQSHSSPMQVYGFVRACLRLLVPGLMGS 480
DB 574 PAAGVCAREKPGQSVAAPEEDTDPRRLVOLLRQSHSSPMQVYGFVRACLRLLVPGLMGS 633
QY 481 RHNERRFLRNTKKEFISLGKHAQLSIQELTWKMSVRDCAWLRSPGCVGCPAAEHLRBEI 540
DB 634 RHNERRFLRNTKKEFISLGKHAQLSIQELTWKMSVRDCAWLRSPGCVGCPAAEHLRBEI 693
QY 541 LAKFLHLMVSVYVELLSRPFVTTTQKRLFPYRKSVMKLSQSIGIRQHLKRVQRE 600
DB 694 LAKFLHLMVSVYVELLSRPFVTTTQKRLFPYRKSVMKLSQSIGIRQHLKRVQRE 753
QY 601 LSEAEVROHREARPAALLTSRLRFTPKDGLRPIVNMDDYVVGARTFRERKAEHLTSRVKA 660
DB 754 LSEAEVROHREARPAALLTSRLRFTPKDGLRPIVNMDDYVVGARTFRERKAEHLTSRVKA 813
QY 661 LFSVLNYERARRPGLLGASVLGDDDIHRAWTFVLVRQAQPPPPPELYFKVDVTCAYDTI 720
DB 814 LFSVLNYERARRPGLLGASVLGDDDIHRAWTFVLVRQAQPPPPPELYFKVDVTCAYDTI 873
QY 721 PDRLTEVIASIIKPQNTYCVRRYAVVQKAAGHVRKAFKSHVSTLTDLQPYMRQFVAHL 780
DB 874 PDRLTEVIASIIKPQNTYCVRRYAVVQKAAGHVRKAFKSHVSTLTDLQPYMRQFVAHL 933
QY 781 QETSPDRDAVVEQSSSLNEASSGLFDVFLRFMCHAVRIRKSVVQCGIPQGSILSTL 840
DB 934 QETSPDRDAVVEQSSSLNEASSGLFDVFLRFMCHAVRIRKSVVQCGIPQGSILSTL 993
QY 841 LCSLCYGDMEKFLFAGIRDRDGLLLRLVDDFLLVTPHLTHAKTFLRTLVRGVPYECVNL 900
DB 994 LCSLCYGDMEKFLFAGIRDRDGLLLRLVDDFLLVTPHLTHAKTFLRTLVRGVPYECVNL 1053
QY 901 RKTVVNFFVEDEALGGTAFVQMPAGLFPWCGLLDTRTLEVQSDSYSSYARTSIRASLTF 960

Db 1054 RKTUVNPEDEALGCTAFVQMPAHGLFPWCGLLDTRTLEQSDYSYARTSIRASLTP 1113
Qy 961 NRGFKAGNMRKULFGVLRKCHSLFDLQVNSLQTVCTNIYKILLQAVRFHACVQLQP 1020
Db 1114 NRGFKAGNMRKULFGVLRKCHSLFDLQVNSLQTVCTNIYKILLQAVRFHACVQLQP 1173
Qy 1021 FHQQWKNKPTFLRVIDSTASLCYSILKAKNAGSLGAKGAGPLPSEAVOMLCHOAPLL 1080
Db 1174 FHQQWKNKPTFLRVIDSTASLCYSILKAKNAGSLGAKGAGPLPSEAVOMLCHOAPLL 1233
Qy 1081 KLTHRRVTYVPLGSLRTAQQLSRKLPGLTTLTALEAAANPALPSDFKTIILD 1132
Db 1234 KLTHRRVTYVPLGSLRTAQQLSRKLPGLTTLTALEAAANPALPSDFKTIILD 1285

RESULT 27

US-08-912-951-314
; Sequence 314, Application US/08912951
; Patent No. 6475789
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; APPLICANT: Lingner, Joachim
; APPLICANT: Nakamura, Toru
; APPLICANT: Chapman, Karen B.
; APPLICANT: Morin, Gregg B.
; APPLICANT: Harley, Calvin
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: HUMAN TELOMERASE CATALYTIC SUBUNIT: DIAGNOSTIC AND
; TITLE OF INVENTION: THERAPEUTIC METHODS
; NUMBER OF SEQUENCES: 335
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/912,951
; FILING DATE: 14-AUG-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/854,050
; FILING DATE: 09-MAY-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/851,843
; FILING DATE: 06-MAY-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph T.
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-002600US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300

; INFORMATION FOR SEQ ID NO: 314:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1285 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-912-951-314

Query Match 100.0%; Score 5961; DB 4; Length 1285;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MPRAPRCRAVRSLLRSHYREVLPPLATFVRRLPGPCWRLVQRGDPAAPALVAQCCLVCVPW 60
Db 154 MPRAPRCRAVRSLLRSHYREVLPPLATFVRRLPGPCWRLVQRGDPAAPALVAQCCLVCVPW 213
Qy 61 DARPPPAAPSFQVSCUKELVARVQLRCLCRGAKNVLAFGFALLDARGGGPEAFTTSVR 120
Db 214 DARPPPAAPSFQVSCUKELVARVQLRCLCRGAKNVLAFGFALLDARGGGPEAFTTSVR 273
Qy 121 SYLPTVTDALRGSGAWGLLLRRVGGDDVLVHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180
Db 274 SYLPTVTDALRGSGAWGLLLRRVGGDDVLVHLLARCALFVLVAPSCAYQVCGPPLYQLGA 333
Qy 181 ATQARPPPHASGPRRLRGGERANVHSVREAGVPLGLPAPGARRRGGSASRSLPLPKRPRR 240
Db 334 ATQARPPPHASGPRRLRGGERANVHSVREAGVPLGLPAPGARRRGGSASRSLPLPKRPRR 393
Qy 241 GAPEPERTVGGGSAWHPGRTGCPSDRGFCVSPARPAEATSEALSGALSTRSHSPSVG 300
Db 394 GAPEPERTVGGGSAWHPGRTGCPSDRGFCVSPARPAEATSEALSGALSTRSHSPSVG 453
Qy 301 ROHHAGPSTSRPRPMDTFCPPVYAEKTHFLYSSGDKQLRPSFLSSLPSTLGARRL 360
Db 454 ROHHAGPSTSRPRPMDTFCPPVYAEKTHFLYSSGDKQLRPSFLSSLPSTLGARRL 513
Qy 361 VETIFLGSRPWMPGTPRRLPRLPORYWQMRPLFLELLGNHACQPYGULLKTHCFLRAAVT 420
Db 514 VETIFLGSRPWMPGTPRRLPRLPORYWQMRPLFLELLGNHACQPYGULLKTHCFLRAAVT 573
Qy 421 PAAGVCAREKPOGSAVAPEEEDTPRRLVOLLROHSSFPWQYGVFVACLRRLVPPGLWGS 480
Db 574 PAAGVCAREKPOGSAVAPEEEDTPRRLVOLLROHSSFPWQYGVFVACLRRLVPPGLWGS 633
Qy 481 RHNERFLRNTKFFISLGKHAKLSLQBLTWQMSVRDCAWLRSPGVGCPAAEHRLREBI 540
Db 634 RHNERFLRNTKFFISLGKHAKLSLQBLTWQMSVRDCAWLRSPGVGCPAAEHRLREBI 693
Qy 541 LAKELHWMSSVYVVELLRSFYVTTTFOKNRLEFYRKSVMKLSQSGIROIHLKRVOLRE 600
Db 694 LAKELHWMSSVYVVELLRSFYVTTTFOKNRLEFYRKSVMKLSQSGIROIHLKRVOLRE 753
Qy 601 LSEAEVRQHREARPAALLTSRLRFPKPDGLRPIVNMDYVVGARTFRREKRAERLTSRYKA 660
Db 754 LSEAEVRQHREARPAALLTSRLRFPKPDGLRPIVNMDYVVGARTFRREKRAERLTSRYKA 813
Qy 661 LFSVLNYERARRPGLLGASVLGLDDIHRWRTFVLVRQAQPPPELFPVKVDVTGAYDTI 720
Db 814 LFSVLNYERARRPGLLGASVLGLDDIHRWRTFVLVRQAQPPPELFPVKVDVTGAYDTI 873
Qy 721 PDRLTEVIASIIKPQNTYCVRRYAVVQKAAGHVRKAFKSHVSTLTLDQPMRQFVAHL 780
Db 874 PDRLTEVIASIIKPQNTYCVRRYAVVQKAAGHVRKAFKSHVSTLTLDQPMRQFVAHL 933
Qy 781 QETSPLRDAVVIEOSSSINEASSGLFDVFLRFMCHAVRIRGKSYVQCGIPQGSILSTL 840
Db 934 QETSPLRDAVVIEOSSSINEASSGLFDVFLRFMCHAVRIRGKSYVQCGIPQGSILSTL 993
Qy 841 LCSLCYGD MENKLPAGIRRDGLLRLVDDFLLVTPHLLTHAKTFLRTLVRGVPEYGCVNIL 900
Db 994 LCSLCYGD MENKLPAGIRRDGLLRLVDDFLLVTPHLLTHAKTFLRTLVRGVPEYGCVNIL 1053

901 RKTVMNPFVEDEALGTAFAVQMPAHGLFPWCGLLDTRTLEVOSSDYSSVARTSIRASLTF 960
 1054 RKTVMNPFVEDEALGTAFAVQMPAHGLFPWCGLLDTRTLEVOSSDYSSVARTSIRASLTF 1113
 961 NGFKAGNRNRKLFGLVRLKCHSLFLDLQVNSLQTVCTNIYKILLLOAYRFHACVLQLP 1020
 1114 NGFKAGNRNRKLFGLVRLKCHSLFLDLQVNSLQTVCTNIYKILLLOAYRFHACVLQLP 1173
 1021 FHOQVKNPTFFLRVISTASLCSYLKAKNAGMSLGAKGAGPLPSEAVQMLCHQAFLL 1080
 1174 FHOQVKNPTFFLRVISTASLCSYLKAKNAGMSLGAKGAGPLPSEAVQMLCHQAFLL 1233
 1081 KLTHRVTVVPLGLSLRTAQOLSRKLPCTTTTALFAAANPALPSPDKTILD 1132
 1234 KLTHRVTVVPLGLSLRTAQOLSRKLPCTTTTALFAAANPALPSPDKTILD 1285

RESULT 28

US-09-402-181B-600
 ; Sequence 600, Application US/09402181B
 ; Patent No. 6610839

GENERAL INFORMATION:

APPLICANT: Cech, Thomas R.
 ; Lingner, Joachim
 ; Nakamura, Toru
 ; Chapman, Karen B.
 ; Morin, Gregg B.
 ; Harley, Calvin B.
 ; Andrews, William H.

TITLE OF INVENTION: Human Telomerase Catalytic Subunit

NUMBER OF SEQUENCES: 633

CORRESPONDENCE ADDRESS:

ADDRESSEE: Townsend and Townsend and Crew LLP
 ; STREET: Two Embarcadero Center, Eighth Floor
 ; CITY: San Francisco
 ; STATE: California
 ; COUNTRY: USA

ZIP: 94111-3834

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/402,181B

FILING DATE: 29-Sep-1997

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/724,643

FILING DATE: 01-OCT-1996

APPLICATION NUMBER: US 08/844,419

FILING DATE: 18-APR-1997

APPLICATION NUMBER: US 08/846,017

FILING DATE: 25-APR-1997

APPLICATION NUMBER: US 08/851,843

FILING DATE: 06-MAY-1997

APPLICATION NUMBER: US 08/854,050

FILING DATE: 09-MAY-1997

APPLICATION NUMBER: US 08/911,312

FILING DATE: 14-AUG-1997

APPLICATION NUMBER: US 08/912,951

FILING DATE: 14-AUG-1997

APPLICATION NUMBER: US 08/915,503

FILING DATE: 14-AUG-1997

APPLICATION NUMBER: WO PCT/US97/17885

FILING DATE: 01-OCT-1997

ATTORNEY/AGENT INFORMATION:

NAME: Ausebus, Scott L.

REGISTRATION NUMBER: 42,271

REFERENCE/DOCKET NUMBER: 015389-002620US

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 576-0200

TELEFAX: (415) 576-0300

INFORMATION FOR SEQ ID NO: 600:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 1285 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: <Unknown>
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; FEATURE:
 ; NAME/KEY: Protein
 ; LOCATION: 1..1285
 ; OTHER INFORMATION: /note= "fusion protein composed of
 ; enterokinase cleavable, his tagged
 ; thiorodoxin moiety and full length hTERT"
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 600:
 ; US-09-402-181B-600

Query Match 100.0%; Score 5961; DB 4; Length 1285;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MPAPRCRAVRSLRLSHYREVLPPLATFVRRLLGPOQGRMLVQVGDPAAFRALVAQCLVCPW 60
 DB 154 MPAPRCRAVRSLRLSHYREVLPPLATFVRRLLGPOQGRMLVQVGDPAAFRALVAQCLVCPW 213
 QY 61 DARPPPAAPSFQVSCLEKELVARVLQRLCERGAKNVLAFFGALLDGAAGGPPPEAFTTSYR 120
 DB 214 DARPPPAAPSFQVSCLEKELVARVLQRLCERGAKNVLAFFGALLDGAAGGPPPEAFTTSYR 273
 QY 121 SYLPTNTVDALRGSGAWGLLRVGDVLLVHLLARCALFVLVAPSCAYQVCPPLYLQGA 180
 DB 274 SYLPTNTVDALRGSGAWGLLRVGDVLLVHLLARCALFVLVAPSCAYQVCPPLYLQGA 333
 QY 181 ATQARPPPHASGPRRLCERAWNHSVREAGVPLGLPAGARRRGSASRSPLPKRPRR 240
 DB 334 ATQARPPPHASGPRRLCERAWNHSVREAGVPLGLPAGARRRGSASRSPLPKRPRR 393
 QY 241 GAAPEPERTVQGGSWAHPGTRGSDRGFCVVSAPARPAEATSLLEGALSGTRHSHPSVG 300
 DB 394 GAAPEPERTVQGGSWAHPGTRGSDRGFCVVSAPARPAEATSLLEGALSGTRHSHPSVG 453
 QY 301 ROHAGPSTSRPRPMDTPCPVVAETKHFYSSGDKQLRPSFLLSLRSLTGARL 360
 DB 454 ROHAGPSTSRPRPMDTPCPVVAETKHFYSSGDKQLRPSFLLSLRSLTGARL 513
 QY 361 VETIFLGRPMWPGTPRELPRLPQYQWMPRLFELLLGNHACQPGVLLKTHCPRAAAT 420
 DB 514 VETIFLGRPMWPGTPRELPRLPQYQWMPRLFELLLGNHACQPGVLLKTHCPRAAAT 573
 QY 421 PAAAGVCAREKPGQGSVAAPPEEDTDPRRLVQLLRQHSPPQVYGFVRACLRLRVPGLWGS 480
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 QY 481 RHNERFLRNTKCFISLGHAKLSLOELTWKMSVRDCAWLRRSPGCVGCPVAAEHLREBI 540
 DB 634 RHNERFLRNTKCFISLGHAKLSLOELTWKMSVRDCAWLRRSPGCVGCPVAAEHLREBI 693
 QY 541 LAKFLHLMVSVYVVELLSRFFVTTTTPQKRLFFYKRSVMSKLSQSIGIROLKXVOLRE 600
 DB 694 LAKFLHLMVSVYVVELLSRFFVTTTTPQKRLFFYKRSVMSKLSQSIGIROLKXVOLRE 753
 QY 601 LSEAEVROHREARPALTSRLRFIPKPDGLRPIVNMDDVVGARTFRERKRAERLTSRVKA 660
 DB 754 LSEAEVROHREARPALTSRLRFIPKPDGLRPIVNMDDVVGARTFRERKRAERLTSRVKA 813
 QY 661 LFSVLNVERARRPGLLGASVLGLDDIHRAWRTFVLRLVRAQDPPPELYFVKVDVDTGAYDTI 720
 DB 814 LFSVLNVERARRPGLLGASVLGLDDIHRAWRTFVLRLVRAQDPPPELYFVKVDVDTGAYDTI 873
 QY 721 PDRLTEVIAIIPQNTYCVRRYAVVQAAHGHVRKAFKSHVSTLTDLQPMROFVAHL 780
 DB 874 PDRLTEVIAIIPQNTYCVRRYAVVQAAHGHVRKAFKSHVSTLTDLQPMROFVAHL 933
 QY 781 QETSPLRDAVVIEQSSSLNEASSGLFDVFLRPMCHAVRIRGKSVVQCQGIQSGISLSTL 840

Db 934 QETSLRDVIEQSSSNEASSGLDFVFLPMCHAVRIKSVQCGIPQSGIISLTL 993
Qy 841 LCSLCYGMENKLFAGIRDDGLLLRLVDFFLLVTPHLTHAKTFLRLTVRGVPEYGCVVNL 900
Db 994 LCSLCYGMENKLFAGIRDDGLLLRLVDFFLLVTPHLTHAKTFLRLTVRGVPEYGCVVNL 1053
Qy 901 RKTUVNPFVEBALGGTAFVQMPAHGLFPWCGLLLDTRTLEVSQSYSSYARTSIRASLTF 960
Db 1054 RKTUVNPFVEBALGGTAFVQMPAHGLFPWCGLLLDTRTLEVSQSYSSYARTSIRASLTF 1113
Qy 961 NRGFKAGNRMRKLGVLRLKCHSLFDLQVNSLQVCTNLYKILLQAYRHFACVLQLP 1020
Db 1114 NRGFKAGNRMRKLGVLRLKCHSLFDLQVNSLQVCTNLYKILLQAYRHFACVLQLP 1173
Qy 1021 FHQQWKNPFFLRVISDTASLCYSILKAKNAGMSLGAKGAGPLPSEAVQWLCHQAFLL 1080
Db 1174 FHQQWKNPFFLRVISDTASLCYSILKAKNAGMSLGAKGAGPLPSEAVQWLCHQAFLL 1233
Qy 1081 KLTHRVTVVPLLSLRTAQOLSKLPGTTLTALBAANPALPSDFKTIILD 1132
Db 1234 KLTHRVTVVPLLSLRTAQOLSKLPGTTLTALBAANPALPSDFKTIILD 1285

RESULT 29

US-09-721-456-600
; Sequence 600, Application US/09721456
; Patent No. 6617110
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; Lingner, Joachim
; Nakamura, Toru
; Chapman, Karen B.
; Morin, Gregg B.
; Harley, Calvin B.
; Andrews, William H.
; TITLE OF INVENTION: Human Telomerase Catalytic Subunit
; NUMBER OF SEQUENCES: 727
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/721,456
; FILING DATE: 22-NOV-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/974,549A
; FILING DATE: 19-NOV-1997
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; APPLICATION NUMBER: US 08/851,843
; FILING DATE: 06-MAY-1997
; APPLICATION NUMBER: US 08/854,050
; FILING DATE: 09-MAY-1997
; APPLICATION NUMBER: US 08/911,312
; FILING DATE: 14-AUG-1997
; APPLICATION NUMBER: US 08/912,951
; FILING DATE: 14-AUG-1997
; APPLICATION NUMBER: US 08/915,503
; FILING DATE: 14-AUG-1997

; APPLICATION NUMBER: WO PCT/US97/17618
; FILING DATE: 01-OCT-1997
; APPLICATION NUMBER: WO PCT/US97/17885
; FILING DATE: 01-OCT-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph Ted
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-002610US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 600:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1285 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..1285
; OTHER INFORMATION: /note= "fusion protein composed of
; thiorodoxin moiety and full length hTERT"
; SEQUENCE DESCRIPTION: SEQ ID NO: 600:
US-09-721-456-600

Query Match 100.0%; Score 5961; DB 4; Length 1285;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MPAPRCRAVRSLLRSHYREVLPVPLATFVRLGPGWRLVQSGDPAAFRAUVAQCLVCVPW 60
Db 154 MPAPRCRAVRSLLRSHYREVLPVPLATFVRLGPGWRLVQSGDPAAFRAUVAQCLVCVPW 213
Qy 61 DARPPAAPSPFQVSCUKELVARVLQRLCERGAKNLAFGALLDARGGPEAFTTSVR 120
Db 214 DARPPAAPSPFQVSCUKELVARVLQRLCERGAKNLAFGALLDARGGPEAFTTSVR 273
Qy 121 SYLPTVTDALRGSGAWGLLLRRVGGDVLVHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180
Db 274 SYLPTVTDALRGSGAWGLLLRRVGGDVLVHLLARCALFVLVAPSCAYQVCGPPLYQLGA 333
Qy 181 ATQARPPPHASGPRRLRGCEAMNHSVREAGVPLGLPAGARRRGGSASRSLPLPKRPRR 240
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Qy 301 RQHHAGPPSTSRPPRWDTPCPCPVYAEYKIFLYSSGDKQLRPSFLLSSRPSLTGARRL 360
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Db 754 LSEAEVQRHREARBPALLTSRLRPIPKPDGLRPIVMNDYVVGARTPRREKRAERLTSRVKA 813
QY 661 LFSVLNYERARRPGLLGASVLGLDDIHRARWTFVLVRRAQDPPPELYFVKVDVTGAYDTI 720
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Db 934 QETSLRDAVTEQSSSLEASSGLFDVFLRPMCHHAVIRKSVYQCGI PQSGTSLTL 993
QY 841 LCSLCYGMENKLFAGIRRDGLLLRLVDLFTLPHLTHAKTFLRLVRGVPYCGVNL 900
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Db 1054 RKTVNFVPEDEALGGTAFVQMPAHLFPWCGLLLDTRTLEVSQSYSSYARTSIRASLTF 1113
QY 961 NRGPKAGNRMRKLGVLRLKCHSLFLDLQVNSLOTVCNTIYKILLQAYRHFACVLOLP 1020
Db 1114 NRGPKAGNRMRKLGVLRLKCHSLFLDLQVNSLOTVCNTIYKILLQAYRHFACVLOLP 1173
QY 1021 FHQYWKNTPTFLRIVISDTASLCYILKAKNAGMSLGAKGAGPLPSEAVQWLCHQAFIL 1080
Db 1174 FHQYWKNTPTFLRIVISDTASLCYILKAKNAGMSLGAKGAGPLPSEAVQWLCHQAFIL 1233
QY 1081 KLTHRVTVYVPLGLSLRTAQTSKLPGLTTLTALBAANPALPSDFKTILD 1132
Db 1234 KLTHRVTVYVPLGLSLRTAQTSKLPGLTTLTALBAANPALPSDFKTILD 1285

RESULT 30

US-08-974-549A-344
; Sequence 344, Application US/08974549A
; Patent No. 6166178

GENERAL INFORMATION:

; APPLICANT: Cech, Thomas R.
; APPLICANT: Lingner, Joachim
; APPLICANT: Nakamura, Toru
; APPLICANT: Chapman, Karen B.
; APPLICANT: Morin, Gregg B.
; APPLICANT: Harley, Calvin B.
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: Human Telomerase Catalytic Subunit
; NUMBER OF SEQUENCES: 727
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834

; COMPUTER TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/974,549A
; FILING DATE: 19-NOV-1997
; CLASSIFICATION: 536

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/846,017

; FILING DATE: 25-APR-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/851,843
; FILING DATE: 06-MAY-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/854,050
; FILING DATE: 09-MAY-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/911,312
; FILING DATE: 14-AUG-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/912,951
; FILING DATE: 14-AUG-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/915,503
; FILING DATE: 14-AUG-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/US97/17618
; FILING DATE: 01-OCT-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/US97/17885
; FILING DATE: 01-OCT-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph Red
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-002610US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 344:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1132 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-974-549A-344

Query Match 99.8%; Score 5952; DB 3; Length 1132;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1130; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MPRAPRCRAVRSLLRSHYREVLPATFVRRLGPGQWRVLVQRGDPAAFRALVAQCLVCPWM 60
Db 1 MPRAPRCRAVRSLLRSHYREVLPATFVRRLGPGQWRVLVQRGDPAAFRALVAQCLVCPWM 60
QY 61 DARPPAPSPROVSCLELVARVLCRCERAKNVLAFGALLDARGGPEAFTTSVR 120
Db 61 DARPPAPSPROVSCLELVARVLCRCERAKNVLAFGALLDARGGPEAFTTSVR 120
QY 121 SYLPTNTVDALRGSGAWGLLLRRVGDVVLVHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180
Db 121 SYLPTNTVDALRGSGAWGLLLRRVGDVVLVHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180
QY 181 ATQARPPPHAGPPRRRLGRCERAWNHSVREAGVPLGAPAGARRRGSSASRSLPLPKRRR 240
Db 181 ATQARPPPHAGPPRRRLGRCERAWNHSVREAGVPLGAPAGARRRGSSASRSLPLPKRRR 240
QY 241 GAAPEPERTVPGQGSWAHPGTRGSDRGFCVSPARPAEATSLGALSCTRHSHPVG 300
Db 241 GAAPEPERTVPGQGSWAHPGTRGSDRGFCVSPARPAEATSLGALSCTRHSHPVG 300
QY 301 RQHAGPPSTSRPPRMDTPCPVVAETKHFYSSGDKQLRPSFLLSSLRPSLTGARRL 360
Db 301 RQHAGPPSTSRPPRMDTPCPVVAETKHFYSSGDKQLRPSFLLSSLRPSLTGARRL 360
QY 361 VETIFLGSRPMPGTPRRLPQRYMOMRFLFLELGNHACQCPYGVLLKTHCPLRAAVT 420
Db 361 VETIFLGSRPMPGTPRRLPQRYMOMRFLFLELGNHACQCPYGVLLKTHCPLRAAVT 420
QY 421 PAAGVCAREKPGQGSVAAPAEEDTDPRLVQLLRQHSHPWQYVGFVRACLRRLVPPGLWS 480
Db 421 PAAGVCAREKPGQGSVAAPAEEDTDPRLVQLLRQHSHPWQYVGFVRACLRRLVPPGLWS 480

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QY 481 RHNRERFLRNTKFKTSLGKHAKLSLOELTWKMSVRDCAWLRSPGVCPVPAEHLREEI 540
Db 481 RHNRERFLRNTKFKTSLGKHAKLSLOELTWKMSVRDCAWLRSPGVCPVPAEHLREEI 540
QY 541 LAKFLHMLSVVVELLSFFVVTETTFQKNRLFYRKSVMKLSQSIGIRQHLKRVOLRE 600
Db 541 LAKFLHMLSVVVELLSFFVVTETTFQKNRLFYRKSVMKLSQSIGIRQHLKRVOLRE 600
QY 601 LSEARVROHREARPAALLSRIRFPKPDGLRPIVNMDDYVVGARTPRRKRERLTTSRVKA 660
Db 601 LSEARVROHREARPAALLSRIRFPKPDGLRPIVNMDDYVVGARTPRRKRERLTTSRVKA 660
QY 661 LFSVLNYERARRPGLGASVLGLDDIHRARTFVLVRQAQPPPELYFVKVDVTCAYDTI 720
Db 661 LFSVLNYERARRPGLGASVLGLDDIHRARTFVLVRQAQPPPELYFVKVDVTCAYDTI 720
QY 721 PODRLTEVIASIIKQNTYCVRRYAVVQKAAGHVRKAFKSHVSTLTDLQPMRQFVAHL 780
Db 721 PODRLTEVIASIIKQNTYCVRRYAVVQKAAGHVRKAFKSHVSTLTDLQPMRQFVAHL 780
QY 781 QETSPLRDAVIEQSSSLNEASSGLFDVFLRPMCHAVIRKGSYVQCQGIPOQSILSTL 840
Db 781 QETSPLRDAVIEQSSSLNEASSGLFDVFLRPMCHAVIRKGSYVQCQGIPOQSILSTL 840
QY 841 LCSLCYGDMENKLFAGIRRDGLLRLVDDELLVTPHLTHAKTFLRTLVRGVPEYCCVNL 900
Db 841 LCSLCYGDMENKLFAGIRRDGLLRLVDDELLVTPHLTHAKTFLRTLVRGVPEYCCVNL 900
QY 901 RKTVMNFPVEDEALGGTAVQMPAHGLFPWCGLLDTRTLEVSQSYSSYARTSIRASLTF 960
Db 901 RKTVMNFPVEDEALGGTAVQMPAHGLFPWCGLLDTRTLEVSQSYSSYARTSIRASLTF 960
QY 961 NRGFKAGNRMRKLGVLRLKCHSLFDLQVNSLQTVCTNIYKILLQAYRFHACVLQLP 1020
Db 961 NRGFKAGNRMRKLGVLRLKCHSLFDLQVNSLQTVCTNIYKILLQAYRFHACVLQLP 1020
QY 1021 FHQQVWKNTPTFLRIVISDTASLCYSILKAKNAGMSLGAKGAGPLPSEAVOMLCHQAFLL 1080
Db 1021 FHQQVWKNTPTFLRIVISDTASLCYSILKAKNAGMSLGAKGAGPLPSEAVOMLCHQAFLL 1080
QY 1081 KLTHRVTVYVPLGLSLRTAQOLSKLPCTTITALEAANPALPSDFKTILD 1132
Db 1081 KLTHRVTVYVPLGLSLRTAQOLSKLPCTTITALEAANPALPSDFKTILD 1132
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RESULT 31

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US-09-402-181B-344
; Sequence 344, Application US/09402181B
; Patent No. 6610839
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GENERAL INFORMATION:

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; APPLICANT: Cech, Thomas R.
; Lingner, Joachim
; Nakamura, Toru
; Chapman, Karen B.
; Morin, Gregg B.
; Harley, Calvin B.
; Andrews, William H.
```

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; TITLE OF INVENTION: Human Telomerase Catalytic Subunit
```

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; NUMBER OF SEQUENCES: 633
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; CORRESPONDENCE ADDRESS:
```

```
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
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; COMPUTER READABLE FORM:
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; MEDIUM TYPE: Floppy disk
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; COMPUTER: IBM PC compatible
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; OPERATING SYSTEM: PC-DOS/MS-DOS
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; SOFTWARE: Patent in Release #1.0, Version #1.30
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; CURRENT APPLICATION DATA:
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; APPLICATION NUMBER: US/09/402,181B
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; FILING DATE: 29-Sep-1997
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; APPLICATION NUMBER: US 08/851,843
; FILING DATE: 06-MAY-1997
; APPLICATION NUMBER: US 08/854,050
; FILING DATE: 09-MAY-1997
; APPLICATION NUMBER: US 08/911,312
; FILING DATE: 14-AUG-1997
; APPLICATION NUMBER: US 08/912,951
; FILING DATE: 14-AUG-1997
; APPLICATION NUMBER: US 08/915,503
; FILING DATE: 14-AUG-1997
; APPLICATION NUMBER: WO PCT/US97/17885
; FILING DATE: 01-OCT-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Ausenhus, Scott L.
; REGISTRATION NUMBER: 42,271
; REFERENCE/DOCKET NUMBER: 015389-002620US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 344:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1132 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 344:
US-09-402-181B-344
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Query Match 99.8%; Score 5952; DB 4; Length 1132;

Best Local Similarity 99.8%; Pred. No. 0;

Matches 1130; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

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Db 1 MPAPRCRAVRSLLRSHYREVLPVPLATFVRRLGPGQWRLVQRGDDPAAPRALVAQCVCVPM 60
QY 61 DAREPPAAPSPRQVSCLELVARVLQRLCERGAKNVLAFGFALLDGGARGGPEAFTTSVR 120
Db 61 DAREPPAAPSPRQVSCLELVARVLQRLCERGAKNVLAFGFALLDGGARGGPEAFTTSVR 120
QY 121 SYLPTNTVDALRGSGANGLLRRVGGDDVLLHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180
Db 121 SYLPTNTVDALRGSGANGLLRRVGGDDVLLHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180
QY 181 ATOARPPPHASGPRRRRLGCERAWNHSVREAGVPLGLPAPGARRRGGSSASRSILPKRRPR 240
Db 181 ATOARPPPHASGPRRRRLGCERAWNHSVREAGVPLGLPAPGARRRGGSSASRSILPKRRPR 240
QY 241 GAAPERTPVQGSWAHPGRTGRPSDRGFCVSPARPAEATSLGALSCTRHSHPVG 300
Db 241 GAAPERTPVQGSWAHPGRTGRPSDRGFCVSPARPAEATSLGALSCTRHSHPVG 300
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Db 301 RQHHAGPSTSRPPRPMWDTCPVPVYAEKHFYSSGDKQLRPSFLLSLPSLTGARRL 360
QY 361 VETIFLGSRRPMPGTPRRLPRLPORYQWMRPLFLELLGNHAQCPYGVLLKTHCPRAAVT 420
Db 361 VETIFLGSRRPMPGTPRRLPRLPORYQWMRPLFLELLGNHAQCPYGVLLKTHCPRAAVT 420
QY 421 PAAGVCAREKPGQSVAAPEEEDTDRRLVQLLRQHSHPWQYGVFVRACLRRLVPPGLNGS 480
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QY 421 PAAGVAREKPOGSAVAPEEEDTPRRVLVOLLROHSSPMQVYGFVRACLRRLVPPGLWS 480
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QY 481 RHNERRFLRNTKFFISLGHAKLSLOELTWKSVDRDCAWLRRSPGVGCVPAAEHLRLEEI 540
Db 481 RHNERRFLRNTKFFISLGHAKLSLOELTWKSVDRDCAWLRRSPGVGCVPAAEHLRLEEI 540
QY 541 LAKFLHMLSVVVELLSFFVTETTFQKNRLFFYRKSVMSKLSQSIGIRQHLKRVQLRE 600
Db 541 LAKFLHMLSVVVELLSFFVTETTFQKNRLFFYRKSVMSKLSQSIGIRQHLKRVQLRE 600
QY 601 LSEAEVROHREARPAALTSLRFPKPDGLRPIVNMVYVVGARTFRREKRAERLTSRVKA 660
Db 601 LSEAEVROHREARPAALTSLRFPKPDGLRPIVNMVYVVGARTFRREKRAERLTSRVKA 660
QY 661 LFSVLNTERARRPGLGASVLGLDDIHRAMWTFVLVRVAQDPPPELYFVKVDVTGAYDTI 720
Db 661 LFSVLNTERARRPGLGASVLGLDDIHRAMWTFVLVRVAQDPPPELYFVKVDVTGAYDTI 720
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Db 721 PQDRLTEVIASIIKPONTYCVRRYAVVQKAAHGHVRKAFKSHVSTLTDLPYMQFVAHL 780
QY 781 QETSLRDAVVEIOSSSINEASSGLFDVFLRFMCHHVRIRGKSVVOCQIPQGSILSTL 840
Db 781 QETSLRDAVVEIOSSSINEASSGLFDVFLRFMCHHVRIRGKSVVOCQIPQGSILSTL 840
QY 841 LCSLCYGMENKLFAGIRRDGLLRLVDDFLVTPHLLTHAKTFLRTLVRGVPEYGCVVNL 900
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Db 961 NRGFKAGNRMRKLFVGLRLKCHSLFDLQVNSLQTVCTNLYKILLQAYRFAHCVIQLP 1020
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Db 1021 FHQQWKNPTFFLRVISDTASLCYSILKAKNAGMSLGAAGPLPSEAVQWLCHQAFLL 1080
QY 1081 KLTHRVTVYVPLLSLRTAQOLSRKLPGETTITALEAANPALPSDFKTIILD 1132
Db 1081 KLTHRVTVYVPLLSLRTAQOLSRKLPGETTITALEAANPALPSDFKTIILD 1132

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RESULT 33

US-08-974-549A-628
Sequence 628, Application US/08974549A
Patent No. 6166178

GENERAL INFORMATION:

APPLICANT: Cech, Thomas R.
APPLICANT: Lingner, Joachim
APPLICANT: Nakamura, Toru
APPLICANT: Chapman, Karen B.
APPLICANT: Morin, Gregg B.
APPLICANT: Harley, Calvin B.
APPLICANT: Andrews, William H.
TITLE OF INVENTION: Human Telomerase Catalytic Subunit
NUMBER OF SEQUENCES: 727

CORRESPONDENCE ADDRESS:

ADDRESSEE: Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

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; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/974,549A
; FILING DATE: 19-NOV-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/851,843
; FILING DATE: 06-MAY-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/854,050
; FILING DATE: 09-MAY-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/911,312
; FILING DATE: 14-AUG-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/912,951
; FILING DATE: 14-AUG-1997
; APPLICATION NUMBER: US 08/915,503
; FILING DATE: 14-AUG-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/US97/17618
; FILING DATE: 01-OCT-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/US97/17885
; FILING DATE: 01-OCT-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph Ted
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-002610US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 628:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1407 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..1407
; OTHER INFORMATION: /note="fusion protein composed of
; OTHER INFORMATION: enhanced green fluorescent protein
; OTHER INFORMATION:
; OTHER INFORMATION: 5' untranslated region of hTERT mRNA and
; OTHER INFORMATION: hTERT protein sequence"
; US-08-974-549A-628

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Query Match 99.8%; Score 5952; DB 3; Length 1407;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1130; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MPRAPRCRAVRSLLRSHYREVLPATFVRLPGQWRLVQRGDPAAFRALVAQCILVCVPW 60
Db 276 MPRAPRCRAVRSLLRSHYREVLPATFVRLPGQWRLVQRGDPAAFRALVAQCILVCVPW 335
QY 61 DARPPPAAPSFQVSCIKELVARVLQRLCERGAKNVLAFGPALLDARGGPPFAFTTSVR 120
Db 336 DARPPPAAPSFQVSCIKELVARVLQRLCERGAKNVLAFGPALLDARGGPPFAFTTSVR 395
QY 121 SYLPNTVTDALRGSGAWGLLLRRVGDDVLVHLLARCALFVLVAPSCAYQVCGPPPLYQLGA 180

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Db 396 STLPNTVTDALRSGAWGLLRRVGDVVLHLLARCALFVLVAPSCAYQVCGPPLYQLCA 455
QY 181 ATOARPPPHASPRRLGGERAWNSVREAGVPLGLPAGARRRGSGASRSPLPKRPR 240
Db 456 ATOARPPPHASPRRLGGERAWNSVREAGVPLGLPAGARRRGSGASRSPLPKRPR 515
QY 241 GAAPPERTPVQGSWAHPGRTGRGSDRGFCVVSPPARPAEATSLEGALSGTRHSHPSVG 300
Db 516 GAAPPERTPVQGSWAHPGRTGRGSDRGFCVVSPPARPAEATSLEGALSGTRHSHPSVG 575
QY 301 ROHAGPPSTSRPPRWDTPCPVVAETHKFLYSSGDKQLPSPFLLSLRSLTGARRL 360
Db 576 ROHAGPPSTSRPPRWDTPCPVVAETHKFLYSSGDKQLPSPFLLSLRSLTGARRL 635
QY 361 VETIFLGRPMWPGTPRRLPRLPQRYWQMRPLFELLLGNHACQPYGVLLKTHCPRAAVT 420
Db 636 VETIFLGRPMWPGTPRRLPRLPQRYWQMRPLFELLLGNHACQPYGVLLKTHCPRAAVT 695
QY 421 PAAGVCAREKPGQGSVAAPPEEDTPRRLVQLLRQHSSPMQVYGFVRACLRLRVPGLMGS 480
Db 696 PAAGVCAREKPGQGSVAAPPEEDTPRRLVQLLRQHSSPMQVYGFVRACLRLRVPGLMGS 755
QY 481 RHNERFLRNTKFTSLGKHAKLSLOELTWKMSVRDCAWLRSPGVGCVPAAEHRLREBI 540
Db 756 RHNERFLRNTKFTSLGKHAKLSLOELTWKMSVRDCAWLRSPGVGCVPAAEHRLREBI 815
QY 541 LAKFLHMLMSVVVVELLSFFVVTETTFQKNRLFVRKSVWSKLOSIGIRQHLKRVQURE 600
Db 816 LAKFLHMLMSVVVVELLSFFVVTETTFQKNRLFVRKSVWSKLOSIGIRQHLKRVQURE 875
QY 601 LSEAEVRQHREARPAALLTSRLFIKPKDGLRIVNMDYVVGARTFRREKRAERLTSRVKA 660
Db 876 LSEAEVRQHREARPAALLTSRLFIKPKDGLRIVNMDYVVGARTFRREKRAERLTSRVKA 935
QY 661 LFSVLNVRARRPGLLGASVLGLDDIHRARWTFVLVRADQPPPELYFKVDVDTGAYDTI 720
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QY 721 PODRLTEVIASIIKPNQTYCVRYAVQKAAHGHVRKAFKSHVSTLTDLQPMRQFVAHL 780
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QY 841 LCSLCYGMENKLFAGIRRDGLLRLVDDFLVTPHLTHAKTFLRTLVRGVEPYGCVNVL 900
Db 1116 LCSLCYGMENKLFAGIRRDGLLRLVDDFLVTPHLTHAKTFLRTLVRGVEPYGCVNVL 1175
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Db 1236 NRGFKAGNMRKLFGLVKLCHSLFDLDQVNSLOTVCNIIYKILLQAYRPHACVLQLP 1295
QY 1021 FHOQVWKNPTFLRVIDSTASICYILKAKNAGMSLGAKGAAGPLPSEAVOMLCHQAFLL 1080
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QY 1081 KLTRHRVTYVPLGLSLRTAQTOLSKLPGTTLTALAAANPALPSDFKTILD 1132
Db 1356 KLTRHRVTYVPLGLSLRTAQTOLSKLPGTTLTALAAANPALPSDFKTILD 1407

RESULT 34

US-08-912-951-334

; Sequence 334, Application US/08912951

; Patent No. 6475789

; GENERAL INFORMATION:

APPLICANT: Cech, Thomas R.
APPLICANT: Lingner, Joachim
APPLICANT: Nakamura, Toru
APPLICANT: Chapman, Karen B.
APPLICANT: Morin, Gregg B.
APPLICANT: Harley, Calvin
APPLICANT: Andrews, William H.
TITLE OF INVENTION: HUMAN TELOMERASE CATALYTIC SUBUNIT: DIAGNOSTIC AND
TITLE OF INVENTION: THERAPEUTIC METHODS
NUMBER OF SEQUENCES: 335
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: United States of America
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/912,951
FILING DATE: 14-AUG-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002600US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 334:
SEQUENCE CHARACTERISTICS:
LENGTH: 1407 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-912-951-334

Query Match 99.8%; Score 5952; DB 4; Length 1407;
Best Local Similarity 99.8%; Fred. No. 0;
Matches 1130; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MPAPRCRAVRSLLRSHYREVLPPLATFVRRLLGPOGWRLLVQRGDPAAFRALVAQCLVCPW 60
Db 276 MPAPRCRAVRSLLRSHYREVLPPLATFVRRLLGPOGWRLLVQRGDPAAFRALVAQCLVCPW 335
QY 61 DARPPPAAPSPQVSCSKLKVRLQRLCERGAKNVLAFGFAALLDARGGPPPEAFTTSVR 120
Db 336 DARPPPAAPSPQVSCSKLKVRLQRLCERGAKNVLAFGFAALLDARGGPPPEAFTTSVR 395

Matches 1130; Conservative 1; Mismatches 1; Indels 0; Gaps 0;			
QY	1	MPRAPRCRAVRSLLRSHYREVLPATFVRLRGQGWRLVQRGDPAARALVAQCLVCPW	60
Db	276	MPRAPRCRAVRSLLRSHYREVLPATFVRLRGQGWRLVQRGDPAARALVAQCLVCPW	335
QY	61	DARPPAAPSPROVSCLEKELVARVQLRCERGAQKVLARGFALLDQARGGPPPEATTTSVR	120
Db	336	DARPPAAPSPROVSCLEKELVARVQLRCERGAQKVLARGFALLDQARGGPPPEATTTSVR	395
QY	121	SYLPTNTVDALRGSGAWGLLRVDDVLLHLLARCALFVLVAPSCAYOVCGPPPLYQLGA	180
Db	396	SYLPTNTVDALRGSGAWGLLRVDDVLLHLLARCALFVLVAPSCAYOVCGPPPLYQLGA	455
QY	181	ATOARPPPHASGPRRLGCERAMNHSVREAGVPLGLPAPGARRRGSASRSLPLKRRR	240
Db	456	ATOARPPPHASGPRRLGCERAMNHSVREAGVPLGLPAPGARRRGSASRSLPLKRRR	515
QY	241	GAAPERTPVCGSWAHGRTGRGSDRGFCVVSAPARPAEATSLGALSGTRHSHPSVG	300
Db	516	GAAPERTPVCGSWAHGRTGRGSDRGFCVVSAPARPAEATSLGALSGTRHSHPSVG	575
QY	301	ROHAGPSTSPRPPMDTPCPVVAETHKFLYSSGDKQLRPSFLLSRLSLTGARRL	360
Db	576	ROHAGPSTSPRPPMDTPCPVVAETHKFLYSSGDKQLRPSFLLSRLSLTGARRL	635
QY	361	VETIFLGRPMWPGTPRRLPRLPQRYWQMRPLFELLLGNHQAQPYGVLLKTHCPLRAAVT	420
Db	636	VETIFLGRPMWPGTPRRLPRLPQRYWQMRPLFELLLGNHQAQPYGVLLKTHCPLRAAVT	695
QY	421	PAAGVCAEKPOGSVAABEEDTPRRLVQLLRQHSHPQVYGFVRACLRLVPPGLMGS	480
Db	696	PAAGVCAEKPOGSVAABEEDTPRRLVQLLRQHSHPQVYGFVRACLRLVPPGLMGS	755
QY	481	RINERFLRNTKFFLSLGHAKLSLQELTWKMSVRDCAWLRSPGCVGCPAAEHLRBEI	540
Db	756	RINERFLRNTKFFLSLGHAKLSLQELTWKMSVRDCAWLRSPGCVGCPAAEHLRBEI	815
QY	541	LAKFLHLMSSVYVVELLSFFVYVTTTQKNLFFYRKSVMKLSQSIGIRQHLKRVQRE	600
Db	816	LAKFLHLMSSVYVVELLSFFVYVTTTQKNLFFYRKSVMKLSQSIGIRQHLKRVQRE	875
QY	601	LSEAVRQHREARPAALLTSRLRFPKPDGLRPIVNMVYVVGARTFRREKRAERLTSRVKA	660
Db	876	LSEAVRQHREARPAALLTSRLRFPKPDGLRPIVNMVYVVGARTFRREKRAERLTSRVKA	935
QY	661	LFSVLNYERARPPGLGASVLGLDDIHRARWTFVLVRAQDPPPELYFVKVDVTGAYDTI	720
Db	936	LFSVLNYERARPPGLGASVLGLDDIHRARWTFVLVRAQDPPPELYFVKVDVTGAYDTI	995
QY	721	PODLRTEVTASIIKQNTYCVRRYAVVQAAHGHVKAQKSHVSTLTLDQPMRQFVAHL	780
Db	996	PODLRTEVTASIIKQNTYCVRRYAVVQAAHGHVKAQKSHVSTLTLDQPMRQFVAHL	1055
QY	781	QTSPLRDAVVIQSSSLEASGLDFVFLRPMCHHAVIRGKSVYVQCGIPQGSILSTL	840
Db	1056	QTSPLRDAVVIQSSSLEASGLDFVFLRPMCHHAVIRGKSVYVQCGIPQGSILSTL	1115
QY	841	LCSLCYGDMEKLPAGIRDDGLLLRLVDDFLVTPHLLTHAKTFLRLVRGVEYCVNVL	900
Db	1116	LCSLCYGDMEKLPAGIRDDGLLLRLVDDFLVTPHLLTHAKTFLRLVRGVEYCVNVL	1175
QY	901	RKTVNVFVDEALGATFVQMPAGLPPWCGLLDTRTLEVSQSYSSVARTSIRASLTF	960
Db	1176	RKTVNVFVDEALGATFVQMPAGLPPWCGLLDTRTLEVSQSYSSVARTSIRASLTF	1235
QY	961	NRGFAGRNMRRLFGVLRLLKCHSLFDLQVNSLQTVCTNIYKILLQAYRFHACVQLP	1020
Db	1236	NRGFAGRNMRRLFGVLRLLKCHSLFDLQVNSLQTVCTNIYKILLQAYRFHACVQLP	1295
QY	1021	FHQQVWKNPFTFLRIVISDTASLCYSILKAKNAGMSLGAKGAGPLPSEAVQWLCHQAFLL	1080
Db	1296	FHQQVWKNPFTFLRIVISDTASLCYSILKAKNAGMSLGAKGAGPLPSEAVQWLCHQAFLL	1355

QY 1081 KLTRHRTVTVPLGLSLRTAQTSKRLPGTTLTALAAAAANPALPSDFKTILD 1132
Db 1356 KLTRHRTVTVPLGLSLRTAQTSKRLPGTTLTALAAAAANPALPSDFKTILD 1407

RESULT 36

US-09-721-456-628
; Sequence 628, Application US/09721456
; Patent No. 6617110

GENERAL INFORMATION:

APPLICANT: Cech, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin B.
Andrews, William H.

TITLE OF INVENTION: Human Telomerase Catalytic Subunit
NUMBER OF SEQUENCES: 727
CORRESPONDENCE ADDRESS:

ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/721,456
FILING DATE: 22-NOV-1997
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/974,549A
FILING DATE: 19-NOV-1997
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/911,312
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: WO PCT/US97/17618
FILING DATE: 01-OCT-1997
APPLICATION NUMBER: WO PCT/US97/17885
FILING DATE: 01-OCT-1997

ATTORNEY/AGENT INFORMATION:

NAME: Apple, Randolph Ted
REGISTRATION NUMBER: 36,429

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300

SEQUENCE CHARACTERISTICS:

LENGTH: 1407 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: protein

379 VETIFLGRPMWPGTFRRLPRLPQRYWQWPLFLELLGNHQAQCPYGVLLKTHCLPLRAAVT 438
421 PAAGVCAREKPGSGVAAPDEEDTDRRLVOLLROHSSPMOVYGFVRACLRRLVPPGLMGS 480
439 PAAGVCAREKPGSGVAAPDEEDTDRRLVOLLROHSSPMOVYGFVRACLRRLVPPGLMGS 498
481 RHNERFLRNTKFTISLGHAKLSLQELTWKMSVRDCAWLRSPGVGCVPAAEHLRBEI 540
499 RHNERFLRNTKFTISLGHAKLSLQELTWKMSVRDCAWLRSPGVGCVPAAEHLRBEI 558
541 LAKFLHLMVSVVVELLSFFVYTTTQKNLFFYRKSVWSKLOSIGIRQHLLKRVQURE 600
559 LAKFLHLMVSVVVELLSFFVYTTTQKNLFFYRKSVWSKLOSIGIRQHLLKRVQURE 618
601 LSEAEVROHREARPAALLTSRLRFIPKPGDLRPIVNMVYVVGARTFRREKRAERLTSRVKA 660
619 LSEAEVROHREARPAALLTSRLRFIPKPGDLRPIVNMVYVVGARTFRREKRAERLTSRVKA 678
661 LFSVLNTERARRPGLLGASVLGLDDIHRARWTFVLVRQAQDPPPELYFKVDVTCAYDTI 720
679 LFSVLNTERARRPGLLGASVLGLDDIHRARWTFVLVRQAQDPPPELYFKVDVTCAYDTI 738
721 PODRLTEVIASIIKQNTYCVRRYAVQKAHGHVRKAFKSHVSTLTDLQPMRQFVAHL 780
739 PODRLTEVIASIIKQNTYCVRRYAVQKAHGHVRKAFKSHVSTLTDLQPMRQFVAHL 798
781 QSTSLRDAVTEQSSNEASSGLPDLFLRPMCHHVRIRGKSVVQCGIPQGSILSTL 840
799 QSTSLRDAVTEQSSNEASSGLPDLFLRPMCHHVRIRGKSVVQCGIPQGSILSTL 858
841 LCSCYGMENKLFAGIRRDGLLLRLVDDFLVTPHLLTHAKTFLRTLVRGVPEYGCVVNL 900
859 LCSCYGMENKLFAGIRRDGLLLRLVDDFLVTPHLLTHAKTFLRTLVRGVPEYGCVVNL 918
901 RKTVPNPFVEBALGGTAFVQMPANGLFPWCGLLDDTRTLEVQSDYSYVARTSIRASLTF 960
919 RKTVPNPFVEBALGGTAFVQMPANGLFPWCGLLDDTRTLEVQSDYSYVARTSIRASLTF 978
961 NRGFKAGNMRKLGVLRLKCHSLFLDLQVNSLQTVCTNIYKILLQAYRPHACVLOLP 1020
979 NRGFKAGNMRKLGVLRLKCHSLFLDLQVNSLQTVCTNIYKILLQAYRPHACVLOLP 1038
1021 FHOQWKNPTFLRIVISDTASLCYILKAKNAGMSLGAKGAGPLPSEAVQWLCHQAFLL 1080
1039 FHOQWKNPTFLRIVISDTASLCYILKAKNAGMSLGAKGAGPLPSEAVQWLCHQAFLL 1098
1081 KLTRHRTVTVPLGLSLRTAQTLQSLKLPFTTL-----TALEAANPAL 1123
1099 KLTRHRTVTVPLGLSLRTGKYAASEAPGDDADCPGGRSQPGTALRLQDHPGL 1151

RESULT 38
US-08-974-549A-5
; Sequence 5, Application US/08974549A
; Patent No. 6166178
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; APPLICANT: Lingner, Joachim
; APPLICANT: Nakamura, Toru
; APPLICANT: Chapman, Karen B.
; APPLICANT: Morin, Gregg B.
; APPLICANT: Harley, Calvin B.
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: Human Telomerase Catalytic Subunit
; NUMBER OF SEQUENCES: 727
; CORRESPONDENCE ADDRESS:
; ADDRESS: Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/974,549A
; FILING DATE: 19-NOV-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/851,843
; FILING DATE: 06-MAY-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/854,050
; FILING DATE: 09-MAY-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/911,312
; FILING DATE: 14-AUG-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/912,951
; FILING DATE: 14-AUG-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/915,503
; FILING DATE: 14-AUG-1997
; APPLICATION NUMBER: WO PCT/US97/17618
; FILING DATE: 01-OCT-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/US97/17885
; FILING DATE: 01-OCT-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph Ted
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-002610US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 807 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-974-549A-5

Query Match 68.0%; Score 4052; DB 3; Length 807;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 763; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPRAPRCRAVRSLLRSHYREVLPATFVRRILGPQGWRLVQRGDPAAFRALVAQCLVCPW 60
Db 1 MPRAPRCRAVRSLLRSHYREVLPATFVRRILGPQGWRLVQRGDPAAFRALVAQCLVCPW 60
QY 61 DAREPPAAPSPROVSCIKELVARVLQRLCERCAKNVLAFGFALLDARGGPEAFTTSVR 120
Db 61 DAREPPAAPSPROVSCIKELVARVLQRLCERCAKNVLAFGFALLDARGGPEAFTTSVR 120
QY 121 SYLNTVTTDALRGSGAWGLLRRVDDVLLHLLARCALFVLVAPSCAYQVCGPPPLYQLGA 180
Db 121 SYLNTVTTDALRGSGAWGLLRRVDDVLLHLLARCALFVLVAPSCAYQVCGPPPLYQLGA 180
QY 181 ATQARPPPHASGPRRRLLGCERAMNHSVREAGVPLGLPAGARRRGGSASRSLPLPKRPR 240
Db 181 ATQARPPPHASGPRRRLLGCERAMNHSVREAGVPLGLPAGARRRGGSASRSLPLPKRPR 240

QY 241 GAAPEPRTVPGQSWAHPTGTRGSDRGFCVSPARPAEATSLGALSCTRSHSPSVG 300
Db 241 GAAPEPRTVPGQSWAHPTGTRGSDRGFCVSPARPAEATSLGALSCTRSHSPSVG 300
QY 301 ROHAGPSTSRPPRPWDTPCPVVAETKHFYSSGDKQLRPSFLSSLRPSLTGARRL 360
Db 301 ROHAGPSTSRPPRPWDTPCPVVAETKHFYSSGDKQLRPSFLSSLRPSLTGARRL 360
QY 361 VETIFLGSRPMPGTPRRLPRLPQRYWQMRPLFLELLGNHAQCPYGVLLKTHCPRAAVT 420
Db 361 VETIFLGSRPMPGTPRRLPRLPQRYWQMRPLFLELLGNHAQCPYGVLLKTHCPRAAVT 420
QY 421 PAAGVCAREKPGQSWAAPEEDTDPRLVQLLRQHSSPWQYGVFVRACLRRLVPPGLWGS 480
Db 421 PAAGVCAREKPGQSWAAPEEDTDPRLVQLLRQHSSPWQYGVFVRACLRRLVPPGLWGS 480
QY 481 RHNERFLRNTKFPISLGKHAQLSLQELTWKMSVRDCAWLRRSPGVGCVPAEHLRREEI 540
Db 481 RHNERFLRNTKFPISLGKHAQLSLQELTWKMSVRDCAWLRRSPGVGCVPAEHLRREEI 540
QY 541 LAKFLHMLMSVYVVELLSFFVTTTQKNRLFYRKSVMKLSQSIGIRQHLKRVQLRE 600
Db 541 LAKFLHMLMSVYVVELLSFFVTTTQKNRLFYRKSVMKLSQSIGIRQHLKRVQLRE 600
QY 601 LSEAEVRQHRREARPAALLTSRLRFPKPDGLRPIVMMDYVVGARTFRREKRAERLTSRVKA 660
Db 601 LSEAEVRQHRREARPAALLTSRLRFPKPDGLRPIVMMDYVVGARTFRREKRAERLTSRVKA 660
QY 661 LFSVLNYERARRPGLGASVLGLDDIHRAWRTFVLRVQAQPPPELYFVKVDVTGAYDTI 720
Db 661 LFSVLNYERARRPGLGASVLGLDDIHRAWRTFVLRVQAQPPPELYFVKVDVTGAYDTI 720
QY 721 PQDRLETVIASIIRKQNTYCYVRRYAVVQKAAHGHVRKAFKSHV 763
Db 721 PQDRLETVIASIIRKQNTYCYVRRYAVVQKAAHGHVRKAFKSHV 763

RESULT 39
US-08-912-951-5
; Sequence 5, Application US/08912951
; Patent No. 6475789
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; APPLICANT: Lingner, Joachim
; APPLICANT: Nakamura, Toru
; APPLICANT: Chapman, Karen B.
; APPLICANT: Morin, Gregg B.
; APPLICANT: Harley, Calvin
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: HUMAN TELOMERASE CATALYTIC SUBUNIT: DIAGNOSTIC AND
; THERAPEUTIC METHODS
; NUMBER OF SEQUENCES: 335
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/912,951
; FILING DATE: 14-AUG-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/854,050
; FILING DATE: 09-MAY-1997
; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/851,843
; FILING DATE: 06-MAY-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph T.
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-002600US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 807 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-912-951-5
Query Match 68.0%; Score 4052; DB 4; Length 807;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 763; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MPRAPRCRAVRSLLRSHYREVLPATFVRRLPGQWELVORGDPAAFRALVAQCCLVCPWM 60
Db 1 MPRAPRCRAVRSLLRSHYREVLPATFVRRLPGQWELVORGDPAAFRALVAQCCLVCPWM 60
QY 61 DARPPPAAPSFROVSCIKELVARVLQRLCERGAKNVLAFFGALLDARGGPEAFTTSVR 120
Db 61 DARPPPAAPSFROVSCIKELVARVLQRLCERGAKNVLAFFGALLDARGGPEAFTTSVR 120
QY 121 SYLPNTVTDALRGSGAWGLLLRRVGGDDVLVHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180
Db 121 SYLPNTVTDALRGSGAWGLLLRRVGGDDVLVHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180
QY 181 ATQARPPPHASGPRRLGRCERAMNHSVREAGVPLGLPAPGARRRGGSASRLPLPKRPRR 240
Db 181 ATQARPPPHASGPRRLGRCERAMNHSVREAGVPLGLPAPGARRRGGSASRLPLPKRPRR 240
QY 241 GAAPEPRTVPGQSWAHPTGTRGSDRGFCVSPARPAEATSLGALSCTRSHSPSVG 300
Db 241 GAAPEPRTVPGQSWAHPTGTRGSDRGFCVSPARPAEATSLGALSCTRSHSPSVG 300
QY 301 ROHAGPSTSRPPRPWDTPCPVVAETKHFYSSGDKQLRPSFLSSLRPSLTGARRL 360
Db 301 ROHAGPSTSRPPRPWDTPCPVVAETKHFYSSGDKQLRPSFLSSLRPSLTGARRL 360
QY 361 VETIFLGSRPMPGTPRRLPRLPQRYWQMRPLFLELLGNHAQCPYGVLLKTHCPRAAVT 420
Db 361 VETIFLGSRPMPGTPRRLPRLPQRYWQMRPLFLELLGNHAQCPYGVLLKTHCPRAAVT 420
QY 421 PAAGVCAREKPGQSWAAPEEDTDPRLVQLLRQHSSPWQYGVFVRACLRRLVPPGLWGS 480
Db 421 PAAGVCAREKPGQSWAAPEEDTDPRLVQLLRQHSSPWQYGVFVRACLRRLVPPGLWGS 480
QY 481 RHNERFLRNTKFPISLGKHAQLSLQELTWKMSVRDCAWLRRSPGVGCVPAEHLRREEI 540
Db 481 RHNERFLRNTKFPISLGKHAQLSLQELTWKMSVRDCAWLRRSPGVGCVPAEHLRREEI 540
QY 541 LAKFLHMLMSVYVVELLSFFVTTTQKNRLFYRKSVMKLSQSIGIRQHLKRVQLRE 600
Db 541 LAKFLHMLMSVYVVELLSFFVTTTQKNRLFYRKSVMKLSQSIGIRQHLKRVQLRE 600

Db 541 LAKFLHLMSSVYVVELLSFFVYVTTTQKNRLFYRKSVMSKLSQSIGIRHQLKRVQLRE 600
QY 601 LSEAEVRQREARPAALLSRLEFIPKPDGLRPIVNMDDYVVGARTFRREKRAERLTSRVKA 660
Db 601 LSEAEVRQREARPAALLSRLEFIPKPDGLRPIVNMDDYVVGARTFRREKRAERLTSRVKA 660
QY 661 LFSVLNTERARRPGLLGASVLGLDDIHRAWRTFVLVRVAQDPPPELYFVKVDVTGAYDTI 720
Db 661 LFSVLNTERARRPGLLGASVLGLDDIHRAWRTFVLVRVAQDPPPELYFVKVDVTGAYDTI 720
QY 721 PDRLTEVIASIIKPQNTYCVRRYAVVQAAHGHVRKAFKSHV 763
Db 721 PDRLTEVIASIIKPQNTYCVRRYAVVQAAHGHVRKAFKSHV 763

RESULT 40

US-09-402-181B-5
; Sequence 5, Application US/09402181B
; Patent No. 6610839
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; ; Lingner, Joachim
; ; Nakamura, Toru
; ; Chapman, Karen B.
; ; Morin, Gregg B.
; ; Harley, Calvin B.
; ; Andrews, William H.
; TITLE OF INVENTION: Human Telomerase Catalytic Subunit
; NUMBER OF SEQUENCES: 633
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/402,181B
; FILING DATE: 29-Sep-1997
; CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; APPLICATION NUMBER: US 08/851,843
; FILING DATE: 06-MAY-1997
; APPLICATION NUMBER: US 08/854,050
; FILING DATE: 09-MAY-1997
; APPLICATION NUMBER: US 08/911,312
; FILING DATE: 14-AUG-1997
; APPLICATION NUMBER: US 08/912,951
; FILING DATE: 14-AUG-1997
; APPLICATION NUMBER: US 08/915,503
; FILING DATE: 14-AUG-1997
; APPLICATION NUMBER: WO PCT/US97/17885
; FILING DATE: 01-OCT-1997

ATTORNEY/AGENT INFORMATION:
; NAME: Ausenhus, Scott L.
; REGISTRATION NUMBER: 42,271
; REFERENCE/DOCKET NUMBER: 015389-00262005
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:

; LENGTH: 807 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-09-402-181B-5

Query Match 68.0%; Score 4052; DB 4; Length 807;

Best Local Similarity 100.0%; Pred. No. 0;
Matches 763; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPRAPRCBAVRSLLRSHYREVLPPLATFVRRLLGPOGWRVLVQRGDDPAAFALVAQCILVCVPM 60
Db 1 MPRAPRCBAVRSLLRSHYREVLPPLATFVRRLLGPOGWRVLVQRGDDPAAFALVAQCILVCVPM 60
QY 61 DARPPPAAPSPROVSCLELVARVLRQRCERGAKNVLAFFGALLDARGGPPPEAFTTSVR 120
Db 61 DARPPPAAPSPROVSCLELVARVLRQRCERGAKNVLAFFGALLDARGGPPPEAFTTSVR 120
QY 121 SYLPTNTVDALRGSGANGLLRRVGGDDVLVHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180
Db 121 SYLPTNTVDALRGSGANGLLRRVGGDDVLVHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180
QY 181 ATQARPPPHASGPRRRRLGGERAWNHSVREAGVPLGLPAPGARRRGGSASRSLPLPKRPRR 240
Db 181 ATQARPPPHASGPRRRRLGGERAWNHSVREAGVPLGLPAPGARRRGGSASRSLPLPKRPRR 240
QY 241 GAAPERTPVQGSWAHPGRTGRGFCVSPARPAEATSLLEGALSCTRSHSPSVG 300
Db 241 GAAPERTPVQGSWAHPGRTGRGFCVSPARPAEATSLLEGALSCTRSHSPSVG 300
QY 301 RQHHAGPSTSRPPMDTPCPVYAEYTKHFLYSYGKQELRPSFLSSLRPSLTGARRL 360
Db 301 RQHHAGPSTSRPPMDTPCPVYAEYTKHFLYSYGKQELRPSFLSSLRPSLTGARRL 360
QY 361 VETIFLGSRPMPGTPRRRLPRLPQRYQWRPLFLELLGNHQAQCPYGVLLKTHCPRAAVT 420
Db 361 VETIFLGSRPMPGTPRRRLPRLPQRYQWRPLFLELLGNHQAQCPYGVLLKTHCPRAAVT 420
QY 421 PAAGVCAREKPGQSVAAPEEEDTPRRLVQLRQHSPPQVYGVFVACRLRLVPPGLWGS 480
Db 421 PAAGVCAREKPGQSVAAPEEEDTPRRLVQLRQHSPPQVYGVFVACRLRLVPPGLWGS 480
QY 481 RHNERRFLRNTKFIISLGKHAQLSIQELTWKMSVRDCAWLRSPGVCVPAAEHLRBEI 540
Db 481 RHNERRFLRNTKFIISLGKHAQLSIQELTWKMSVRDCAWLRSPGVCVPAAEHLRBEI 540
QY 541 LAKFLHLMSSVYVVELLSFFVYVTTTQKNRLFYRKSVMSKLSQSIGIRHQLKRVQLRE 600
Db 541 LAKFLHLMSSVYVVELLSFFVYVTTTQKNRLFYRKSVMSKLSQSIGIRHQLKRVQLRE 600
QY 601 LSEAEVRQREARPAALLSRLEFIPKPDGLRPIVNMDDYVVGARTFRREKRAERLTSRVKA 660
Db 601 LSEAEVRQREARPAALLSRLEFIPKPDGLRPIVNMDDYVVGARTFRREKRAERLTSRVKA 660
QY 661 LFSVLNTERARRPGLLGASVLGLDDIHRAWRTFVLVRVAQDPPPELYFVKVDVTGAYDTI 720
Db 661 LFSVLNTERARRPGLLGASVLGLDDIHRAWRTFVLVRVAQDPPPELYFVKVDVTGAYDTI 720
QY 721 PDRLTEVIASIIKPQNTYCVRRYAVVQAAHGHVRKAFKSHV 763
Db 721 PDRLTEVIASIIKPQNTYCVRRYAVVQAAHGHVRKAFKSHV 763

RESULT 41

US-09-721-456-5
; Sequence 5, Application US/09721456
; Patent No. 6617110
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; ; Lingner, Joachim
; ; Nakamura, Toru
; ; Chapman, Karen B.

Morin, Gregg B.
Harley, Calvin B.
Andrews, William H.
TITLE OF INVENTION: Human Telomerase Catalytic Subunit
NUMBER OF SEQUENCES: 727
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/721,456
FILING DATE: 22-NOV-1997
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/974,549A
FILING DATE: 19-NOV-1997
APPLICATION NUMBER: US/08/724,643
FILING DATE: 01-OCT-1996
APPLICATION NUMBER: US/08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US/08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US/08/851,843
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US/08/854,050
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US/08/911,312
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US/08/912,951
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US/08/915,503
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: WO PCT/US97/17618
FILING DATE: 01-OCT-1997
APPLICATION NUMBER: WO PCT/US97/17885
FILING DATE: 01-OCT-1997

ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph Ted
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002610US
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300

INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 807 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 5:

Query Match 68.0%; Score 4052; DB 4; Length 807;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 763; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 MPRAPCRAVRLSLRSHRYEVLPLATFVRRLLGPGQWRVLRQGDPAAFRALVAQCLVCPW 60
1 MPRAPCRAVRLSLRSHRYEVLPLATFVRRLLGPGQWRVLRQGDPAAFRALVAQCLVCPW 60
61 DARPPAAPSPROVSLCKELVARVLQRLCEGAKNVLAFGALLDARGGPPPEAFTTSVR 120
61 DARPPAAPSPROVSLCKELVARVLQRLCEGAKNVLAFGALLDARGGPPPEAFTTSVR 120
121 SYLPNTVTDALRGSGAWGLLLRRVGGDDVLVHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180

Db 121 SYLPNTVTDALRGSGAWGLLLRRVGGDDVLVHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180
Qy 181 ATQARPPPHASGRRRLGRCERAWNHSVREAGVPLGLPAPGARRRRGSSASRLPLPKPRR 240
Db 181 ATQARPPPHASGRRRLGRCERAWNHSVREAGVPLGLPAPGARRRRGSSASRLPLPKPRR 240
Qy 241 GAAPPERTPVGGSWAHQTRGPGSDRGFCVVSPPARPAEATSLGALSSTRHSHPSVG 300
Db 241 GAAPPERTPVGGSWAHQTRGPGSDRGFCVVSPPARPAEATSLGALSSTRHSHPSVG 300
Qy 301 ROHHAGPPSTSRPRPMDTPCPVYAEKTHFLYSSGDKQLRPSFLSSLRPSLTGARRL 360
Db 301 ROHHAGPPSTSRPRPMDTPCPVYAEKTHFLYSSGDKQLRPSFLSSLRPSLTGARRL 360
Qy 361 VETIFLGSRRPMPGTPRRLLPRLPQRYQWMPRLFLLELLGNHAQCPYGVLLKTHCPLRAAVT 420
Db 361 VETIFLGSRRPMPGTPRRLLPRLPQRYQWMPRLFLLELLGNHAQCPYGVLLKTHCPLRAAVT 420
Qy 421 PAAGVCAREKPGQSVAAPEEEDTPRRLVOLLROHSSPWQYGVFVRACTLRRLVPPGLWGS 480
Db 421 PAAGVCAREKPGQSVAAPEEEDTPRRLVOLLROHSSPWQYGVFVRACTLRRLVPPGLWGS 480
Qy 481 RHNERRELRNTKXFIISGKHAKLSLOELTWKMSVRDCAWLRSSPGVGCVPAAEHLREEI 540
Db 481 RHNERRELRNTKXFIISGKHAKLSLOELTWKMSVRDCAWLRSSPGVGCVPAAEHLREEI 540
Qy 541 LAKFLHLMSSVYVVELLRSFFYVTTTTFQKNRFFYFKSVMSKLSQISGIRQHLKRVQLRE 600
Db 541 LAKFLHLMSSVYVVELLRSFFYVTTTTFQKNRFFYFKSVMSKLSQISGIRQHLKRVQLRE 600
Qy 601 LSEAEVRQHREARPAALTSRLRIPKPDGLRPIVNMDDYVVGARTFPRKKAERLTSRVKA 660
Db 601 LSEAEVRQHREARPAALTSRLRIPKPDGLRPIVNMDDYVVGARTFPRKKAERLTSRVKA 660
Qy 661 LFSVLNYERARRPGLLGASVLGLDDIHRAWRTFVLVRADODPPPELYFVKVDVTGAYDTI 720
Db 661 LFSVLNYERARRPGLLGASVLGLDDIHRAWRTFVLVRADODPPPELYFVKVDVTGAYDTI 720
Qy 721 PQDLTEVIASIIKPQNTYCVRRYAVVQKAAHGHVRKAFKSHV 763
Db 721 PQDLTEVIASIIKPQNTYCVRRYAVVQKAAHGHVRKAFKSHV 763

RESULT 42

US-08-851-843A-217
Sequence 217, Application US/08851843A
Patent No. 6093809
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
APPLICANT: Lingner, Joachim
APPLICANT: Nakamura, Toru
APPLICANT: Chapman, Karen B.
APPLICANT: Morin, Gregg B.
APPLICANT: Harley, Calvin
APPLICANT: Andrews, William H.
TITLE OF INVENTION: No. 6093809el Telomerase
NUMBER OF SEQUENCES: 225
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: United States of America
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/851,843A
FILING DATE: 06-MAY-1997

QY	732	IIKPONTYCVRRYAVVQKAAHGHVRKAFKSHVSTLTDLQPYMRQFVAHLQETSPLRDAVV	79
DB	603	IIKPONTYCVRRYAVVQKAAHGHVRKAFKSHVSTLTDLQPYMRQFVAHLQXNSPLRDAVV	662
QY	792	IEQSSSINEASSGLFDVFLPMCHHVRIRGKSVQCOGIPQSGIILSTLLCSLCYGDME	851
DB	663	IEQSSSINEASSGLFDVFLPMCHHVRIRGKSVQCOGIPQSGIILSTLLCSLCYGDME	722
QY	852	KLFIAGIRRDGLLLRLVDDFLVTPHLLTHAKTFLRTLVGRVPEYGVVNLKTKTVNFPVED	911
DB	723	KLFIAGIRRDGLLLRLVDDFLVTPHLLTHAKTFLRTLVGRVPEYGVVNLKTKTVNFPVED	762
QY	912	EALGGTAFVQMPAHGLPPWCGLLDTRTLEVSQSDYSYARTSTRASITFNRGPKAGNMR	971
DB	783	EALGGTAFVQMPAHGLPPWCGLLDTRTLEVSQSDYSYARTSTRASITFNRGPKAGNMR	842
QY	972	RKLFVGLRLKCHSLFLDLQVNSLQTVCTNLYKILLQAVRFHACVLQLPHQOQWKNPTF	103
DB	843	RKLFVGLRLKCHSLFLDLQVNSLQTVCTNLYKILLQAVRFHACVLQLPHQOQWKNPTF	902
QY	1032	FLRVIDTASLCYSILKAKNAGSLGAKGAAGPLPSEAVQWLCHQAFLLKLTFRHRTVYVP	109
DB	903	FLRVIDTASLCYSILKAKNAGSLGAKGAAGPLPSEAVQWLCHQAFLLKLTFRHRTVYVP	962
QY	1092	LLGSLRTAQQLSRKLPGLTTLTALAANAANPALPSDFKTILD	1132
DB	963	LLGSLRTAQQLSRKLPGLTTLTALAANAANPALPSDFKTILD	1003
RESULT 43			
US-08-974-549A-336			
; Sequence 336, Application US/08974549A			
; Patent No. 6166178			
; GENERAL INFORMATION:			
; APPLICANT: Cech, Thomas R.			
; APPLICANT: Lingner, Joachim			
; APPLICANT: Nakamura, Toru			
; APPLICANT: Chapman, Karen B.			
; APPLICANT: Morin, Gregg B.			
; APPLICANT: Harley, Calvin B.			
; APPLICANT: Andrews, William H.			
; TITLE OF INVENTION: Human Telomerase Catalytic Subunit			
; NUMBER OF SEQUENCES: 727			
; CORRESPONDENCE ADDRESS:			
; ADDRESSEE: Townsend and Townsend and Crew LLP			
; STREET: Two Embarcadero Center, Eighth Floor			
; CITY: San Francisco			
; STATE: California			
; COUNTRY: USA			
; ZIP: 94111-3834			
; COMPUTER READABLE FORM:			
; MEDIUM TYPE: Floppy disk			
; COMPUTER: IBM PC compatible			
; OPERATING SYSTEM: PC-DOS/MS-DOS			
; SOFTWARE: Patent In Release #1.0, Version #1.30			
; CURRENT APPLICATION DATA:			
; APPLICATION NUMBER: US/08/974,549A			
; FILING DATE: 19-NOV-1997			
; CLASSIFICATION: 536			
; PRIOR APPLICATION DATA:			
; APPLICATION NUMBER: US 08/724,643			
; FILING DATE: 01-OCT-1996			
; PRIOR APPLICATION DATA:			
; APPLICATION NUMBER: US 08/844,419			
; FILING DATE: 18-APR-1997			
; PRIOR APPLICATION DATA:			
; APPLICATION NUMBER: US 08/846,017			
; FILING DATE: 25-APR-1997			
; PRIOR APPLICATION DATA:			
; APPLICATION NUMBER: US 08/851,843			
; FILING DATE: 06-MAY-1997			
; PRIOR APPLICATION DATA:			
; APPLICATION NUMBER: US 08/854,050			

Query Match	64.1%	Score 3819.5;	DB 3;	Length 1003;
Best Local Similarity	78.7%;	Pred. No. 0;		
Matches 788;	Conservative 23;	Mismatches 123;	Indels 67;	Gaps 18;
Qy	163	APS-CAVQVCGPPLYQLGAAQTQARPPHAGSGPRRL-----GCERAWNHSHVRAGVPLG	215	
Db	39	APTXCAGRC-----TSBALXLRP-----GPRHILXDPXASGIORAWNHSHVRAGVPLG	87	
Qy	216	LPAPGARRGGGASRSLPLPKPR- RGAAPERT--PVGQSWAHPGQTR-GFSDRGFC	271	
Db	88	CQ---PRVRGGAGVPAEVCRCPRGPGVALPLSRSGRPLGRG---PGFTRAGRLDR-VT	139	
Qy	272	VVS-----PAP-----AREATSEALSGTRHSHPSVCRQ--HAGPSTSRP	313	
Db	140	VSVWCHLPDPKPKPLMRVSLRATRPHWAASTTRAPHRHGHVHGLALFGVRR-	198	
Qy	314	PREWDTPCPVVAETKHFLYSGDKQLRPSLLSLRPSLTGARRLVETITFLGSRPWP	373	
Db	199	----DQALPLLRQXHC-----XPPSYSI-YLRPSLTGVREVRGDXLSGRPWP	244	
Qy	374	GTPRRLPLRQRYWQMRPLFLELLGNHAQCYPGVLLK--THCPLRAAVTPAAGVCAREK	431	
Db	245	GFPAGCPACPSXTKGCGPCFWSCLGTRTSAPTGCSSRRRTARCELRSPPQPVVS--VPGRSP	302	
Qy	432	QGSVAPEEDTDPRLVOLLRQHSSPWQYGFVRACLRLVPPGLWGRNRRFLANT	491	
Db	303	RALWRPFRNRNTDPRLLVOLLRQHSSPWQYGFVRACLRLVPPGLWGRNRRFLANT	362	
Qy	492	KKFISLGKIAKLSQBLTWKMSVRDCAWLRRSPGVGCVPAABHRLREILAKFLHLMV	551	
Db	363	KKFISLGKIAKLSQBLTWKMSVRDCAWLRRSPGVGCVPAABHRLREILAKFLHLMV	422	
Qy	552	YVVELLRSPFYVTTTFQKNRLFVYKKSVMKLSQSIGIRQHLKRVOLRELSEAEVRQHRE	611	
Db	423	YVVELLRSPFYVTTTFQKNRLFVYKKSVMKLSQSIGIRQHLKRVOLRELSEAEVRQHRE	482	
Qy	612	ARPALTSRLRFTPKPDGRLPIVNDYVVGARTFREKRAELTTSRVKALFVNLNFERAR	671	
Db	483	ARPALTSRLRFTPKPDGRLPIVNDYVVGARTFREKRAELTTSRVKALFVNLNFERAR	542	
Qy	672	RPGLLGASVLGLDDIHRAWRTFVLVRAQDPPPELVFKVDVTGAYDTIPQDRLTEVIAS	731	

CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002930US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 217:
SEQUENCE CHARACTERISTICS:
LENGTH: 1003 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-854-050-217

Query Match 64.1%; Score 3819.5; DB 3; Length 1003;
Best Local Similarity 78.7%; Pred. No. 0;
Matches 788; Conservative 23; Mismatches 123; Indels 67; Gaps 18;

QY 163 APS-CAYQVCGPPLYQLGAATQARPPHAGSRRRL-----GGERAWNHSVREAGVPLG 215
DB 39 APTXCAGRRCC-----TSSALXLRP-----GPRHTLXDPXASGIQORAWNHSVREAGVPLG 87
QY 216 LPAGARRGGSASRLPLPKRPR-rgaaPEERT--PVGQSWAHPGKTR-GPSDRGFC 271
DB 88 CQ---PRVGGAGAVPAEVCRCPRGPGVALPLSRGRLGRG---PGPTRAGRLDR-VT 139
QY 272 VVS-----PAP-----AEEATSEALSGTRSHSPVGRQ--HAGAPSTSRP 313
DB 140 VVSVMCHLPDPKPKPLNRVRLARATPHWAASTTRAPHRHGHVGHLSGVR-- 198
QY 314 PRPWPTCPVVAETKFLYSGDKEQRLSPSLSLRPSLTGARRLVETIFLGSRRPWP 373
DB 199 ---DOALPLLRQXHC-----XPPSVSI-YLPSLTGVREVRGDXLSGSRPWP 244
QY 374 GTPRLRLPQRYWQMRPLFLELGNHAQCPVGVLLK--THCPLRAAVTPAAGVCAREK 431
DB 245 GPPAGCAPCPSXGKCGCFWSCGLGTRSAPTGCSRRRTARCELSPQOPVS--VPGRSP 302
QY 432 QGSVAAPBEEDTDRLLVQLRQHSPPQVYGFVACLRRLVPPGLWGRHNERFLRNT 491
DB 303 RALWRPPRRNTDRLLVQLRQHSPPQVYGFVACLRRLVPPGLWGRHNERFLRNT 362
QY 492 KKFISLGHKAKLSQELTWKMSVRDCAWLRSPGVGCVPAAEHRLREELAKFLHLMV 551
DB 363 KKFISLGHKAKLSQELTWKMSVRDCAWLRSPGVGCVPAAEHRLREELAKFLHLMV 422
QY 552 YVVELLRFFVYTTTFOQNRLLFFVYKSVWSKLQSIGIRQHLKRVOLRELSEAEVQHRE 611
DB 423 YVVELLRFFVYTTTFOQNRLLFFVYKSVWSKLQSIGIRQHLKRVOLRELSEAEVQHRE 482
QY 612 APALLTSLRLPIPKPDGLRPIVNNDYVVGARTPREKRAELTGRVVALPSVLNVERAR 671
DB 493 APALLTSLRLPIPKPDGLRPIVNNDYVVGARTPREKRAELTGRVVALPSVLNVERAR 542
QY 672 RPLLGASVLGDDTHRAWRTPVLAVRAQDPPPELYFVKVDVGTGAYDTIPQDLRTEVIAS 731
DB 543 RPLLGASVLGDDTHRAWRTPVLAVRAQDPPPELYFVKVDVGTGAYDTIPQDLRTEVIAS 602
QY 732 IIPQNTYCVRYAVVQAAHGHVRKAFKSHVSTLTLDLPYMRQFVAHLQETSPILRDVAV 791
DB 603 IIPQNTYCVRYAVVQAAHGHVRKAFKSHVSTLTLDLPYMRQFVAHLQXNSPLRDVAV 662
QY 792 IEQSSSLNEASGLPDLVFLRFMCHAVIRGKSVYVQCGIPQGSILSTLLCSLCYGDVME 851
DB 663 IEQSSSLNEASGLPDLVFLRFMCHAVIRGKSVYVQCGIPQGSILSTLLCSLCYGDVME 722

QY 852 KLFAGIRDRGLLRVDDFLVTPHLTHAKTFLRTRVGVPEYGCVVNLRTKTVNFPVED 911
DB 723 KLFAGIRDRGLLRVDDFLVTPHLTHAKTFLRTRVGVPEYGCVVNLRTKTVNFPVED 782
QY 912 EALGGTAFVQMPAHGLFPWCGLLLDTRILEVQSDYSSYARTSIRASLTFNRGFKAGRNMR 971
DB 783 EALGGTAFVQMPAHGLFPWCGLLLDTRILEVQSDYSSYARTSIRASLTFNRGFKAGRNMR 842
QY 972 RKLFGVLRKCHSLFLDLQVNSLQVCTNIIYKILLQAYRPHACVQLQPLPFFHOQVWKNPTF 1031
DB 843 RKLFGVLRKCHSLFLDLQVNSLQVCTNIIYKILLQAYRPHACVQLQPLPFFHOQVWKNPTF 902
QY 1032 FLRVISDTASLCYSILKAKNAGMSLGAKGAGPLPSEAVQMLCHQAFLLKLTRHRTVYVP 1091
DB 903 FLRVISDTASLCYSILKAKNAGMSLGAKGAGPLPSEAVQMLCHQAFLLKLTRHRTVYVP 962
QY 1092 LLGSLRTAQTOLSRKLPCTTTLTALEAAANPALPSDFKTILD 1132
DB 963 LLGSLRTAQTOLSRKLPCTTTLTALEAAANPALPSDFKTILD 1003

RESULT 45
US-09-430-323-217
; Sequence 217, Application US/09430323
; Patent No. 6309867
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; Lingner, Joachim
; Nakamura, Toru
; Chapman, Karen B.
; Morin, Gregg B.
; Harley, Calvin
; Andrews, William H.
; TITLE OF INVENTION: No. 6309867el Telomerase
; NUMBER OF SEQUENCES: 225
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/430,323
; FILING DATE: 29-Oct-1999
; CLASSIFICATION: <unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/854,050
; FILING DATE: 09-MAY-1997
; APPLICATION NUMBER: US 08/851,843
; FILING DATE: 06-MAY-1997
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph T.
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-002930US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 217:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1003 amino acids
; TYPE: amino acid

	Best Local Similarity	78.7%; Pred. No. 0;	Matches	789; Conservative	23; Mismatches	123; Indels	67; Gaps	18;
Qy	163	APS--CAYQVCGPPLYQLGAAATQARP	PPPHASGPRRL-----GGERAMNHSVREAGVPLG	215				
Db	39	APTXCAGRRCC-----TSSALLXLRP----	GRPHTLXDPXASGIQRAMNHSVREAGVPLG	87				
Qy	216	LPAPGABRRGSASRSILPKRRP--RGAAP	EPERT--PVCGSWAHVPGRTT--GPSDRGFC	271				
Db	88	CO---PRVRGGAGAVPAEVCRCPRG	GVALLPSGSRPLGRG-----EGPTRAGRLDR--VT	139				
Qy	272	VVS-----PAPP-----AEEATS	LEGALSGTRHSHPSVGRO--HHAGPPPSRSP	313				
Db	140	VVSVMCHLPDPKPKPLWRVRS	LARATPTHPWAASITTRAPHPRGHVILGHALSPGVYR--	198				
Qy	314	PRPWTCCPVVYATKHFLYSSGDK	EQRLSPSFLSSLRPSLGTGARRLIVETIFLGSRRPMP	373				
Db	199	----DQALPILLRRQXHC-----	XPPSYSI--YLRPISLTGVREVRGDXLSGSRPMP	244				
Qy	374	GTPRRRLPRLPQRYWQMPLELLEL	IGNHAQCPYGVLLK--THCPLRAAVTAAAGVCAREKP	431				
Db	245	GFAGCPCACPSXGKCGPCF	MSCLGTTTSAPTGCSSRTRCARCELSPPQVPS--VPGRSP	302				
Qy	432	QGSVAAPPEEDTDPRLRLVOLL	ROHSSPWQVYGFVRACLRRLVPPGLWGSRHNERRFLRNT	491				
Db	303	RALWRP	RRRNTDPRRLVOLLROHSSPWQVYGFVRACLRRLVPPGLWGSRHNERRFLRNT	362				
Qy	492	KKFTISLGKHA	KLISQELTWKMSVRDCAWLRRSPGVCPVAAEHLREIILAKFLHLMMSV	551				
Db	363	KKFTISLGKHA	KLISQELTWKMSVRDCAWLRRSPGVCPVAAEHLREIILAKFLHLMMSV	422				
Qy	552	YVVELLRSFFVVTETTFQKRL	LFYRKSVMSKLOSIGIROHLKRVQLRELSAEVRQHRE	611				
Db	423	YVVELLRSFFVVTETTFQKRL	LFYRKSVMSKLOSIGIROHLKRVQLRELSAEVRQHRE	482				
Qy	612	ARPALLTSRLRFIPKPDGLRPI	VNMDYVVGARTFRREKRAERLTSRKVALFSVLNYSERAR	671				
Db	483	ARPALLTSRLRFIPKPDGLRPI	VNMDYVVGARTFRREKRAERLTSRKVALFSVLNYSERAR	542				
Qy	672	RPGLLGASVLGLDDIHRAWRT	FVILVRQAOPPPPELYFVKVDVTGAYDTIIPQDRLTEVIAS	731				
Db	543	RPGLLGASVLGLDDIHRAWRT	FVILVRQAOPPPPELYFVKVDVTGAYDTIIPQDRLTEVIAS	602				
Qy	732	IIIPQNTYCYRRYAVVQKAAH	GVKAPKFSHVSTLTDLPQYMRQFVAHLQETSPLRDAVV	791				
Db	603	IIIPQNTYCYRRYAVVQKAAH	GVKAPKFSHVSTLTDLPQYMRQFVAHLQXNSPLRDAVV	662				
Qy	792	IEOSSSLSNEASSGLFDVFLR	FMCHHAVRIKGSVVQCQGIPOGSILSTLLCSLCYGDWEN	851				
Db	663	IEOSSSLSNEASSGLFDVFLR	FMCHHAVRIKGSVVQCQGIPOGSILSTLLCSLCYGDWEN	722				
Qy	852	KLFPAGIRRDGLLRLVDDFL	LVTPHPLTHAKTFLRTLVRGPEYGCVVNLAKTVVNFPPVED	911				
Db	723	KLFPAGIRRDGLLRLVDDFL	LVTPHPLTHAKTFLRTLVRGPEYGCVVNLAKTVVNFPPVED	782				
Qy	912	EALGGTAFVQMPAHGLFPWCG	LLDTRTLEVSQSDYSYARTSTRASLTFRGFKAGNMR	971				
Db	783	EALGGTAFVQMPAHGLFPWCG	LLDTRTLEVSQSDYSYARTSTRASLTFRGFKAGNMR	842				
Qy	972	RKLPFVLRLLKCHSLFLDLQNS	LQTVCTNITYKILLQAYRFACVLQLPFHQQVWKNPTE	1031				
Db	843	RKLPFVLRLLKCHSLFLDLQNS	LQTVCTNITYKILLQAYRFACVLQLPFHQQVWKNPTE	902				
Qy	1032	FLRVISDTASLCYSILKAKNAG	MSLGAAGPLPSEAVQWLCHQAFLLKLTRHRVTYVP	1091				
Db	903	FLRVISDTASLCYSILKAKNAG	MSLGAAGPLPSEAVQWLCHQAFLLKLTRHRVTYVP	962				
Qy	1092	LLGSLRTAQOLSKLP	GGTTLTALAAAAANPALPSDFDKTILD	1132				
Db	963	LLGSLRTAQOLSKLP	GGTTLTALAAAAANPALPSDFDKTILD	1003				

RESULT 47

US-09-721-456-336
; Sequence 336, Application US/09721456
; Patent No. 6617110
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; Lingner, Joachim
; Nakamura, Toru
; Chapman, Karen B.
; Morin, Gregg B.
; Harley, Calvin B.
; Andrews, William H.
; TITLE OF INVENTION: Human Telomerase Catalytic Subunit
; NUMBER OF SEQUENCES: 727
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/721,456
; FILING DATE: 22-No. 6617110-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/974,549A
; FILING DATE: 19-NOV-1997
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; APPLICATION NUMBER: US 08/851,843
; FILING DATE: 06-MAY-1997
; APPLICATION NUMBER: US 08/854,050
; FILING DATE: 09-MAY-1997
; APPLICATION NUMBER: US 08/911,312
; FILING DATE: 14-AUG-1997
; APPLICATION NUMBER: US 08/912,951
; FILING DATE: 14-AUG-1997
; APPLICATION NUMBER: US 08/915,503
; FILING DATE: 14-AUG-1997
; APPLICATION NUMBER: WO PCT/US97/17618
; FILING DATE: 01-OCT-1997
; APPLICATION NUMBER: WO PCT/US97/17885
; FILING DATE: 01-OCT-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph Ted
; REGISTRATION NUMBER: 36,429
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 336:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1003 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 336:
US-09-721-456-336

Query Match	64.1%;	Score 3819.5;	DB 4;	Length 1003;
Best Local Similarity	78.7%;	Pred. No. 0;		
Matches 788; Conservative	23;	Mismatches 123;	Indels 67;	Gaps 18;


```

; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-042-460-2

Query Match
Best Local Similarity 58.8%; Score 3505; DB 4; Length 1122;
Matches 719; Conservative 122; Mismatches 260; Indels 52; Gaps 13;

QY 1 MPAPRCRAVRLSLRSHYREVLPATFVRRLLGPGQWRLVQRGDPAAFRALVAQCLVCPW 60
DQ 1 MTRAPRCPAVRLSLRSHYREVLPATFVRRLLGPGQWRLVQRGDPAAFRALVAQCLVCPW 60
QY 61 DARPPAPAPSPQVSCLEKELVARVQLRCEKAKVLAARGPALLDGAAGPPPEAFTTSVR 120
DQ 61 GSQPPADLSFQVSLKELVARVQLRCEKAKVLAARGPALLDGAAGPPPEAFTTSVR 120
QY 121 SYLPTNTVDALRGSGAGWGLLRVGGDVLVHLARCALFVLVAPSCAVQVCCPPLVCLGA 180
DQ 121 SYLPTNTVIELRVSGAWMLLRLSRVGGDVLVHLARCALFVLVAPSCAVQVCCPPLVCLGA 180
QY 181 ATQARPPPHAS-GPRLRLG-----CERAMNHSVREAGVPLGLPAPGARRRGGSASRS 231
DQ 181 TTDIWPVSASVYRTPVGRNFTNLRFLOQIKSSRQEQAPKPLAFSRGTKHLSTSTIS 240
QY 232 LPLPKRPRGAAPERTPVGGGWAHPGRTGRSDRGFCVVSAPR-----PABEATSL 286
DQ 241 VPSAKKARCYPVPRVEEGP-----HRQVLTPSGKSW-VPSPARSPVPPTAEKDLSSK 292
QY 287 GALSCTRSHSPVGRQHAGPSTSRPPRPWDTCPVVAETKHFYSSGD-KEQLRPSF 345
DQ 293 GKVSLSUS-GVCCCKHKPSSTLSLPPKQNAFQLRP-PIETRHFLYSGRGGQERLNPSF 350
QY 346 LLSLRPSLTGARRIVETIFLGRSWMMPGTTPRLPQRYWQMPPLFLELGNHAQCPY 405
DQ 351 LLSNLQPNLTGARRIVEIFLGRSPTSGPLCRTHLSRYWQMPPLFQOLLVNHACQY 410
QY 406 GVLLKTHCPLEAA-----VTPAAGVCAAREKPGGSAAPBEDTDPRLVOLLRQHSFPQY 462
DQ 411 VLLRSHCRFTANQVTDAL-----NTSPPHMLDLLRLHSPFWQY 452
QY 463 GFVRACLRLVPPGLWGRSHNERRFLNTKKISLGKHAFLSLOELTWKMSVRDCAWLR 522
DQ 453 GFLRACLCKVWSASLWGTTHNERRFFNKLKPFISLGKYGKLSLOELMMKMKVEDCHWLS 512
QY 523 SPGVGCVPAAEHRLREELILAKLHLMWSVYVVELLRSFFYVTTTFQKRLFFYKRSVNS 582
DQ 513 SPGRDVPAAEHLREELILATFLWMDTYVYVQLRSFFYITESTFQKRLFFYKRSVNS 572
QY 583 KLSIGIRQHLKRVQLRELSEAEVQHRREARPAALLTSRLRFTPKDGLRPIVNM DYVGA 642
DQ 573 KLSIGVRQHLRVRRLRELSEAEVQHRHODTWLAMPICRLRFTPKDGLRPIVNM DYVGA 632
QY 643 RTFREKRAERLTSVKALFVNLNTERARRPGLLGASVLGLDDIHRMRTFVLRVRAQDP 702
DQ 633 RALGRKQQAQHTQRLKTLFSLMANTERTKPHLMGSSVLGMNDIYRTWRAFLVRLALDQ 692
QY 703 PPFLYFVKVDVTGAYDTTIPQDRLTEVIASIIK-PONTYCVRRYAVVQKAAHGHVRKAFKS 761
DQ 693 TPRTMVFVADVTGADAIPOGLKQEVVANNIRHSESTYCIRQYAVVRKDSQQVHKSFRR 752
QY 762 HVSTLTDLQPMYRQFVAHLQET--SPLRDVAVIEQSSSLNEASSGLFDVFLRFMCHAVR 819
DQ 753 QVTTLSDLQPMYRQFVAHLQET--SPLRDVAVIEQSSSLNEASSGLFDVFLRFMCHAVR 812
QY 820 IRGKSYVQCGIPQSSILSTLLCSLCYGDMEKLFAGIRRDGLLRLVDDFLVTPHLLTH 879
DQ 813 IGDRCYTCQCGIPQSSILSTLLCSLCYGDMEKLFAGIRRDGLLRLVDDFLVTPHLLTH 872
QY 880 AKTFLRTLVRGPEYGCYVNVNPFVDEALGGTAFVQMPAHGLFPWCGLLDTRT 939
DQ 873 AKTFLRTLVRGPEYGCYVNVNPFVDEALGGTAFVQMPAHGLFPWCGLLDTRT 932
QY 940 LEVQSDYSSYARTSIRASLTNRFKAGNMRKLFGLVRLKCHSLFLDLQVNSLQTVCT 999

```

933 LEVFCDSYGAQTSIKTSLTFSQVFAKGTWENKLSVLRLKCHGLFLDLQVNSLQTVCT 992
1000 NIYKILLQAVRFHACVQLQPHQVQWKNPTFFLRVISTASLCVYSILKAKNAGSLGAK 1059
993 NIYKIFLQAVRFHACVQLQPHQVQWKNPTFFLRVISTASLCVYSILKAKNAGSLGAK 1052
1060 GAAGPLPSEAVQWLCHQAFLLKLTHRVYVYVVELLRSFTAQTLQSRKLPGLTTLTALAAA 1119
1053 GS---FPPEAAHWLCYQAFLLKLAHSAHVIYKCLGLPLRTAQLCKLPEATMTILKAAA 1109
1120 NPALPSDFKTILD 1132
1110 DPALSTDFQTILD 1122

RESULT 49
US-09-582-924B-12
; Sequence 12, Application US/09582924B
; Patent No. 6608188
; GENERAL INFORMATION:
; APPLICANT: CHUGAI SEIVAKU KABUSHIKI KAISHA
; TITLE OF INVENTION: No. 6608188el Gene Having Reverse Transcriptase Motif
; FILE REFERENCE: 46124-5034-US
; CURRENT APPLICATION NUMBER: US/09/582,924B
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: JP 10/13232
; PRIOR FILING DATE: 1998-01-08
; PRIOR APPLICATION NUMBER: JP 10/33584
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: JP 10/139177
; PRIOR FILING DATE: 1998-05-06
; PRIOR APPLICATION NUMBER: PCT/JP99/00039
; PRIOR FILING DATE: 1999-01-08
; NUMBER OF SEQ ID NOS: 13
; SEQ ID NO 12
; LENGTH: 622
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION:
US-09-582-924B-12

Query Match 52.6%; Score 3134; DB 4; Length 622;
Best Local Similarity 97.9%; Pred. No. 4.5e-280;
Matches 610; Conservative 3; Mismatches 6; Indels 4; Gaps 1;

QY 510 WKMSVRDCAWLRSPGVGCVPAAEHRLREELILAKLHLMWSVYVVELLRSFFYVTTTTPQ 569
DQ 4 WRLTRAVILAR---VGCVPAAEHRLREELILAKLHLMWSVYVVELLRSFFYVTTTTPQ 59
QY 570 KNLFFYFKSVWSKLSIGIRQHLKRVQLRELSEAEVQHRREARPAALLTSRLRFTPKDPG 629
DQ 60 KNLFFYFKSVWSKLSIGIRQHLKRVQLRELSEAEVQHRREARPAALLTSRLRFTPKDPG 119
QY 630 LRPIVNM DYVGAARTFREKRAERLTSVKALFVNLNTERARRPGLLGASVLGLDDIHRM 689
DQ 120 LRPIVNM DYVGAARTFREKRAERLTSVKALFVNLNTERARRPGLLGASVLGLDDIHRM 179
QY 690 WRTFVLVRAQDPPELYFVKVDVTGAYDTTIPQDRLTEVIASIIK-PONTYCVRRYAVVQK 749
DQ 180 WRTFVLVRAQDPPELYFVKVDVTGAYDTTIPQDRLTEVIASIIK-PONTYCVRRYAVVQK 239
QY 750 AAHGHVRKAFKSHVSTLTDLPYMRQFVAHLQETSPLRDVAVIEQSSSLNEASSGLFDV 809
DQ 240 AAHGHVRKAFKSHVSTLTDLPYMRQFVAHLQETSPLRDVAVIEQSSSLNEASSGLFDV 299
QY 810 LRFMCHAVRIRGKSYVQCGIPQSSILSTLLCSLCYGDMEKLFAGIRRDGLLRLVDD 869
DQ 300 LRFMCHAVRIRGKSYVQCGIPQSSILSTLLCSLCYGDMEKLFAGIRRDGLLRLVDD 359
QY 870 FLLVTPHLLTHAKTFLRTLVRGPEYGCYVNVNPFVDEALGGTAFVQMPAHGLFP 929

Db 360 FLLVTPHLTHAKTFLRTLVRGVPYGCVVNLRKTVVNPVPEDEALGGTAFVQMPAHGLFP 419
Qy 930 WCGLLDTRTLEVDSSYARTSIRASLTNNRGFKAGNNRRKLFVGLRLKCHSLFLDL 989
Db 420 WCGLLDTRTLEVDSSYARTSIRASLTNNRGFKAGNNRRKLFVGLRLKCHSLFLDL 479
Qy 990 QVNSIQVCTNYYKILLQAVRFHACVLOLPHQOVWKNPTFFELRVISDTSASLCYSILKA 1049
Db 480 QVNSIQVCTNYYKILLQAVRFHACVLOLPHQOVWKNPTFFELRVISDTSASLCYSILKA 539
Qy 1050 KNAGMSLGAKGAGPLPSEAVQWLCHQAFLLKLTFRHRYVYVPLLGSLRTAQTOLSRKLP 1109
Db 540 KNAGMSLGAKGAGPLPSEAVQWLCHQAFLLKLTFRHRYVYVPLLGSLRTAQTOLSRKLP 599
Qy 1110 TTLEAAAAANPALPSDPKTILD 1132
Db 600 TTLEAAAAANPALPSDPKTILD 622

RESULT 50

US-09-582-924B-10
; Sequence 10, Application US/09582924B
; Patent No. 6608188
; GENERAL INFORMATION:
; APPLICANT: CHUGAI SEIYAKU KABUSHIKI KAISHA
; TITLE OF INVENTION: No. 6608188el Gene Having Reverse Transcriptase Motif
; FILE REFERENCE: 46124-5034-US
; CURRENT APPLICATION NUMBER: US/09/582,924B
; CURRENT FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: JP 10/13232
; PRIOR FILING DATE: 1998-01-08
; PRIOR APPLICATION NUMBER: JP 10/33584
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: JP 10/139177
; PRIOR FILING DATE: 1998-05-06
; PRIOR APPLICATION NUMBER: PCT/JP99/00039
; PRIOR FILING DATE: 1999-01-08
; NUMBER OF SEQ ID NOS: 13
; SEQ ID NO 10
; LENGTH: 438
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION:
US-09-582-924B-10

Query Match 36.6%; Score 2184; DB 4; Length 438;
Best Local Similarity 97.0%; Pred. No. 1.2e-192;
Matches 425; Conservative 3; Mismatches 6; Indels 4; Gaps 1;
Qy 510 WMSVDRDCAWLRSPGCVGCPAAEHRRLREEILAKFLHLMMSVYVVELLRSFFYVTTTFQ 569
Db 4 WLTTRAVILAR---VGCVPAAEHRRLREEILAKFLHLMMSVYVVELLRSFFYVTTTFQ 59
Qy 570 KNRLFFYKSVMSKLSQSIGIQLKRVOLRELSAEVQREARPAALLTSRLRTPKPDG 629
Db 60 KNRLFFYKSVMSKLSQSIGIQLKRVOLRELSAEVQREARPAALLTSRLRTPKPDG 119
Qy 630 LRPIVNDYVVGARTFRREKRAERLTSRVKALFSVLNYERARRPGLLGASVLGLDDIHRA 689
Db 120 LRPIVNDYVVGARTFRREKRAERLTSRVKALFSVLNYERARRPGLLGASVLGLDDIHRA 179
Qy 690 WRTFVLVRADQPPPELVFKVDVTGAYDTIPQDRLTEVIASIIKPQNTYCVRRYAVVQK 749
Db 180 WRTFVLVRADQPPPELVFKVDVTGAYDTIPQDRLTEVIASIIKPQNTYCVRRYAVVQK 239
Qy 750 AAHGHRKAFKSHVSTLTDLPYMQFVAHLQETSPLRDADVIEQSSSINEASSGLFDVF 809
Db 240 AAHGHRKAFKSHVSTLTDLPYMQFVAHLQETSPLRDADVIEQSSSINEASSGLFDVF 299
Qy 810 LRFMCHHAVIRGKSVYVQCGIPQGSILSTLLCSLCYGDMMENKLPAGIRRDGLLRVDD 869
Db 300 LRFMCHHAVIRGKSVYVQCGIPQGSILSTLLCSLCYGDMMENKLPAGIRRDGLLRVDD 359

Qy 870 FLLVTPHLTHAKTFLRTLVRGVPYGCVVNLRKTVVNPVPEDEALGGTAFVQMPAHGLFP 929
Db 360 FLLVTPHLTHAKTFLRTLVRGVPYGCVVNLRKTVVNPVPEDEALGGTAFVQMPAHGLFP 419
Qy 930 WCGLLDTRTLEVDSSYARTSIRASLTNNRGFKAGNNRRKLFVGLRLKCHSLFLDL 989
Db 420 WCGLLDTRTLEVDSSYARTSIRASLTNNRGFKAGNNRRKLFVGLRLKCHSLFLDL 479
Qy 990 QVNSIQVCTNYYKILLQAVRFHACVLOLPHQOVWKNPTFFELRVISDTSASLCYSILKA 1049
Db 480 QVNSIQVCTNYYKILLQAVRFHACVLOLPHQOVWKNPTFFELRVISDTSASLCYSILKA 539

Search completed: August 5, 2005, 14:22:37
Job time : 66 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 5, 2005, 14:04:32 ; Search time 175 Seconds
(without alignments)
2501.787 Million cell updates/sec

Title: US-10-053-758-225
Perfect score: 5961
Sequence: 1 MFPRAPRCRAVRSLLRSHYRE.....TALSAANPALPSPDFKTLTD 1132

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:.*
1: Geneseqp1980s:.*
2: Geneseqp1990s:.*
3: Geneseqp2000s:.*
4: Geneseqp2001s:.*
5: Geneseqp2002s:.*
6: Geneseqp2003as:.*
7: Geneseqp2003bs:.*
8: Geneseqp2004s:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	5961	100.0	1132	2 AAW46957	Aaw46957 Human tel
2	5961	100.0	1132	2 AAW90251	Aaw90251 Human cat
3	5961	100.0	1132	2 AAY28881	Aay28881 Human tel
4	5961	100.0	1132	2 AAY32090	Aay32090 Human tel
5	5961	100.0	1132	2 AAY43621	Aay43621 A human t
6	5961	100.0	1132	2 AAY25680	Aay25680 Human tel
7	5961	100.0	1132	4 AAG64859	Aag64859 Heart mus
8	5961	100.0	1132	4 AAG64329	Aag64329 Human pro
9	5961	100.0	1132	4 AAB99930	Aab99930 Human tel
10	5961	100.0	1132	4 AAB82765	Aab82765 Human tel
11	5961	100.0	1132	5 AAE29226	Aae29226 Human tel
12	5961	100.0	1132	5 AAU72735	Aau72735 Human tel
13	5961	100.0	1132	6 ABR42384	Abr42384 Human tel
14	5961	100.0	1132	6 ABR42063	Abr42063 Human tel
15	5961	100.0	1132	6 ABP56676	Abp56676 Human tel
16	5961	100.0	1132	6 ABR58045	Abr58045 Human tel
17	5961	100.0	1132	7 ADD21420	Add21420 Human TER
18	5961	100.0	1132	7 ADH72743	Adh72743 Human pro
19	5961	100.0	1132	8 ADG70114	Adg70114 hTERT pro
20	5961	100.0	1132	8 ADG90599	Adg90599 Human TER
21	5961	100.0	1132	8 ADI82172	Adi82172 Human tel
22	5961	100.0	1132	8 ADR70482	Adr70482 Human tel
23	5961	100.0	1154	2 AAW61350	Aaw61350 Human tel
24	5961	100.0	1189	2 AAW47008	Aaw47008 Glutathio
25	5955	99.9	1285	2 AAW47000	Aaw47000 HIS tagge

ALIGNMENTS

RESULT 1

AAW46957
ID AAW46957 standard; protein; 1132 AA.

AC AAW46957;

XX
XX
DT 13-AUG-1998 (first entry)

DE Human telomerase reverse transcriptase.

XX
KW Human; telomerase reverse transcriptase; hTERT; TRT; diagnosis; prognosis;
KW cell proliferation; cancer; ageing; ribonucleoprotein.

XX Homo sapiens.

PN GB2317891-A.

PD 08-APR-1998.

XX
XX
PF 01-OCT-1997; 97GB-00020890.

XX
XX
PR 01-OCT-1996; 96US-00724643.

PR 18-APR-1997; 97US-00844419.

PR 25-APR-1997; 97US-00846017.

PR 06-MAY-1997; 97US-00851843.

PR 09-MAY-1997; 97US-00854050.

PR 14-AUG-1997; 97US-00911312.

PR 14-AUG-1997; 97US-00912951.

XX (GERO-) GERON CORP.

XX (UYTE-) UNIV TECHNOLOGY CORP.

PI Cech TR, Lingner J, Nakamura T, Chapman KB, Morin GB, Harley CB;

PI Andrews WH;

DR WPI; 1998-171633/16.

DR N-PSDB; AAW22379.

XX Pure and recombinant human Telomerase Reverse Transcriptase and its

PT variants - are useful in the diagnosis, prognosis and treatment of cell

XX proliferation conditions especially cancer and ageing.

PS Claim 3; Fig 17; 387pp; English.

XX The present sequence represents human telomerase reverse transcriptase

CC (hTERT), which is a ribonucleoprotein. The present invention also

CC describes the following methods: (A) determining whether a test compound

CC is a modulator of hTERT, by detecting the change in hTERT recombinant
CC protein or polynucleotide, on administration of the compound; (B)
CC preparation of recombinant telomerase by contacting a protein preparation
CC of hTERT with a telomerase RNA component; (C) detection of the hTERT RNA or
CC protein in a sample by binding a relevant probe to the sample and
CC detecting the complex formed or in the case of RNA detection, amplifying
CC the product and correlating the presence of complex or amplification
CC product with presence of hTERT in the sample; and (D) increasing the
CC proliferation of a vertebrate cell by increasing hTERT expression; and (E)
CC the use of an agent that causes an increase in cell vertebrate cell
CC proliferation to create a medicament that inhibits ageing. A protein
CC preparation of hTERT and the polynucleotide encoding hTERT can be used in
CC the manufacture of medicaments for inhibiting the effect of ageing or
CC cancer. Inhibitors of telomerase activity can be used to treat conditions
CC that are associated with high telomerase activity. A protein preparation
CC of hTERT can also be used in the new methods

XX SQ Sequence 1132 AA;

Query Match 100.0%; Score 5961; DB 2; Length 1132;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPAPRCRAVRLSHRYEVLPLATFVRRLLGPGQWRVLVQRGDDPAAPALVAQCILVCVPW 60
DB 1 MPAPRCRAVRLSHRYEVLPLATFVRRLLGPGQWRVLVQRGDDPAAPALVAQCILVCVPW 60

QY 61 DARPPPAAPSPROVSKLXELVARVLQRLCERGAKNVLAFFGALLDGGAGGPEAFTTSVR 120
DB 61 DARPPPAAPSPROVSKLXELVARVLQRLCERGAKNVLAFFGALLDGGAGGPEAFTTSVR 120

QY 121 SYLNTVTDALRGSGAWGLLRRVDDVLVHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180
DB 121 SYLNTVTDALRGSGAWGLLRRVDDVLVHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180

QY 181 ATOARPPPHASGPRRLCERAWNHSVREAGVPLGLPAPGARRRGGASRSLPLPKPRR 240
DB 181 ATOARPPPHASGPRRLCERAWNHSVREAGVPLGLPAPGARRRGGASRSLPLPKPRR 240

QY 241 GAAPEPERTVPGQSWAHFGRTRGSDRGFCVSPARPAEATSLGALSCTRHSHPVSG 300
DB 241 GAAPEPERTVPGQSWAHFGRTRGSDRGFCVSPARPAEATSLGALSCTRHSHPVSG 300

QY 301 RQHAGPPSTSRPRPMDTPCPVVAETKHFYLSGDKQLRPSFLSSLPSTGARRL 360
DB 301 RQHAGPPSTSRPRPMDTPCPVVAETKHFYLSGDKQLRPSFLSSLPSTGARRL 360

QY 361 VETIFLGSRPWMPGTFRPLPRLPORYWOMRPLFLELLGNHAQCPVGLLTKHCPLRAVT 420
DB 361 VETIFLGSRPWMPGTFRPLPRLPORYWOMRPLFLELLGNHAQCPVGLLTKHCPLRAVT 420

QY 421 PAAGVCAREKPGQSWAAPEEDTPRRLVQLLRQHSFSPQVYGFVRACLRRLVPPGLWGS 480
DB 421 PAAGVCAREKPGQSWAAPEEDTPRRLVQLLRQHSFSPQVYGFVRACLRRLVPPGLWGS 480

QY 481 RHNERFLRNTKFKFISLGHAKLSLOELTWKMSVRDCAWLRSPGVGCVPAEHLRLEEI 540
DB 481 RHNERFLRNTKFKFISLGHAKLSLOELTWKMSVRDCAWLRSPGVGCVPAEHLRLEEI 540

QY 541 LAKFLHLWMSVYVVELLSFFVTETTFQKNRLLPFYKSVMSKLSQIGIROHLKRVQLE 600
DB 541 LAKFLHLWMSVYVVELLSFFVTETTFQKNRLLPFYKSVMSKLSQIGIROHLKRVQLE 600

QY 601 LSEAFVQRHREARPALLSRLRIFPKPDGLRPIVNMDDYVVGARTFRREKRAERLTSRYKA 660
DB 601 LSEAFVQRHREARPALLSRLRIFPKPDGLRPIVNMDDYVVGARTFRREKRAERLTSRYKA 660

QY 661 LFSVLNFERARRPGLLGASVLGLDDIHRAWTFVLVRQAQDPPPELYFKVVDVTGAYDTI 720
DB 661 LFSVLNFERARRPGLLGASVLGLDDIHRAWTFVLVRQAQDPPPELYFKVVDVTGAYDTI 720

QY 721 PQDLRTEVIASIIKPNTYCVRRYAVVQKAAHGHVRKAFKSHVSTLTDLQPYMQFVAHL 780

DB 721 PQDLRTEVIASIIKPNTYCVRRYAVVQKAAHGHVRKAFKSHVSTLTDLQPYMQFVAHL 780

QY 781 QETSPLRDVAVIEQSSSLNEASSGLFDVFLRFMCHHVRIRKSGSYVQCQGIPOGSIISTL 840

DB 781 QETSPLRDVAVIEQSSSLNEASSGLFDVFLRFMCHHVRIRKSGSYVQCQGIPOGSIISTL 840

QY 841 LCSLCYGDGMENKLPAGIRRDGLLLRLVDDFLVTPHLLTHAKTFLRTLVRGVPYGCVVNL 900

DB 841 LCSLCYGDGMENKLPAGIRRDGLLLRLVDDFLVTPHLLTHAKTFLRTLVRGVPYGCVVNL 900

QY 901 RKTWNPFVDEALGGTAFVQMPAHGLFPWCGLLDDTRTLEVSQSDYSYARTSRASLTF 960

DB 901 RKTWNPFVDEALGGTAFVQMPAHGLFPWCGLLDDTRTLEVSQSDYSYARTSRASLTF 960

QY 961 NRGFAGRNMRRLFGVLRLLKCHSLFLDLQVNSLQTVCTNIYKILLQAYRHFACVLQLP 1020

DB 961 NRGFAGRNMRRLFGVLRLLKCHSLFLDLQVNSLQTVCTNIYKILLQAYRHFACVLQLP 1020

QY 1021 FHQOVWKNPTFFLRVISDTSALCYSLKAKNAGSLGAKGAGPLPSEAVQWLCHQAFLL 1080

DB 1021 FHQOVWKNPTFFLRVISDTSALCYSLKAKNAGSLGAKGAGPLPSEAVQWLCHQAFLL 1080

QY 1081 KLTRHRVTVYVPLGLSLRTAQTQLSRKLPGTTLTAAEAANPALPSDFKTILD 1132

DB 1081 KLTRHRVTVYVPLGLSLRTAQTQLSRKLPGTTLTAAEAANPALPSDFKTILD 1132

RESULT 2

AAW90251

ID AAW90251 standard; protein; 1132 AA.

XX AC AAW90251;

XX DT 24-MAY-1999 (first entry)

XX DE Human catalytic telomerase sub-unit protein.

XX KW Human; catalytic telomerase subunit; therapy; diagnosis; hTC; assay; modulator; treatment; inhibit; cellular disorder; death; defect; cancer; ageing; antisense; neoplastic cell; telomerase-related condition; tumour cell.

XX OS Homo sapiens.

XX PN WO9859040-A2.

XX PD 30-DEC-1998.

XX PF 09-JUN-1998; 98WO-EP003468.

XX PR 20-JUN-1997; 97DE-01026329.

XX PR 26-MAR-1998; 98DE-01013274.

XX PR 14-APR-1998; 98DE-01016496.

XX PA (FARB) BAYER AG.

XX PI Hagen G, Siegmund H, Weichel W, Wick M, Zubov D;

XX PS WPI; 1999-081276/07.

XX PT N-PSDB; AAV72117.

XX PT New catalytically active subunit of human telomerase - used in the modulation of telomerase activity, particularly for treating cancer and ageing.

XX PS Claim 2; Fig 2; 76pp; German.

XX CC This sequence represents a novel human catalytic telomerase sub-unit (hTC). This protein can be used in screening assays to identify modulators of telomerase and to treat or inhibit cellular disorders, death, defects and/or other pathological processes involving telomerase, particularly cancer and ageing (also suitable for this are agents that stimulate, inhibit or mimic the activity of the subunit). Antisense

CC nucleic acids inhibit telomerase action (by binding to specific mRNA),
CC particularly in neoplastic cells and may be expressed in vivo. Antibodies
CC and fragments of the protein, used as probes or primers, are used to
CC diagnose telomerase-related conditions (especially neoplasia) by (i)
CC detecting abnormal levels of the subunit protein in body fluids or
CC tissues or (ii) by measuring the amount of the encoding nucleic acid.
CC Expression of the nucleic acid encoding the subunit mRNA is confined to
CC tumour cells, in contrast to the ubiquitous expression of the telomerase
CC RNA subunit

XX SQ Sequence 1132 AA;

Query Match 100.0%; Score 5961; DB 2; Length 1132;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPAPRCRAVSLRSHYREVLPATFVRRLGPOGMRVLVORGDPAAFALVAQCVCVPW 60
DB 1 MPAPRCRAVSLRSHYREVLPATFVRRLGPOGMRVLVORGDPAAFALVAQCVCVPW 60

QY 61 DARPPAAPSPROVSKLXELVARVLQRCERGAKNVLAFFGALLDARGGPEAFTTSVR 120
DB 61 DARPPAAPSPROVSKLXELVARVLQRCERGAKNVLAFFGALLDARGGPEAFTTSVR 120

QY 121 SYLNTVTDALRGSGAWGALLRRVGDVLLHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180
DB 121 SYLNTVTDALRGSGAWGALLRRVGDVLLHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180

QY 181 ATOARPPHAGSPRRRLCERAWNSVREAGVPLGLPARGARRGSGASRSILPLKRRR 240
DB 181 ATOARPPHAGSPRRRLCERAWNSVREAGVPLGLPARGARRGSGASRSILPLKRRR 240

QY 241 GAAPPERTPVQGSWAHPGRTGSDRGFCVSPARPAEATSLGALSGTRHSHPSVG 300
DB 241 GAAPPERTPVQGSWAHPGRTGSDRGFCVSPARPAEATSLGALSGTRHSHPSVG 300

QY 301 RQHAGPSTSRPPRPMDTPCPVYATKHFLLYSSGDKQLRPSFLLSRPSLTGARRL 360
DB 301 RQHAGPSTSRPPRPMDTPCPVYATKHFLLYSSGDKQLRPSFLLSRPSLTGARRL 360

QY 361 VETIFLGRPMWPGTFRPLRPLRQYQWMPRLFLELLGNHAQCPYGVLLKTHCPLRAAVT 420
DB 361 VETIFLGRPMWPGTFRPLRPLRQYQWMPRLFLELLGNHAQCPYGVLLKTHCPLRAAVT 420

QY 421 PAAGVCAREKPGQSVAAPEEDTDPRRLVQLLRQHSPPQVYGFVRACLRRLVPPGLWGS 480
DB 421 PAAGVCAREKPGQSVAAPEEDTDPRRLVQLLRQHSPPQVYGFVRACLRRLVPPGLWGS 480

QY 481 RHNERFLRNTKFTISLGHAKLSIQELTWKMSVRDCAWLRSPGVCVPAAEHRLREEI 540
DB 481 RHNERFLRNTKFTISLGHAKLSIQELTWKMSVRDCAWLRSPGVCVPAAEHRLREEI 540

QY 541 LAKFLHMLSVVVBELLSPFFVTETTTQKNRLLFFYKRSVMSKLSQIGIRHLKRVQURE 600
DB 541 LAKFLHMLSVVVBELLSPFFVTETTTQKNRLLFFYKRSVMSKLSQIGIRHLKRVQURE 600

QY 601 LSEAEVROHREARPAALLTSRLRPIPKDGLRPIVNMDDVVGARTFRKRAERLTSRYKA 660
DB 601 LSEAEVROHREARPAALLTSRLRPIPKDGLRPIVNMDDVVGARTFRKRAERLTSRYKA 660

QY 661 LFSVLNYSERARRPGLLGASVLGLDDIHRARTFVLVRQAQDPPPELYFVKVDVTGAYDTI 720
DB 661 LFSVLNYSERARRPGLLGASVLGLDDIHRARTFVLVRQAQDPPPELYFVKVDVTGAYDTI 720

QY 721 PQDLTEVIASIIKQNTYCVRRYAVVQAAHGHVRKAFKSHVSTLTDLQPMRFVAHL 780
DB 721 PQDLTEVIASIIKQNTYCVRRYAVVQAAHGHVRKAFKSHVSTLTDLQPMRFVAHL 780

QY 781 QSTPLRDAVLEQSSSNEASSGLFDVFLRPMCHAVRIRKSVQCGIPQGSILSTL 840
DB 781 QSTPLRDAVLEQSSSNEASSGLFDVFLRPMCHAVRIRKSVQCGIPQGSILSTL 840

QY 841 LCCLCYGDMENKLPAGIRRDGLLLRLVDVDFLLVTPHLLTHAKTFLTLVRGVPYGCVVNL 900

DB 841 LCCLCYGDMENKLPAGIRRDGLLLRLVDVDFLLVTPHLLTHAKTFLTLVRGVPYGCVVNL 900
QY 901 RKTVVNPVEDEALGGTAFVQMPAHGLPPWCGLLDDTLETVQSDYSSYARTSIRASLTF 960
DB 901 RKTVVNPVEDEALGGTAFVQMPAHGLPPWCGLLDDTLETVQSDYSSYARTSIRASLTF 960
QY 961 NRGFKAGNMRKLFVGLRLKCHSLFLDLQVNSLQTVCTNIYKILLQAYRFHACVQLQP 1020
DB 961 NRGFKAGNMRKLFVGLRLKCHSLFLDLQVNSLQTVCTNIYKILLQAYRFHACVQLQP 1020

QY 1021 FHOQVWKNPTFFLRVVISDTASLCYSILKAKNAGSLGAKGAGPLPSEAVOWLCHOAFLL 1080
DB 1021 FHOQVWKNPTFFLRVVISDTASLCYSILKAKNAGSLGAKGAGPLPSEAVOWLCHOAFLL 1080

QY 1081 KLTRHRTVTVYVPLLGLSRLTAQTLRSKLPGLTTLTALEAAANPALPSDFKTIID 1132
DB 1081 KLTRHRTVTVYVPLLGLSRLTAQTLRSKLPGLTTLTALEAAANPALPSDFKTIID 1132

RESULT 3
AAY28881
ID AAY28881 standard; protein; 1132 AA.
XX AC AAY28881;
XX DT 17-JAN-2000 (first entry)
XX DE Human telomerase reverse transcriptase protein.
XX KW Human telomerase reverse transcriptase protein; hTERT; telomerase; hEST2;
KW catalytic protein component; cell proliferative capacity; DNA primer;
KW telomerase substrate; telomeric DNA synthesis; cell immortality;
KW neoplastic phenotype; diagnostic application; prognostic application;
KW telomerase related condition; cancer; therapeutic agent;
KW telomerase expression; telomerase activity.
XX OS Homo sapiens.
XX FH Key Location/Qualifiers
FT Misc-difference 608 /note= "Corresponds to cac codon"
FT FT
XX PN WO9950279-A1.
XX PD 07-OCT-1999.
XX PF 31-MAR-1999; 99WO-US007160.
XX PR 31-MAR-1998; 98US-00052919.
XX PA (GERO-) GERON CORP.
XX PI (UYTE-) UNIV TECHNOLOGY CORP.
XX PI Cech TR, Lingner J, Nakamura T, Chapman KB, Morin GB, Harley CB;
XX Andrews WH;
XX DR WPI; 1999-610834/52.
XX DR N-PSDB; AAZ08150.
XX XX Antisense polynucleotides for human telomerase reverse transcriptase used
XX for diagnosing or treating cancer.
XX PS Claim 2; Fig 2; 31pp; English.
XX CC The present sequence is human telomerase reverse transcriptase protein.
CC This is the catalytic protein component of telomerase and is also
CC referred to as hEST2. hTERT has the ability to extend a DNA primer that
CC functions as a telomerase substrate for telomeric DNA synthesis. This
CC correlates with cell proliferative capacity, cell immortality, and the
CC development of a neoplastic phenotype. Human TERT antisense
CC oligonucleotides are useful for diagnostic or prognostic applications to
CC telomerase related conditions, including cancer. They are also useful as

therapeutic agents, for inhibition of telomerase expression and activity										
CC	SQ Sequence 1132 AA;									
XX										
SQ										
Query Match	100.0%; Score 5961; DB 2; Length 1132;									
Best Local Similarity	100.0%; Pred. No. 0;									
Matches 1132; Conservative	0; Mismatches 0; Indels 0; Gaps 0;									
QY	1	MPRAPRCRAVRSLLRSHYREVLP	PLATFVRRLGPGQWRVLVQ	RGDPAAFRALVAQCLVCVPW	60					
DB	1	MPRAPRCRAVRSLLRSHYREVLP	PLATFVRRLGPGQWRVLVQ	RGDPAAFRALVAQCLVCVPW	60					
QY	61	DARPPAAPSPROVSCLELVARVL	ORLCERCAGKXVLAFA	LGDGARGGPEAFTTSVR	120					
DB	61	DARPPAAPSPROVSCLELVARVL	ORLCERCAGKXVLAFA	LGDGARGGPEAFTTSVR	120					
QY	121	SYLPTNTVDALRGSGAGWGLLR	RVGDDVLVHLARCALFVL	VAPSCAYQVCGPPLYQLGA	180					
DB	121	SYLPTNTVDALRGSGAGWGLLR	RVGDDVLVHLARCALFVL	VAPSCAYQVCGPPLYQLGA	180					
QY	181	ATQARPPPHASGPRRLCERAMNHS	VREAGVPLGLPAPGARRRGGSASRSLPLPKRPRR	240						
DB	181	ATQARPPPHASGPRRLCERAMNHS	VREAGVPLGLPAPGARRRGGSASRSLPLPKRPRR	240						
QY	241	GAAPEPERTVGQGSWAHPGRT	RGPSDRGFCVSPARPAEATS	LEGALSGTRHSHPSVG	300					
DB	241	GAAPEPERTVGQGSWAHPGRT	RGPSDRGFCVSPARPAEATS	LEGALSGTRHSHPSVG	300					
QY	301	ROHAGPPSTRPPRPMWDTCP	PPVVAETKFLYSSGDK	KEQLRPSFLSSRLPSLTGARRL	360					
DB	301	ROHAGPPSTRPPRPMWDTCP	PPVVAETKFLYSSGDK	KEQLRPSFLSSRLPSLTGARRL	360					
QY	361	VETIFLGSRPMPGTPRRLPRL	PQRYQWMBPLFELLGNH	AQCPYGVLLKTHCPLRAAVT	420					
DB	361	VETIFLGSRPMPGTPRRLPRL	PQRYQWMBPLFELLGNH	AQCPYGVLLKTHCPLRAAVT	420					
QY	421	PAAGVCAREKPGQGSVAAP	EEEDTPRRLVOLLRQHSS	PWQYGVFRACLRRLVPPGLWS	480					
DB	421	PAAGVCAREKPGQGSVAAP	EEEDTPRRLVOLLRQHSS	PWQYGVFRACLRRLVPPGLWS	480					
QY	481	RHNERRFLRNTKFTSLGKHAK	LISOELTWKMSVRDC	AWLRSPGVCVPAAEHRLREEI	540					
DB	481	RHNERRFLRNTKFTSLGKHAK	LISOELTWKMSVRDC	AWLRSPGVCVPAAEHRLREEI	540					
QY	541	LAKFLHLMVSVVVELLSR	FFVTETTFQKNRLF	FFYKSVMSKLSQSIGIRQHLKRVQRE	600					
DB	541	LAKFLHLMVSVVVELLSR	FFVTETTFQKNRLF	FFYKSVMSKLSQSIGIRQHLKRVQRE	600					
QY	601	LSEAEVROHREAR	PALLTSRLRFTPKPDGLR	PIVNMVVGARTFRREKRAERLTSRVKA	660					
DB	601	LSEAEVROHREAR	PALLTSRLRFTPKPDGLR	PIVNMVVGARTFRREKRAERLTSRVKA	660					
QY	661	LFSVLNYERARRPGLLGAS	VLGLDDIHRAWRTFVL	RVAQDPPPELVFKVDVTGAYDTI	720					
DB	661	LFSVLNYERARRPGLLGAS	VLGLDDIHRAWRTFVL	RVAQDPPPELVFKVDVTGAYDTI	720					
QY	721	PQDRLTEVIASIIKPQNTY	CVRRYAVVQKAANGHV	KAFAKSHVSTLTDLPYMQFVAHL	780					
DB	721	PQDRLTEVIASIIKPQNTY	CVRRYAVVQKAANGHV	KAFAKSHVSTLTDLPYMQFVAHL	780					
QY	781	QETSPLRDAVIEQSSS	LINEASSGLFDVFLRF	MCCHAVIRKGSYVOCGIPGGSILSTL	840					
DB	781	QETSPLRDAVIEQSSS	LINEASSGLFDVFLRF	MCCHAVIRKGSYVOCGIPGGSILSTL	840					
QY	841	LCSLCYGDMEKMLFAGIR	DDGLLRVDDFLVTPH	LTHAKTFLRTLVRGVPYGCVVNL	900					
DB	841	LCSLCYGDMEKMLFAGIR	DDGLLRVDDFLVTPH	LTHAKTFLRTLVRGVPYGCVVNL	900					
QY	901	RKTVVNPFVEALGCTA	FVOMPAGHLFPWCGL	LLDTRTLEVSQDYSYARTSTRASLTP	960					
DB	901	RKTVVNPFVEALGCTA	FVOMPAGHLFPWCGL	LLDTRTLEVSQDYSYARTSTRASLTP	960					
QY	961	NRGPKAGRMRRKLF	GVLRKCHSLFLDLQ	VNSLQVCTNIYKILLQAYRFHACVLQLP	1020					

Db	961	NRGFKAGNMRKLF	GVLRKCHSLFLDLQVNSLQT	CTNIYKILLQAYRFHACVLQLP	1020																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																													</
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Db 1 MPAPRCRAVRSLSRSHYREVLPFLATFVRRLGPOGRLVQRGDPAAFRALVAQCLVCPW 60
QY 61 DARPPAAPSPROVSKLKLVARVLQRLCERGAKNVLAFGFALLDARGGPPPEAFTTSVR 120
Db 61 DARPPAAPSPROVSKLKLVARVLQRLCERGAKNVLAFGFALLDARGGPPPEAFTTSVR 120
QY 121 SYLVNTVTDALRGSGANGLLLRVGDVLLVHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180
Db 121 SYLVNTVTDALRGSGANGLLLRVGDVLLVHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180
QY 181 ATQARPPPHASGPRRLCERAWNSVREAGVPLGLPARGARRGGSASRSILPKRPRR 240
Db 181 ATQARPPPHASGPRRLCERAWNSVREAGVPLGLPARGARRGGSASRSILPKRPRR 240
QY 241 GAAPPERTPVQGSWAHPGTRGSDRGFCVSPARPAEATSLGALSGRTRHSPVSG 300
Db 241 GAAPPERTPVQGSWAHPGTRGSDRGFCVSPARPAEATSLGALSGRTRHSPVSG 300
QY 301 ROHAGPSTSRPPRMDTPCPVVAETKHFLLYSSGDKQLRPSFLLSRPSLTGARRL 360
Db 301 ROHAGPSTSRPPRMDTPCPVVAETKHFLLYSSGDKQLRPSFLLSRPSLTGARRL 360
QY 361 VETIFLGRSPWPCTPRRLPRLPQRYQWRPLFELLLGNHQAQCPYGVLLKTHCPLRAAVT 420
Db 361 VETIFLGRSPWPCTPRRLPRLPQRYQWRPLFELLLGNHQAQCPYGVLLKTHCPLRAAVT 420
QY 421 PAAGVCAREKPGSVAAPPEEDTPRRLVOLLROHSSPWQVYGFVRACLRRLVPPGLWGS 480
Db 421 PAAGVCAREKPGSVAAPPEEDTPRRLVOLLROHSSPWQVYGFVRACLRRLVPPGLWGS 480
QY 481 RHNERFLRNTKFTISLGHAKLSIQELTWKMSVRDCAWLRSPGVCVPAAEHLRREI 540
Db 481 RHNERFLRNTKFTISLGHAKLSIQELTWKMSVRDCAWLRSPGVCVPAAEHLRREI 540
QY 541 LAKFLHMLSVVVELLSFFVYVTTTQKRLFFYRKSVMKLSQIGIRQHLKRVQRE 600
Db 541 LAKFLHMLSVVVELLSFFVYVTTTQKRLFFYRKSVMKLSQIGIRQHLKRVQRE 600
QY 601 LSEAVROHREARPAALLSRFLFKPKDGLRPIVNDVYVVGARTPRRKRERLTSRYKA 660
Db 601 LSEAVROHREARPAALLSRFLFKPKDGLRPIVNDVYVVGARTPRRKRERLTSRYKA 660
QY 661 LFSVLNTERARRPGLLGASVLGLDIIHRAWRTFVLVRAQDPPPELYFKVDVTGAYDTI 720
Db 661 LFSVLNTERARRPGLLGASVLGLDIIHRAWRTFVLVRAQDPPPELYFKVDVTGAYDTI 720
QY 721 PODRLTEVIASIIKPNQTYCVRRYAVQKAAHGHVRKAFKSHVSTLTDLPYMRQFVAHL 780
Db 721 PODRLTEVIASIIKPNQTYCVRRYAVQKAAHGHVRKAFKSHVSTLTDLPYMRQFVAHL 780
QY 781 QETSLRDAVVIQSSSLNEASSGLFDVFLRPMCHAVRIRCKSVYVQCGIPQGSILSTL 840
Db 781 QETSLRDAVVIQSSSLNEASSGLFDVFLRPMCHAVRIRCKSVYVQCGIPQGSILSTL 840
QY 841 LCSLCYGMENKLFAGIRDDGLLLRLLVDFLLVTLTHAKTFLRTLVRGPEYCCVNL 900
Db 841 LCSLCYGMENKLFAGIRDDGLLLRLLVDFLLVTLTHAKTFLRTLVRGPEYCCVNL 900
QY 901 RKTVNVFPVEDEALGGTAFVQMPAHGLFPWCGLLDTLRTLEVQSDYSYVARTSIRASLTF 960
Db 901 RKTVNVFPVEDEALGGTAFVQMPAHGLFPWCGLLDTLRTLEVQSDYSYVARTSIRASLTF 960
QY 961 NRGFKAGNRMRKLFVGLRLKCHSLFLDLQVNSLQTVCTNIYKILLLOAYRFHACVLQLP 1020
Db 961 NRGFKAGNRMRKLFVGLRLKCHSLFLDLQVNSLQTVCTNIYKILLLOAYRFHACVLQLP 1020
QY 1021 FHOQVWKNPTFLRIVISDTASLCYSLKAKNAGMSLGKAGAGPLPSEAVQMLCHOAFL 1080
Db 1021 FHOQVWKNPTFLRIVISDTASLCYSLKAKNAGMSLGKAGAGPLPSEAVQMLCHOAFL 1080
QY 1081 KLTRHRVTYVPLGSLRTAQOLSKRLPGTTLTALAAANPALPSDFKTILD 1132

Db 1081 KLTRHRVTYVPLGSLRTAQOLSKRLPGTTLTALAAANPALPSDFKTILD 1132
RESULT 5
AAY43621
ID AAY43621 standard; protein; 1132 AA.
XX AAY43621;
AC AAY43621;
XX 26-JAN-2000 (first entry)
DT 26-JAN-2000 (first entry)
XX A human telomerase reverse transcriptase (TERT) polypeptide.
DE Human; telomerase reverse transcriptase; TERT; T lymphocyte activation;
XX dendritic cell; telomerase activity; cancer cell; proliferating cell;
KW immunological destruction; telomerase; cancer; proliferation disease.
KW Homo sapiens.
OS
XX WO9950392-A1.
PN 07-OCT-1999.
PD 30-MAR-1999; 99WO-US006898.
XX 31-MAR-1998; 98US-0112006P.
PR (GERO-) GERON CORP.
PA Gaeta FCA;
PI WPI; 1999-610845/52.
XX N-PSDB; AAZ30154.
DR Eliciting an in vivo immune response for prevention and treatment of
PT cancers.
PT Claim 3; Fig 1; 26pp; English.
PS The present sequence represents a human telomerase reverse transcriptase
CC (TERT) polypeptide. The protein is used in the method of the invention.
CC The specification describes a method for activating a T lymphocyte,
CC comprising contacting the T lymphocyte with a dendritic cell that
CC expresses a TERT peptide in the context of a MHC class I or MHC class II
CC molecule. The protein causes induction of an in vivo immunological
CC response to telomerase activity. Cancer cells are characterized by
CC expression of endogenous TERT gene and the presence of detectable
CC telomerase activity. Therefore, by eliciting a specific immune response
CC to TERT or to TERT-expressing cells, it is possible to selectively target
CC proliferating cells for immunological destruction. The method is used for
CC eliciting an in vivo immune response to telomerase by activating a T
CC lymphocyte, and is useful for prevention and treatment of cancers and
CC other proliferation diseases/conditions
SQ Sequence 1132 AA;
Query Match 100.0%; Score 5961; DB 2; Length 1132;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MPAPRCRAVRSLSRSHYREVLPFLATFVRRLGPOGRLVQRGDPAAFRALVAQCLVCPW 60
Db 1 MPAPRCRAVRSLSRSHYREVLPFLATFVRRLGPOGRLVQRGDPAAFRALVAQCLVCPW 60
QY 61 DARPPAAPSPROVSKLKLVARVLQRLCERGAKNVLAFGFALLDARGGPPPEAFTTSVR 120
Db 61 DARPPAAPSPROVSKLKLVARVLQRLCERGAKNVLAFGFALLDARGGPPPEAFTTSVR 120
QY 121 SYLVNTVTDALRGSGANGLLLRVGDVLLVHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180
Db 121 SYLVNTVTDALRGSGANGLLLRVGDVLLVHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180
QY 181 ATQARPPPHASGPRRLCERAWNSVREAGVPLGLPARGARRGGSASRSILPKRPRR 240

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Db 181 ATQARPPHAGPRRLGCRANWHSVREAGVPLGAPGARRGGASRSLPLPKRR 240
Qy 241 GAAPERTPVGQSWAHGTRGSDRGFCVSPARPAEBATSLGALSCTRSHPSVG 300
Db 241 GAAPERTPVGQSWAHGTRGSDRGFCVSPARPAEBATSLGALSCTRSHPSVG 300
Qy 301 RQHAGPSTSRPRPMDTPCPVYAEYKHFYSSGDKQLRPSFLSSLPSTGARRL 360
Db 301 RQHAGPSTSRPRPMDTPCPVYAEYKHFYSSGDKQLRPSFLSSLPSTGARRL 360
Qy 361 VETIFLGSRRPMPGTPRRLPRLPQRYQWMRPLFLELGNHACQPVGVLLKTHCPLRAAVT 420
Db 361 VETIFLGSRRPMPGTPRRLPRLPQRYQWMRPLFLELGNHACQPVGVLLKTHCPLRAAVT 420
Qy 421 PAAGVCAREKPGQSWAAPAEEDTDPRRLVQLLRQHSPPQVYGFVRACLRRLVPPGLWGS 480
Db 421 PAAGVCAREKPGQSWAAPAEEDTDPRRLVQLLRQHSPPQVYGFVRACLRRLVPPGLWGS 480
Qy 481 RHNERFLRNTKFTISLGHAKLSLOELTWKMSVRDCAWLRSPGVCVPAEHLRLEEI 540
Db 481 RHNERFLRNTKFTISLGHAKLSLOELTWKMSVRDCAWLRSPGVCVPAEHLRLEEI 540
Qy 541 LAKFLHLMWSVYVVELLRSFFVYVTTETTFQKRLPFYKSVMSKLSQIGIROHLKRVOLRE 600
Db 541 LAKFLHLMWSVYVVELLRSFFVYVTTETTFQKRLPFYKSVMSKLSQIGIROHLKRVOLRE 600
Qy 601 LSEAEVRQHRARPALLTSRLRPIPKPDGLRPVNMDDYVVGARTFRREKRAERLTSRYKA 660
Db 601 LSEAEVRQHRARPALLTSRLRPIPKPDGLRPVNMDDYVVGARTFRREKRAERLTSRYKA 660
Qy 720 LFSVLNYERARRPGLLGASVIGLDIHRAWTFVLRVAQDPPELFPVKVDVTGAYDTI 720
Db 720 LFSVLNYERARRPGLLGASVIGLDIHRAWTFVLRVAQDPPELFPVKVDVTGAYDTI 720
Qy 780 PQDRLTEVIASIIKPNQYCVRRYAVVOKAAHGHVRKAFKSHVSTLTDLPYMQFVAHL 780
Db 780 PQDRLTEVIASIIKPNQYCVRRYAVVOKAAHGHVRKAFKSHVSTLTDLPYMQFVAHL 780
Qy 840 QETSPLRDAVVEQSSSLEASSGLFDVFLRFMCHHAVIRKGSYVQCQGIPOGSILSTL 840
Db 840 QETSPLRDAVVEQSSSLEASSGLFDVFLRFMCHHAVIRKGSYVQCQGIPOGSILSTL 840
Qy 900 LCSLCYGMENKLFAGIRRDGLLRLVDDFLVTPHLTHAKTFLRTLVRGYPGCVVNL 900
Db 900 LCSLCYGMENKLFAGIRRDGLLRLVDDFLVTPHLTHAKTFLRTLVRGYPGCVVNL 900
Qy 960 RKTVVNPFVEBALGTAFAVQMPAHGLFPWCGLLDDTRTLEVSQSDYSYARTSIRASLTF 960
Db 960 RKTVVNPFVEBALGTAFAVQMPAHGLFPWCGLLDDTRTLEVSQSDYSYARTSIRASLTF 960
Qy 1020 NRGFKAGNRMRKLFVGLRLKCHSLFDLQVNSLQTVCTNIYKILLQAYRFHACVQLQP 1020
Db 1020 NRGFKAGNRMRKLFVGLRLKCHSLFDLQVNSLQTVCTNIYKILLQAYRFHACVQLQP 1020
Qy 1080 FHQWKNKPTFLRVIISTASLCYSILKAKNAGMSLGAKGAGPLPSEAVOWLCHQAPLL 1080
Db 1080 FHQWKNKPTFLRVIISTASLCYSILKAKNAGMSLGAKGAGPLPSEAVOWLCHQAPLL 1080
Qy 1081 KLTRHRVTYVPLGLSLRTAQQLSRKLPGLTTLTALEAANPALSDPKTILD 1132
Db 1081 KLTRHRVTYVPLGLSLRTAQQLSRKLPGLTTLTALEAANPALSDPKTILD 1132
```

RESULT 6

AAV26580

ID AAV26580 standard; protein; 1132 AA.

XX

AC AAV26580;

XX

DT 13-SEP-1999 (first entry)

XX

DE Human telomerase reverse transcriptase (hTERT) enzyme.

```
XX
KW Telomerase reverse transcriptase; TERT; mouse; telomere length assay;
KW immunogen; enzyme; telomerase-mediated DNA replication; human.
OS Homo sapiens.
PN WO9927113-A1.
XX
PD 03-JUN-1999.
XX
PF 25-NOV-1998; 98WO-US025211.
XX
PR 26-NOV-1997; 97US-00979742.
PR 16-MAR-1998; 98US-00042460.
XX
XX (GERO-) GERON CORP.
PA (YESH ) UNIV YESHIVA EINSTEIN COLLEGE.
XX
XX Morin GB, Allsopp R, Depinho R, Greenberg R;
XX WPI; 1999-347722/29.
XX
XX Mouse telomerase reverse transcriptase (mTERT) enzyme proteins and
XX nucleic acids.
XX
XX Disclosure; Fig 3; 135pp; English.
XX
XX The invention relates to a mouse telomerase reverse transcriptase (mTERT)
XX enzyme. Compositions containing mTERT can be used in telomere length
XX assays. Isolated mTERT is useful as an immunogen for the production of
XX monoclonal or polyclonal antibodies. The method is useful for assessing
XX the degree of purification and identification of new mTERT species, such
XX as an mTERT allele, homolog or isoform, or to screen for modulators
XX (antagonists and agonists) of telomerase-mediated DNA replication.
XX Antagonists and agonists of mTERT can be used to modify the activity of
XX other telomerase enzymes such as human TERT (hTERT). The present sequence
XX represents a human TERT enzyme
XX
XX Sequence 1132 AA;
```

```
Query Match 100.0%; Score 5961; DB 2; Length 1132;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MPRAPRCRAVRSLLRSHYREVLPATFVRLGPGQWRLVORGDPAAFRALVAQCLVCVPW 60
Db 1 MPRAPRCRAVRSLLRSHYREVLPATFVRLGPGQWRLVORGDPAAFRALVAQCLVCVPW 60
Qy 61 DARPPPPAAPSFRQVSCLELVARVLQRLCERGAKNVLAFGALLDARGGPEAFTTSVR 120
Db 61 DARPPPPAAPSFRQVSCLELVARVLQRLCERGAKNVLAFGALLDARGGPEAFTTSVR 120
Qy 121 SYLPNTVTDALRSGAGWGLLLRRVGGDDVLVHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180
Db 121 SYLPNTVTDALRSGAGWGLLLRRVGGDDVLVHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180
Qy 181 ATQARPPHAGPRRLGCRANWHSVREAGVPLGAPGARRGGASRSLPLPKRR 240
Db 181 ATQARPPHAGPRRLGCRANWHSVREAGVPLGAPGARRGGASRSLPLPKRR 240
Qy 241 GAAPERTPVGQSWAHGTRGSDRGFCVSPARPAEBATSLGALSCTRSHPSVG 300
Db 241 GAAPERTPVGQSWAHGTRGSDRGFCVSPARPAEBATSLGALSCTRSHPSVG 300
Qy 301 RQHAGPSTSRPRPMDTPCPVYAEYKHFYSSGDKQLRPSFLSSLPSTGARRL 360
Db 301 RQHAGPSTSRPRPMDTPCPVYAEYKHFYSSGDKQLRPSFLSSLPSTGARRL 360
Qy 361 VETIFLGSRRPMPGTPRRLPRLPQRYQWMRPLFLELGNHACQPVGVLLKTHCPLRAAVT 420
Db 361 VETIFLGSRRPMPGTPRRLPRLPQRYQWMRPLFLELGNHACQPVGVLLKTHCPLRAAVT 420
Qy 421 PAAGVCAREKPGQSWAAPAEEDTDPRRLVQLLRQHSPPQVYGFVRACLRRLVPPGLWGS 480
```


Db 421 PAAGVCAREKPGQGSVAAPAEEDTDPRRLVQLLRHSSPWQYGFVRACLRLVPPGLWGS 480
Qy 481 RHNERRFLRNTKFKFISLKGKAKLSLOELTWKMSVDPDCAWLRSPGVCVPAAEHRLREEI 540
Db 481 RHNERRFLRNTKFKFISLKGKAKLSLOELTWKMSVDPDCAWLRSPGVCVPAAEHRLREEI 540
Qy 541 LAKFLHLMMSVYVVELLSRFFVTTTQKNRLLFFYRKSVMKLSQSIGIRHKLKRVQRE 600
Db 541 LAKFLHLMMSVYVVELLSRFFVTTTQKNRLLFFYRKSVMKLSQSIGIRHKLKRVQRE 600
Qy 601 LSEAEVRQHRREARPAALLTSRLRFPKPDGLRPIVNM DYVVGARTFRREKRAERLTSRVKA 660
Db 601 LSEAEVRQHRREARPAALLTSRLRFPKPDGLRPIVNM DYVVGARTFRREKRAERLTSRVKA 660
Qy 661 LFSVLNTERARRPGLLGASVLGLDDIHRARTFVLVRAQDPPPELYFVKVDVTGAYDTI 720
Db 661 LFSVLNTERARRPGLLGASVLGLDDIHRARTFVLVRAQDPPPELYFVKVDVTGAYDTI 720
Qy 721 PQDLRLTEVIASIIKFPNTYCYRRVAVVQAAHGHVRKAFKSHVSTLTDLQPMRQFVAHL 780
Db 721 PQDLRLTEVIASIIKFPNTYCYRRVAVVQAAHGHVRKAFKSHVSTLTDLQPMRQFVAHL 780
Qy 781 QETSPRLDAVVIQSSSLNEASSGLFDVFLRFMCHHAVIRKSYVQCQIPQGSILSTL 840
Db 781 QETSPRLDAVVIQSSSLNEASSGLFDVFLRFMCHHAVIRKSYVQCQIPQGSILSTL 840
Qy 841 LCSLCYGDMEKLFAGIRBDGLLLRLVDDFLVTPHLTHAKTFLTLVRGPEYGCVVNL 900
Db 841 LCSLCYGDMEKLFAGIRBDGLLLRLVDDFLVTPHLTHAKTFLTLVRGPEYGCVVNL 900
Qy 901 RKTVMNPFVEDEALGCTAFVQMPAHGLFPWCGLLDDTRTLEVSQSYSSYARTSIRASLTF 960
Db 901 RKTVMNPFVEDEALGCTAFVQMPAHGLFPWCGLLDDTRTLEVSQSYSSYARTSIRASLTF 960
Qy 961 NRGFKAGRMRRKLFVGLRLKCHSLFDLQVNSLQTVCTNIYKILLQAYRFHACVLQLP 1020
Db 961 NRGFKAGRMRRKLFVGLRLKCHSLFDLQVNSLQTVCTNIYKILLQAYRFHACVLQLP 1020
Qy 1021 PHQVWKNTPTFLRVIDSTASLCYSILKAKNAGSLGAKGAGPLPSEAVQWLCHQAFLL 1080
Db 1021 PHQVWKNTPTFLRVIDSTASLCYSILKAKNAGSLGAKGAGPLPSEAVQWLCHQAFLL 1080
Qy 1081 KLTRHRVTYVPLGLSLRTAQTLRSKLPGLTTLTALAAANPALSDPKTILD 1132
Db 1081 KLTRHRVTYVPLGLSLRTAQTLRSKLPGLTTLTALAAANPALSDPKTILD 1132

RESULT 7

AAG64859

ID AAG64859 standard; protein; 1132 AA.

XX AC AAG64859;

XX DT 21-SEP-2001 (first entry)

XX DE Heart muscle cell differentiation related protein SEQ ID NO: 31.

XX KW Heart muscle cell; human; cell differentiation; heart disease.

XX OS Homo sapiens.

XX PN WO200148151-A1.

XX PD 05-JUL-2001.

XX PF 27-DEC-2000; 2000WO-JP009323.

XX PR 28-DEC-1999; 95JP-00372826.

XX PR 28-FEB-2000; 2000WO-JP001148.

XX PR 02-NOV-2000; 2000WO-JP007741.

XX PA (KYOW) KYOWA HAKKO KOGYO KK.

XX Umezawa A, Hata J, Fukuda K, Ogawa S, Sakurada K, Gojo S;
PI Yamada Y;
XX WPI; 2001-425656/45.
DR N-PSDB; AAH48235.
XX Cells capable of differentiating into cardiomyocytes and originating in
bone marrow or umbilical blood cells for study of cardiomyocyte
differentiation and treatment of heart disease.
XX Claim 87; Page 143-147; 183pp; Japanese.
PS The present invention provides cells originating in the human bone marrow
or umbilical blood cells which are capable of differentiating into
cardiomyocytes. These cells are useful in the treatment of diseases
involving heart muscle degeneration, such as myocardial infarction, and
the study of cardiomyocyte differentiation. The present sequence is a
protein described in the exemplification of the invention
XX Sequence 1132 AA;

Query Match 100.0%; Score 5961; DB 4; Length 1132;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MPAPRCRAVRSLSRSHYREVLPATFVRRLGPGQWRLVORGDPAAPRALVAQCLVCVPM 60
Db 1 MPAPRCRAVRSLSRSHYREVLPATFVRRLGPGQWRLVORGDPAAPRALVAQCLVCVPM 60
Qy 61 DARPPAAPFRQVSCLELVARVLQRLCERGANVLAFAFGALLDGGAGGPEAFTTSVR 120
Db 61 DARPPAAPFRQVSCLELVARVLQRLCERGANVLAFAFGALLDGGAGGPEAFTTSVR 120
Qy 121 SYLNTVTDALRGSGANGLLRRVDDVLVHLLARCALFVLVAPSCAYVQCGPPLYQLGA 180
Db 121 SYLNTVTDALRGSGANGLLRRVDDVLVHLLARCALFVLVAPSCAYVQCGPPLYQLGA 180
Qy 181 ATQARPPHAGSPRRRLGGERANVHVSREACVPLGLPAGARRRGGASRSLLPKRPRR 240
Db 181 ATQARPPHAGSPRRRLGGERANVHVSREACVPLGLPAGARRRGGASRSLLPKRPRR 240
Qy 241 GAAPEPRTVPGQSWAHPCGTRGSDRGFCVSPARPAEATSLGALSSTRHSPSVG 300
Db 241 GAAPEPRTVPGQSWAHPCGTRGSDRGFCVSPARPAEATSLGALSSTRHSPSVG 300
Qy 301 RQHAGPSTSRPRPMDTTPCPVYAEKHPLYSSGDKQLRPSFLSSLPSTGARRL 360
Db 301 RQHAGPSTSRPRPMDTTPCPVYAEKHPLYSSGDKQLRPSFLSSLPSTGARRL 360
Qy 361 VETIFLGSRRPMPGTPRRLPRLPORYWQMRPLFLELLGNHAQCPYVLLKTHCPLRAAVT 420
Db 361 VETIFLGSRRPMPGTPRRLPRLPORYWQMRPLFLELLGNHAQCPYVLLKTHCPLRAAVT 420
Qy 421 PAAGVCAREKPGQGSVAAPAEEDTDPRRLVQLLRHSSPWQYGFVRACLRLVPPGLWGS 480
Db 421 PAAGVCAREKPGQGSVAAPAEEDTDPRRLVQLLRHSSPWQYGFVRACLRLVPPGLWGS 480
Qy 481 RHNERRFLRNTKFKFISLKGKAKLSLOELTWKMSVRDCAWLRSPGVCVPAAEHRLREEI 540
Db 481 RHNERRFLRNTKFKFISLKGKAKLSLOELTWKMSVRDCAWLRSPGVCVPAAEHRLREEI 540
Qy 541 LAKFLHLMMSVYVVELLSRFFVTTTQKNRLLFFYRKSVMKLSQSIGIRHKLKRVQRE 600
Db 541 LAKFLHLMMSVYVVELLSRFFVTTTQKNRLLFFYRKSVMKLSQSIGIRHKLKRVQRE 600
Qy 601 LSEAEVRQHRREARPAALLTSRLRFPKPDGLRPIVNM DYVVGARTFRREKRAERLTSRVKA 660
Db 601 LSEAEVRQHRREARPAALLTSRLRFPKPDGLRPIVNM DYVVGARTFRREKRAERLTSRVKA 660
Qy 661 LFSVLNTERARRPGLLGASVLGLDDIHRARTFVLVRAQDPPPELYFVKVDVTGAYDTI 720
Db 661 LFSVLNTERARRPGLLGASVLGLDDIHRARTFVLVRAQDPPPELYFVKVDVTGAYDTI 720

QY 721 QDRLTEVIASIIKPONTYCVRRYAVVQKAAHGHVRKAFKSHVSTLTDLQYMRQFVAHL 780
 Db 721 QDRLTEVIASIIKPONTYCVRRYAVVQKAAHGHVRKAFKSHVSTLTDLQYMRQFVAHL 780
 QY 781 QETSPLRDAVIEQSSSINEASSGLFDVFLRFMCHHAVIRGKSVQCGIPOGSIILSTL 840
 Db 781 QETSPLRDAVIEQSSSINEASSGLFDVFLRFMCHHAVIRGKSVQCGIPOGSIILSTL 840
 QY 841 LCSLCYGDMEKNLFGIRRDGLLRLVDDFLVTPHLTHAKTFLRTLVRGVPYEGCVVNL 900
 Db 841 LCSLCYGDMEKNLFGIRRDGLLRLVDDFLVTPHLTHAKTFLRTLVRGVPYEGCVVNL 900
 QY 901 RKTVMNPFVEDEALGGTAFVQMPAHGLFPWCGLLDTRTLEVSQSDYSYARTSTRASLTF 960
 Db 901 RKTVMNPFVEDEALGGTAFVQMPAHGLFPWCGLLDTRTLEVSQSDYSYARTSTRASLTF 960
 QY 961 NRGFKAGNMRKLFVGLRLKCHSLFDLQVNSLQVCTNIYKILLQAYRFHACVLQLP 1020
 Db 961 NRGFKAGNMRKLFVGLRLKCHSLFDLQVNSLQVCTNIYKILLQAYRFHACVLQLP 1020
 QY 1021 FHQQVWKNPTFLRLVISDTASLCYSILKAKNAGMSLGAKGAAGPLPSEAVQMLCHQAFLL 1080
 Db 1021 FHQQVWKNPTFLRLVISDTASLCYSILKAKNAGMSLGAKGAAGPLPSEAVQMLCHQAFLL 1080
 QY 1081 KLTHRVTVYVPLGSLRTAQTLQSRKLPDGTTLTALEAAANPALPSDFKTILD 1132
 Db 1081 KLTHRVTVYVPLGSLRTAQTLQSRKLPDGTTLTALEAAANPALPSDFKTILD 1132

RESULT 8

AAG64329 ID AAG64329 standard; protein; 1132 AA.
 XX AC AAG64329;
 XX AC
 XX DT 24-SEP-2001 (first entry)
 XX DE Human protein #2.
 XX KW Angiogenesis; cardiast; cell differentiating agent; bone marrow;
 XX KW heart muscle cell; heart disease; human.
 XX OS Homo sapiens.
 XX FN WO200148149-A1.
 XX PD 05-JUL-2001.
 XX PF 28-FEB-2000; 2000WO-JP001148.
 XX PR 28-DEC-1999; 99JP-00372826.
 XX PA (KYOW) KYOWA HAKKO KOGYO KK.
 XX PI Umezawa A, Hata J, Fukuda K, Ogawa S, Sakurada K;
 XX WPI; 2001-418252/44.
 XX DR N-PSDB; AAH49601.
 XX PT New adult bone marrow-originated cells capable of differentiating into
 XX PT heart muscle cells, applicable as remedies for various heart diseases
 XX PT particularly with damaged heart muscle accompanying degeneration.
 XX PS Disclosure; Page 128-134; 158pp; Japanese.
 XX CC The present invention relates to cells isolated from bone marrow, which
 XX CC are capable of at least differentiating into heart muscle cells. The
 XX CC cells are applicable as remedies for various heart diseases particularly
 XX CC with damaged heart muscle accompanying degeneration. The present sequence
 XX CC was used to illustrate the present invention
 XX Sequence 1132 AA;

Query Match 100.0%; Score 5961; DB 4; Length 1132;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MPRAPRCRAVRSLLRSHYREVLPATFVRILPGQWMLVQGGDPAAPALVAQCCLVCVPW 60
 Db 1 MPRAPRCRAVRSLLRSHYREVLPATFVRILPGQWMLVQGGDPAAPALVAQCCLVCVPW 60
 QY 61 DARPPPAAPSFQVSCCLKELVARVLQRLCERGAKNVLAFGFALLDARGGPEAFTTSVR 120
 Db 61 DARPPPAAPSFQVSCCLKELVARVLQRLCERGAKNVLAFGFALLDARGGPEAFTTSVR 120
 QY 121 SYLPTNTVTDALRGSGAWGLLLRRVGGDVLVHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180
 Db 121 SYLPTNTVTDALRGSGAWGLLLRRVGGDVLVHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180
 QY 181 ATQARPPPHASGRRRLGGERAWNHSVREAGVPLGLPAGARRGGGSASRLPLPKPRR 240
 Db 181 ATQARPPPHASGRRRLGGERAWNHSVREAGVPLGLPAGARRGGGSASRLPLPKPRR 240
 QY 241 GAAPEPERTVGGQSWAHPGRTGRGSDRGFCVVSPPARPAEATSLGALSCTRHSHPVG 300
 Db 241 GAAPEPERTVGGQSWAHPGRTGRGSDRGFCVVSPPARPAEATSLGALSCTRHSHPVG 300
 QY 301 RQHHAGPPSTRPPRWDTPCPVYASTKHFLYSSGDKQOLRPSFLLSRLPSLTGARRL 360
 Db 301 RQHHAGPPSTRPPRWDTPCPVYASTKHFLYSSGDKQOLRPSFLLSRLPSLTGARRL 360
 QY 361 VETIFLGSRDWMPCTPRRLPRLPQRYWQMPFLFLELGNHAQCPYGVLLKTHCPLRAAVT 420
 Db 361 VETIFLGSRDWMPCTPRRLPRLPQRYWQMPFLFLELGNHAQCPYGVLLKTHCPLRAAVT 420
 QY 421 PAAGVCAREKPOGSAVAPEEEDTPRRLVOLLROHSSPWQVYGFVRACLRLVPPGLWGS 480
 Db 421 PAAGVCAREKPOGSAVAPEEEDTPRRLVOLLROHSSPWQVYGFVRACLRLVPPGLWGS 480
 QY 481 RHNERRFLNTKKFISLGKHAJLSLOELTWKMSVRDCAWLRRSGVGCVAAPAEHRLREEI 540
 Db 481 RHNERRFLNTKKFISLGKHAJLSLOELTWKMSVRDCAWLRRSGVGCVAAPAEHRLREEI 540
 QY 541 LAKFLHMLMSVYVVELLRSFFYVTEITFOKNRFFYKRSVMSKLOSTGIROHLKRVQURE 600
 Db 541 LAKFLHMLMSVYVVELLRSFFYVTEITFOKNRFFYKRSVMSKLOSTGIROHLKRVQURE 600
 QY 601 LSEAEVRQHREARPALTSRLRFPKPDGLRPIVNM DYVVGARTFRREKRAERLTSRYKA 660
 Db 601 LSEAEVRQHREARPALTSRLRFPKPDGLRPIVNM DYVVGARTFRREKRAERLTSRYKA 660
 QY 661 LFSVLNYERARRPGLLGASVILGDDIHRWRTFVLVRADQPPPELYFVKVDVTGAYDTI 720
 Db 661 LFSVLNYERARRPGLLGASVILGDDIHRWRTFVLVRADQPPPELYFVKVDVTGAYDTI 720
 QY 721 QDRLTEVIASIIKPONTYCVRRYAVVQKAAHGHVRKAFKSHVSTLTDLQYMRQFVAHL 780
 Db 721 QDRLTEVIASIIKPONTYCVRRYAVVQKAAHGHVRKAFKSHVSTLTDLQYMRQFVAHL 780
 QY 781 QETSPLRDAVIEQSSSINEASSGLFDVFLRFMCHHAVIRGKSVQCGIPOGSIILSTL 840
 Db 781 QETSPLRDAVIEQSSSINEASSGLFDVFLRFMCHHAVIRGKSVQCGIPOGSIILSTL 840
 QY 841 LCSLCYGDMEKNLFGIRRDGLLRLVDDFLVTPHLTHAKTFLRTLVRGVPYEGCVVNL 900
 Db 841 LCSLCYGDMEKNLFGIRRDGLLRLVDDFLVTPHLTHAKTFLRTLVRGVPYEGCVVNL 900
 QY 901 RKTVMNPFVEDEALGGTAFVQMPAHGLFPWCGLLDTRTLEVSQSDYSYARTSTRASLTF 960
 Db 901 RKTVMNPFVEDEALGGTAFVQMPAHGLFPWCGLLDTRTLEVSQSDYSYARTSTRASLTF 960
 QY 961 NRGFKAGNMRKLFVGLRLKCHSLFDLQVNSLQVCTNIYKILLQAYRFHACVLQLP 1020
 Db 961 NRGFKAGNMRKLFVGLRLKCHSLFDLQVNSLQVCTNIYKILLQAYRFHACVLQLP 1020

Qy 1021 FHQVWKNPTFLRIVSDTASLCYSILKAKNAGMSLGAAGPLPSAVQWLCHQAPLL 1080
Db |||||
1021 FHQVWKNPTFLRIVSDTASLCYSILKAKNAGMSLGAAGPLPSAVQWLCHQAPLL 1080
Qy 1081 KLTRHRTVTVPLGLSLRTAQQLSKLPGLTTLTALEAANPALPSDFKTIILD 1132
Db |||||
1081 KLTRHRTVTVPLGLSLRTAQQLSKLPGLTTLTALEAANPALPSDFKTIILD 1132

RESULT 9

AAB99930
ID AAB99930 standard; protein; 1132 AA.
XX
AC AAB99930;
XX
DT 26-SEP-2001 (first entry)
XX
DE Human telomerase protein sequence SEQ ID NO:31.
XX
KW Differentiation; heart muscle cell; cytokine; transcription factor;
KW proliferation; surface antigen; heart disease; cardiomyocyte;
KW bone marrow; umbilical blood cell; heart muscle degeneration;
KW myocardial infarction.

XX Homo sapiens.
OS
XX WO200148150-A1.
XX
XX 05-JUL-2001.
XX
XX 02-NOV-2000; 2000WO-JP007741.
XX
XX 28-DEC-1999; 99JP-00372826.
PR
PR 28-FEB-2000; 2000WO-JP001148.
XX
XX (KTOW) KYOWA HAKKO KOGYO KK.
FA
XX Umezawa A, Hata J, Fukuda K, Ogawa S, Sakurada K, Gojo S;
PI Yamada Y;
PI
XX WPI; 2001-425655/45.
DR
DR N-PSDB; AAH44366.

Cells capable of differentiating into cardiomyocytes and originating in
bone marrow or umbilical blood cells for study of cardiomyocyte
differentiation and treatment of heart disease.
XX
PS Claim 146; Page 137-141; 187pp; Japanese.

XX The present invention describes cells originating in bone marrow or
XX umbilical blood cells which are capable of differentiating into
XX cardiomyocytes. Also described are: (1) cardiomyocytes produced by the
XX differentiation of the cells; (2) a method for carrying out the
XX differentiation into cardiomyocytes, regulated by a promotional and/or
XX inhibitory factor; (3) a method for the differentiation of the cells into
XX cell types other than cardiomyocytes; (4) drug compositions promoting the
XX formation of heart muscle and regeneration of heart tissue which contain
XX the cells; (5) a method for the production of antibodies which recognise
XX the cells, especially antibodies which recognise a surface antigen on the
XX cells; (6) a method for screening factors which promote the proliferation
XX of the cells; (7) a method for immortalising the cells by expressing
XX telomerase in them; (8) drug compositions for the treatment of heart
XX disease which contain the immortalised cells; and (9) cell-free
XX supernatant from the culture of the cells and its use in promoting their
XX differentiation into cardiomyocytes. The cells are used in the treatment
XX of diseases involving heart muscle degeneration, such as myocardial
XX infarction and in the study of cardiomyocyte differentiation. AAH44351 to
XX AAH44409 and AAB99915 to AAB99935 represent sequences used in the
XX exemplification of the present invention

XX Sequence 1132 AA;

Query Match 100.0%; Score 5961; DB 4; Length 1132;

Best Local Similarity 100.0%; Pred. No. 0;
Matches 1132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MPRAPCRAVRSLLRSHYREVLPVPLATFVRRLLGPOGWRILVORGDPAAPALVAQCILCVCPW 60
Db |||||
1 MPRAPCRAVRSLLRSHYREVLPVPLATFVRRLLGPOGWRILVORGDPAAPALVAQCILCVCPW 60
Qy 61 DAREPPAAPSFQVSCIKELVARVLQRLCERGANVLAFGFALLDGAAGGPPPEAFTTSVR 120
Db |||||
61 DAREPPAAPSFQVSCIKELVARVLQRLCERGANVLAFGFALLDGAAGGPPPEAFTTSVR 120
Qy 121 SYLNTVTDALRSGAWGLLLRRVGGDVLVHLLARCALFVLVAPSCAYQVCGPPLYLQGA 180
Db |||||
121 SYLNTVTDALRSGAWGLLLRRVGGDVLVHLLARCALFVLVAPSCAYQVCGPPLYLQGA 180
Qy 181 ATQARPPPHASGPRRRIGCERAMNHSVREAGVPLGLPAPGARRRGGASRSLPLPKRPRR 240
Db |||||
181 ATQARPPPHASGPRRRIGCERAMNHSVREAGVPLGLPAPGARRRGGASRSLPLPKRPRR 240
Qy 241 GAAPEPERTVGGQSWAHPGRTGRGFCVWSPARPAEATSELEGALSCTRSHSPSVG 300
Db |||||
241 GAAPEPERTVGGQSWAHPGRTGRGFCVWSPARPAEATSELEGALSCTRSHSPSVG 300
Qy 301 RQHHAGPPSTSRPPRPMWDTPCPPVYAEKHLFYSYGDEKQLRPSFLSSLRPSLTGARRL 360
Db |||||
301 RQHHAGPPSTSRPPRPMWDTPCPPVYAEKHLFYSYGDEKQLRPSFLSSLRPSLTGARRL 360
Qy 361 VETIFLGSRRPMPGTPRRLPRLPQRYWOMRPLFLELIGNHAQCYPYGVLLKTHCPLRAAVT 420
Db |||||
361 VETIFLGSRRPMPGTPRRLPRLPQRYWOMRPLFLELIGNHAQCYPYGVLLKTHCPLRAAVT 420
Qy 421 PAAGVCAREKPOGSAVAPEEEDTPRRLVOLLROHSSPWQVYGFVRACLRRLLVPPGLWGS 480
Db |||||
421 PAAGVCAREKPOGSAVAPEEEDTPRRLVOLLROHSSPWQVYGFVRACLRRLLVPPGLWGS 480
Qy 481 RHNERRFLRNTKXPISLGKHAQLSLOELTWKMSVRDCAWLRRSPGVGCVPAAEHRLREEI 540
Db |||||
481 RHNERRFLRNTKXPISLGKHAQLSLOELTWKMSVRDCAWLRRSPGVGCVPAAEHRLREEI 540
Qy 541 LAKFLHLWMSVYVVELLRSFFYVTTETTFQKNRLFYFKRSVMSKLOSTGIHQHLKRVQLE 600
Db |||||
541 LAKFLHLWMSVYVVELLRSFFYVTTETTFQKNRLFYFKRSVMSKLOSTGIHQHLKRVQLE 600
Qy 601 LSAEAVRQHREARPAALLTSRLRPIKPDGLRPIVNMVYVVGARTFREKKAERLTSRKA 660
Db |||||
601 LSAEAVRQHREARPAALLTSRLRPIKPDGLRPIVNMVYVVGARTFREKKAERLTSRKA 660
Qy 661 LFSVLNYERARRPGLLGASVLGLDDIHRWRTFVLVRAQDPPPELYFVKVDVTGAYDTI 720
Db |||||
661 LFSVLNYERARRPGLLGASVLGLDDIHRWRTFVLVRAQDPPPELYFVKVDVTGAYDTI 720
Qy 721 PDBLTVIASIIPQNTYCVRRYAVVOKAAHGHVKAFKSHVSTLTDLPYMQFVAHL 780
Db |||||
721 PDBLTVIASIIPQNTYCVRRYAVVOKAAHGHVKAFKSHVSTLTDLPYMQFVAHL 780
Qy 781 QETSPLRDADVIEQSSSLNEASSGLFDVFLRFMCHAVIRGKSYVOCQIPQGSILSTL 840
Db |||||
781 QETSPLRDADVIEQSSSLNEASSGLFDVFLRFMCHAVIRGKSYVOCQIPQGSILSTL 840
Qy 841 LCSLCYGDMEKNLPAFIRRDGLLLRLVDDFLLVTPHLTHAKTFLRTLVRGVPYECVVNL 900
Db |||||
841 LCSLCYGDMEKNLPAFIRRDGLLLRLVDDFLLVTPHLTHAKTFLRTLVRGVPYECVVNL 900
Qy 901 RKTVPNPFVDEALGGTAFVQMPAHGLFPWCGLLLDTRTLEVDQSDYSYARTSTRASLTF 960
Db |||||
901 RKTVPNPFVDEALGGTAFVQMPAHGLFPWCGLLLDTRTLEVDQSDYSYARTSTRASLTF 960
Qy 961 NRGFKAGNRMRRLFGVLRLLKCHSLFDLQVNSIQTVCTNLYKILLQAVRFHACVQLP 1020
Db |||||
961 NRGFKAGNRMRRLFGVLRLLKCHSLFDLQVNSIQTVCTNLYKILLQAVRFHACVQLP 1020
Qy 1021 FHQVWKNPTFLRIVSDTASLCYSILKAKNAGMSLGAAGPLPSAVQWLCHQAPLL 1080
|||

[illegible]

QY 1 MPAPRCRAVRSLLRSHYREVLPATFVRRLGPOGWRLVQRGDPAAFRALVAQCILVCPW 60
DB 1 MPAPRCRAVRSLLRSHYREVLPATFVRRLGPOGWRLVQRGDPAAFRALVAQCILVCPW 60
QY 61 DARPPAAPSPQVSCLELVARVLQRLCERGAKNVLAFFGALLDARGGPPPEAFTTSVR 120
DB 61 DARPPAAPSPQVSCLELVARVLQRLCERGAKNVLAFFGALLDARGGPPPEAFTTSVR 120
QY 121 SYLNTVNTDALRGSGAWGLLLRRVGDVLLVHLLARCALFVLVAPSCAYQVCGPPPLYQLGA 180
DB 121 SYLNTVNTDALRGSGAWGLLLRRVGDVLLVHLLARCALFVLVAPSCAYQVCGPPPLYQLGA 180
QY 181 ATQARPPPHASGPRRLCERAWNHSVREAGVPLGLPAPGARRRGSASRSILPKRPRR 240
DB 181 ATQARPPPHASGPRRLCERAWNHSVREAGVPLGLPAPGARRRGSASRSILPKRPRR 240
QY 241 GAAPPERTPVQGGSWAHGPRTRGSDRGFCVVSAPAEAEATSLGALSGTRHSHPSVG 300
DB 241 GAAPPERTPVQGGSWAHGPRTRGSDRGFCVVSAPAEAEATSLGALSGTRHSHPSVG 300
QY 301 RQHAGPSTSRPPRPMDTPCPVYAEKTHFLYSSGDKQLRPSFLLSLRPSLTGARRL 360
DB 301 RQHAGPSTSRPPRPMDTPCPVYAEKTHFLYSSGDKQLRPSFLLSLRPSLTGARRL 360
QY 361 VETIFLGRPMWPGTRPLRLPQRYQWQRPFLBELGNHAQCPYGVLLKTHCPLRAAVT 420
DB 361 VETIFLGRPMWPGTRPLRLPQRYQWQRPFLBELGNHAQCPYGVLLKTHCPLRAAVT 420
QY 421 PAAGVCAEKPKQGSVAAPPEEDTPRRLVOLLROHSSPMQVYGFVRACILRLVPPGLNGS 480
DB 421 PAAGVCAEKPKQGSVAAPPEEDTPRRLVOLLROHSSPMQVYGFVRACILRLVPPGLNGS 480
QY 481 RHNERFLRNTKFFISLKGHAKLSIQELTWKMSVRDCAWLRSPGVGCPVPAEHLRBEI 540
DB 481 RHNERFLRNTKFFISLKGHAKLSIQELTWKMSVRDCAWLRSPGVGCPVPAEHLRBEI 540
QY 541 LAKFLHMLSVVVBELLRSFFVTETTKQNRLLFPYRKSVWSKLSQIGIRHQLKRVQRE 600
DB 541 LAKFLHMLSVVVBELLRSFFVTETTKQNRLLFPYRKSVWSKLSQIGIRHQLKRVQRE 600
QY 601 LSEAEVQHREARPAALLSRFLFKPKDGLRPVNDVYVVGARTFRERKRAERLTSRYKA 660
DB 601 LSEAEVQHREARPAALLSRFLFKPKDGLRPVNDVYVVGARTFRERKRAERLTSRYKA 660
QY 661 LFSVLNLERARRPGLLGASVLGLDDIHRAWRTFVLVRVAQDPPPELYFKVDVTCAYDTI 720
DB 661 LFSVLNLERARRPGLLGASVLGLDDIHRAWRTFVLVRVAQDPPPELYFKVDVTCAYDTI 720
QY 721 PQDRLTEVIASIIKPNQTYCVRRYAVQKAAHGHVRKAPKSHVSTLTDLPYMRQFVAHL 780
DB 721 PQDRLTEVIASIIKPNQTYCVRRYAVQKAAHGHVRKAPKSHVSTLTDLPYMRQFVAHL 780
QY 781 QETSLRDAVITEQSSSNEASSGLFDVFLRPMCHAVRIRCKSVYQCGIPIQGSILSTL 840
DB 781 QETSLRDAVITEQSSSNEASSGLFDVFLRPMCHAVRIRCKSVYQCGIPIQGSILSTL 840
QY 841 LCSLCYGMENKLFAGIRDDGLLLRLVDDFLVATPHLTHAKTFLTLVRGPEYCCVNL 900
DB 841 LCSLCYGMENKLFAGIRDDGLLLRLVDDFLVATPHLTHAKTFLTLVRGPEYCCVNL 900
QY 901 RKTVVNFPVEDBALGTAFAVQMPAHLFPWCGLLDDTRLEQSDYSYARTSIRASLTF 960
DB 901 RKTVVNFPVEDBALGTAFAVQMPAHLFPWCGLLDDTRLEQSDYSYARTSIRASLTF 960
QY 961 NRGFKAGNRMRKLFVGLKCHSLFLLQVNSLOTVCNTIYKILLQAYRHACVLOLP 1020
DB 961 NRGFKAGNRMRKLFVGLKCHSLFLLQVNSLOTVCNTIYKILLQAYRHACVLOLP 1020
QY 1021 FHOQVWKNTFFLRVISTASICYSLKAKNAGMSLGAKGAGPLPSEAVQWLCHQAFLL 1080
DB 1021 FHOQVWKNTFFLRVISTASICYSLKAKNAGMSLGAKGAGPLPSEAVQWLCHQAFLL 1080
QY 1081 KLTHRVTVTVPLGLSLRTAQQLSRKLPQTTLTALAAANPALPSDFKTILD 1132

DB 1081 KLTHRVTVTVPLGLSLRTAQQLSRKLPQTTLTALAAANPALPSDFKTILD 1132
RESULT 11
AAE29226
ID AAE29226 standard; protein; 1132 AA.
XX AAE29226;
AC AC
DT 27-JAN-2003 (first entry)
XX
DE Human telomerase reverse transcriptase (TERT).
XX Carbohydrate antigen; alpha(1,3)galactosyltransferase; alpha1,3GT; TERT;
KW transgenic; alpha(1,2)fucosyltransferase; alpha1,2FT; human; enzyme;
KW telomerase reverse transcriptase.
XX
OS Homo sapiens.
XX
FN WO200274948-A2.
XX
PD 26-SEP-2002.
XX
PF 21-MAR-2002; 2002WO-CA000378.
XX
PR 21-MAR-2001; 2001US-0277811P.
XX
PA (GERO-) GERON CORP.
XX
PI Denning C, Clark AJ, Schiff JM;
XX
DR WPI; 2002-759895/82.
DR N-PSDB; AAD46821.
XX
PT Mammalian cells, useful for producing animal tissues with carbohydrate
XX antigens that are compatible for transplantation into human patients.
PS Disclosure; Page 34; 7ipp; English.
XX
CC The invention relates to animal tissues with carbohydrate antigens that
CC are compatible for transplantation into human patients. The mammalian
CC cell is inactivated homozygously for expression of alpha(1,3)galactosyl-
CC transferase (alpha1,3GT) gene and comprises a transgene for alpha(1,2)-
CC fucosyltransferase (alpha1,2FT). It is useful for producing animal tissue
CC with carbohydrate antigens that are compatible for transplantation into
CC human patients. The present sequence is human telomerase reverse
CC transcriptase (TERT) used in the invention
SQ Sequence 1132 AA;
Query Match 100.0%; Score 5961; DB 5; Length 1132;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MPAPRCRAVRSLLRSHYREVLPATFVRRLGPOGWRLVQRGDPAAFRALVAQCILVCPW 60
DB 1 MPAPRCRAVRSLLRSHYREVLPATFVRRLGPOGWRLVQRGDPAAFRALVAQCILVCPW 60
QY 61 DARPPAAPSPQVSCLELVARVLQRLCERGAKNVLAFFGALLDARGGPPPEAFTTSVR 120
DB 61 DARPPAAPSPQVSCLELVARVLQRLCERGAKNVLAFFGALLDARGGPPPEAFTTSVR 120
QY 121 SYLNTVNTDALRGSGAWGLLLRRVGDVLLVHLLARCALFVLVAPSCAYQVCGPPPLYQLGA 180
DB 121 SYLNTVNTDALRGSGAWGLLLRRVGDVLLVHLLARCALFVLVAPSCAYQVCGPPPLYQLGA 180
QY 181 ATQARPPPHASGPRRLCERAWNHSVREAGVPLGLPAPGARRRGSASRSILPKRPRR 240
DB 181 ATQARPPPHASGPRRLCERAWNHSVREAGVPLGLPAPGARRRGSASRSILPKRPRR 240
QY 241 GAAPPERTPVQGGSWAHGPRTRGSDRGFCVVSAPAEAEATSLGALSGTRHSHPSVG 300
DB 241 GAAPPERTPVQGGSWAHGPRTRGSDRGFCVVSAPAEAEATSLGALSGTRHSHPSVG 300

361 VETIFLGRSPWPGTPRRLPRLPQRYWQRPFLFELLLGNHQAQCPYGVLLKTHCPLRAAVT 420
421 PAAGVCAREKPGQSVAAPEEEDTDRRLVQLLRQHSHPQVYGFVRACLRRLVPPGLWGS 480
421 PAAGVCAREKPGQSVAAPEEEDTDRRLVQLLRQHSHPQVYGFVRACLRRLVPPGLWGS 480
481 RHNERFLRNTKFIISLGHAKLSLOELTWKMSVRDCAWLRSPGVGCVPAAEHLRREI 540
481 RHNERFLRNTKFIISLGHAKLSLOELTWKMSVRDCAWLRSPGVGCVPAAEHLRREI 540
541 LAKFLHMLSVVYVVELLSFFVYTTTFOKNRLLPFRKSVWSKLSIGIRQHLKRVQRE 600
541 LAKFLHMLSVVYVVELLSFFVYTTTFOKNRLLPFRKSVWSKLSIGIRQHLKRVQRE 600
601 LSEAEVROHREARPAALLSRFLFKPKDGLRPIVNDYVVGARTFRREKRAERLRSVKA 660
601 LSEAEVROHREARPAALLSRFLFKPKDGLRPIVNDYVVGARTFRREKRAERLRSVKA 660
661 LFSVLNTERARRPGLLGASVLGLDDIHRARWTFVLVRQAQDPPPELYFKVDVTGAYDTI 720
661 LFSVLNTERARRPGLLGASVLGLDDIHRARWTFVLVRQAQDPPPELYFKVDVTGAYDTI 720
721 PODRLTEVIASIIKQNTYCVRRYAVQKAAHGHVRKAFKSHVSTLTDLPYMRQFVAHL 780
721 PODRLTEVIASIIKQNTYCVRRYAVQKAAHGHVRKAFKSHVSTLTDLPYMRQFVAHL 780
781 QETSLRDAVTEQSSSNEASSGLPDVFLRPMCHHVRIRKSVVQCGIPQGSILSTL 840
781 QETSLRDAVTEQSSSNEASSGLPDVFLRPMCHHVRIRKSVVQCGIPQGSILSTL 840
841 LCSLCYGMENKLFAGIRRDGLLLRLVDVDFLLVTPHLTHAKTFLRLVRGVEYGCNVNL 900
841 LCSLCYGMENKLFAGIRRDGLLLRLVDVDFLLVTPHLTHAKTFLRLVRGVEYGCNVNL 900
901 RKTVPNPFVEDALGGTAFVQMPAHLFPWCGLLDDTRTLEVQSDYSSYARTSIRASLTF 960
901 RKTVPNPFVEDALGGTAFVQMPAHLFPWCGLLDDTRTLEVQSDYSSYARTSIRASLTF 960
961 NRGFKAGNMRKLPGLVRLKCHSLFLDLQVNSLQTVCTNIYKILLQAYRPHACVLOLP 1020
961 NRGFKAGNMRKLPGLVRLKCHSLFLDLQVNSLQTVCTNIYKILLQAYRPHACVLOLP 1020
1021 FHOQWKNPFTFLRVISDTASLCYILKAKNAGMSLGAKGAGPLPSEAVQWLCHQAFLL 1080
1021 FHOQWKNPFTFLRVISDTASLCYILKAKNAGMSLGAKGAGPLPSEAVQWLCHQAFLL 1080
1081 KLTHRVTVYVPLGLSLRTAQTSRLKPLGTTTLTALEAAANPALPSDFKTILD 1132
1081 KLTHRVTVYVPLGLSLRTAQTSRLKPLGTTTLTALEAAANPALPSDFKTILD 1132

RESULT 13
ID ABR42384
ID ABR42384 standard; protein; 1132 AA.
AC ABR42384;
XX
DT 11-AUG-2003 (first entry)
XX
DE Human telomerase reverse transcriptase.
KW Telomerase reverse transcriptase; TERT; enzyme; RNA interference;
KW short interfering RNA; siRNA; cancer; tumour; cytostatic; contraceptive;
KW immunosuppressive; antifertility; fungicide; antiparasitic;
KW antiinflammatory; human; gene therapy.
OS Homo sapiens.
XX
PN WO2003035667-A2.
XX
PD 01-MAY-2003.
XX

16-OCT-2002; 2002WO-US033065.
XX
22-OCT-2001; 2001US-0345326P.
PR
20-FEB-2002; 2002US-0359196P.
PR
22-MAY-2002; 2002US-0383195P.
XX
(UYRP) UNIV ROCHESTER.
PA
Rowley PT;
XX
WPI: 2003-403336/38.
DR N-PSDB; ACC58039.
XX
Novel double-stranded short interfering RNA having sense and antisense
nucleic acids which are complementary to each other and to target nucleic
acid e.g., telomerase RNA or mRNA encoding telomerase reverse
transcriptase.
XX
Disclosure; Fig 4; 37pp; English.
PS
The present sequence is the protein sequence of human telomerase reverse
transcriptase (TERT). The invention relates to the discovery that double-
stranded interfering RNAs, such as short interfering RNAs (siRNA), which
target telomerase RNA or TERT mRNA are capable of inhibiting telomerase
activity. Inhibition of telomerase in cancer cells leads to telomere
shortening, end-to-end chromosomal fusion, and apoptosis. Interference of
telomerase activity can also be used for treatment of infertility, for
contraception or sterilisation, for immunosuppression, for treatment of
yeast, parasite and fungal infections, and in antiinflammatory therapies.
CC As telomerase is active in a limited number of cell types, e.g. tumour
cells, germline cells, certain stem cells of the haematopoietic system, T
and B cells, sun-damaged skin, and proliferative cervix, most normal
cells are not affected by telomerase RNA interference therapy
XX
SQ Sequence 1132 AA;
Query Match 100.0%; Score 5961; DB 6; Length 1132;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MPRAPRCVAVSLRSHYREVLPATFVRRLLGPGQWRVLVQRGDPAAFALVAQCLVCPW 60
DB 1 MPRAPRCVAVSLRSHYREVLPATFVRRLLGPGQWRVLVQRGDPAAFALVAQCLVCPW 60
QY 61 DARPPAPSPROVSKLKLVARVLQRLCERKAKNVLAFFGALLDAGGPPPEAFTTSVR 120
DB 61 DARPPAPSPROVSKLKLVARVLQRLCERKAKNVLAFFGALLDAGGPPPEAFTTSVR 120
QY 121 SYLPTNTVTDALRGSGANGLLLRVGGDDVLVHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180
DB 121 SYLPTNTVTDALRGSGANGLLLRVGGDDVLVHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180
QY 181 ATQARPPHAGSPRRRLGCERAWNHSVREAGVPLGLPAGARRRGGSASRSLPLKRRPR 240
DB 181 ATQARPPHAGSPRRRLGCERAWNHSVREAGVPLGLPAGARRRGGSASRSLPLKRRPR 240
QY 241 GAAPEPERTVQGSWAHPGTRGSDRGFCVSPARPAEATSLGALSCTRHSHPSVG 300
DB 241 GAAPEPERTVQGSWAHPGTRGSDRGFCVSPARPAEATSLGALSCTRHSHPSVG 300
QY 301 RQHAGPPSTSRPRPMDTPCPVVAETKHYLSSGDKQLRPSPLLSLRPSLTGARRL 360
DB 301 RQHAGPPSTSRPRPMDTPCPVVAETKHYLSSGDKQLRPSPLLSLRPSLTGARRL 360
QY 361 VETIFLGRSPWPGTPRRLPRLPQRYWQRPFLFELLLGNHQAQCPYGVLLKTHCPLRAAVT 420
DB 361 VETIFLGRSPWPGTPRRLPRLPQRYWQRPFLFELLLGNHQAQCPYGVLLKTHCPLRAAVT 420
QY 421 PAAGVCAREKPGQSVAAPEEEDTDRRLVQLLRQHSHPQVYGFVRACLRRLVPPGLWGS 480
DB 421 PAAGVCAREKPGQSVAAPEEEDTDRRLVQLLRQHSHPQVYGFVRACLRRLVPPGLWGS 480
QY 481 RHNERFLRNTKFIISLGHAKLSLOELTWKMSVRDCAWLRSPGVGCVPAAEHLRREI 540

Db	481	RHNERFLRNTKFIISLGHAKLSQELTWKQSVRDCAWLRSPGVGCPAAEHLREEI	540
Qy	541	LAKFLHLWMSYVVVELLRSFFYVTTTFQKNRLFFYRKSVMSKLQSIGIRQHLKRVQLRE	600
Db	541	LAKFLHLWMSYVVVELLRSFFYVTTTFQKNRLFFYRKSVMSKLQSIGIRQHLKRVQLRE	600
Qy	601	LSEAEVQHQREARPALITSLRLFTPDKDGLRPIVNDYVVGARTFREKKAERLTSRVKA	660
Db	601	LSEAEVQHQREARPALITSLRLFTPDKDGLRPIVNDYVVGARTFREKKAERLTSRVKA	660
Qy	661	LFSVLNTERARRPGLLGASVLGLDDIHRAWRTFVLVRADPPPELVFKVDVDTGAYDTI	720
Db	661	LFSVLNTERARRPGLLGASVLGLDDIHRAWRTFVLVRADPPPELVFKVDVDTGAYDTI	720
Qy	721	QDRLTEVIASIIKPQNTYCVRRYAVVQKAAHGHRKAFKSHVSTLTDLPYMRQFVAHL	780
Db	721	QDRLTEVIASIIKPQNTYCVRRYAVVQKAAHGHRKAFKSHVSTLTDLPYMRQFVAHL	780
Qy	781	QETSPLRDADVIEOSSSINEASSGLFQVFLRFPMCHHAVIRGKSVYOCQGIPOGSILSTL	840
Db	781	QETSPLRDADVIEOSSSINEASSGLFQVFLRFPMCHHAVIRGKSVYOCQGIPOGSILSTL	840
Qy	841	LCSLCYGDMENKLPAGIRRDGLLRLVDDFLFLVTPHLTHAKTFLTLVRGVPEYGCVVNL	900
Db	841	LCSLCYGDMENKLPAGIRRDGLLRLVDDFLFLVTPHLTHAKTFLTLVRGVPEYGCVVNL	900
Qy	901	RKTVNVFVEDEALGGTAFVQMPAHGLFPWCGLLLDTRTLEQSDYSYARTSIRASLTFF	960
Db	901	RKTVNVFVEDEALGGTAFVQMPAHGLFPWCGLLLDTRTLEQSDYSYARTSIRASLTFF	960
Qy	961	NRGPKAGNMRRKLPFGLVRLKCHSLFLDLQVNSLQTVCTNIYKILLQAVRFHACVLQLP	1020
Db	961	NRGPKAGNMRRKLPFGLVRLKCHSLFLDLQVNSLQTVCTNIYKILLQAVRFHACVLQLP	1020
Qy	1021	FHQQVKNPTFFFLRVISDTASLCYSILKAKNAGMSLGAKGAAGPLPSEAVQWLCHQAFLL	1080
Db	1021	FHQQVKNPTFFFLRVISDTASLCYSILKAKNAGMSLGAKGAAGPLPSEAVQWLCHQAFLL	1080
Qy	1081	KLTHRRVTVYPLGLSLRTAQTOLSRKLPGTTLTALEAAANPALPSDEKTTILD	1132
Db	1081	KLTHRRVTVYPLGLSLRTAQTOLSRKLPGTTLTALEAAANPALPSDEKTTILD	1132
RESULT 14			
ABR42063			
ID	ABR42063 standard; protein; 1132 AA.		
AC	ABR42063;		
XX			
DT	28-JUL-2003 (first entry)		
XX			
DE	Human telomerase reverse transcriptase.		
XX			
KW	Telomerase reverse transcriptase; TERT: enzyme; RNA interference;		
KW	short interfering RNA; siRNA; cancer; tumour; cytostatic; contraceptive;		
KW	immunosuppressive; antifertility; fungicide; antiparasitic;		
KW	antiinflammatory; human; gene therapy.		
XX			
OS	Homo sapiens.		
XX			
PN	W0203034985-A2.		
XX			
PD	01-MAY-2003.		
XX			
PF	16-OCT-2002; 2002WO-US033146.		
XX			
PR	22-OCT-2001; 2001US-0345326P.		
PR	20-FEB-2002; 2002US-0359196P.		
PR	22-MAY-2002; 2002US-0383195P.		
XX			
XX	(UYRP) UNIV ROCHESTER.		
XX			

Db 601 LSEAEVQHQREARPAALTSRLRIFPKPDGLRPIVNMVYVVGARTFRREKRAERLTSRVKA 660
Qy 661 LFSVLNERRARRPGLGASVLGLDDIHRARWTFVLVRQAQDPPPELYFVKVDVTGAYDTI 720
Db 661 LFSVLNERRARRPGLGASVLGLDDIHRARWTFVLVRQAQDPPPELYFVKVDVTGAYDTI 720
Qy 721 PODRLTEVIASIIKPNQTYCYRRYAVVQKAAGHVRKAFKSHVSTLTLDQPYMRQFVAHL 780
Db 721 PODRLTEVIASIIKPNQTYCYRRYAVVQKAAGHVRKAFKSHVSTLTLDQPYMRQFVAHL 780
Qy 781 QETSPLRDVAVIEQSSSINEASSGLFDVFLRPMCHHVRIRGKSVVQCQGIPOQSILSTL 840
Db 781 QETSPLRDVAVIEQSSSINEASSGLFDVFLRPMCHHVRIRGKSVVQCQGIPOQSILSTL 840
Qy 841 LCSLCYGMENKLPAGIRRDGILLRLVDDFLVTPHLTHAKTFLRLTVRGVPEYGCVVNL 900
Db 841 LCSLCYGMENKLPAGIRRDGILLRLVDDFLVTPHLTHAKTFLRLTVRGVPEYGCVVNL 900
Qy 901 RKTWNFFVEDEALGCTAFVQMPAHLFPWCGLLDITLTVQSDYSSYARTSIRASLTF 960
Db 901 RKTWNFFVEDEALGCTAFVQMPAHLFPWCGLLDITLTVQSDYSSYARTSIRASLTF 960
Qy 961 NRGFKAGNRMRKLFGLVRLKCHSLFDLQVNSLQTVCTNIYKILLQAYRPHACVQLQP 1020
Db 961 NRGFKAGNRMRKLFGLVRLKCHSLFDLQVNSLQTVCTNIYKILLQAYRPHACVQLQP 1020
Qy 1021 FHQQWKNPTFFLRVISDTASLCYILKAKNAGMSLGAAGPLPSEAVQWLCHQAFLL 1080
Db 1021 FHQQWKNPTFFLRVISDTASLCYILKAKNAGMSLGAAGPLPSEAVQWLCHQAFLL 1080
Qy 1081 KLTHRVTVYVPLGLSLRTAQTLRSKLPFGTTLTALAAANPALPSDFKTIID 1132
Db 1081 KLTHRVTVYVPLGLSLRTAQTLRSKLPFGTTLTALAAANPALPSDFKTIID 1132

RESULT 15

ABP56676
ID ABP56676 standard; protein; 1132 AA.
XX AC ABP56676;
XX DT 25-MAR-2003 (first entry)
XX DE Human telomerase reverse transcriptase protein SEQ ID NO:2.
XX KW Human; telomerase reverse transcriptase; enzyme; hTERT; chromosome 5;
KW vulnery; antiulcer; epithelial cell migration promoter; wound;
KW epithelisation; skin wound; lesion; burn; surgical incision; ulcer;
KW epithelial cell; keratinocyte; epidermal; mucosal.
XX OS Homo sapiens.
XX FN WO200291999-A2.
XX PD 21-NOV-2002.
XX PF 09-MAY-2002; 2002WO-US014867.
XX PR 09-MAY-2001; 2001US-0289903P.
XX PA (GERO-) GERON CORP.
XX PI Jiang X, Chiu C, Harley CB;
XX WPI; 2003-120591/11.
DR N-PSDB; ABZ22474.
XX Composition for treating wounds and enhancing epithelization of a skin
PT surface, comprises vector encoding telomerase reverse transcriptase or
PT telomerized epithelial cells on a microparticle or a matrix.
XX PS Disclosure; Page 32; 68pp; English.
XX

CC The present invention describes a pharmaceutical composition (I) comprising a vector encoding telomerase reverse transcriptase (TERT) in an excipient or device, or comprises telomerized epithelial cells on a microparticle or a matrix suitable for topical administration or administration to a wound site. (I) has vulnery and antiulcer activities and can be used to promote epithelial cell migration. (I) is useful for treating a wound and enhancing epithelisation of a skin surface. The wound is especially skin wound including acute lesion such as traumatic lesion, burn, or surgical incision, chronic lesion such as chronic venous ulcer, diabetic ulcer or compression ulcer and the wound is further monitored for closure. The telomerase activity or TERT expression is increased in epithelial cells at the site of treatment and also in fibroblasts or endothelial cells at the site of treatment. The epithelial cells are especially keratinocytes. A polynucleotide encoding TERT is useful for the preparation of a medicament for treatment of a wound or an epithelial surface in a human or animal. An epithelial cell with increased telomerase activity or increased expression of TERT is useful for preparation of a medicament for the treatment of a wound in a human or animal. (I) is also useful for treating wounds of other epidermal surfaces including mucosal surfaces such as bronchus, mouth, nose, oesophagus, stomach, or intestine. The present sequence represents human TERT (hTERT), which is given in the exemplification of the present invention. hTERT is located to chromosome 5
XX
SQ Sequence 1132 AA;

Query Match 100.0%; Score 5961; DB 6; Length 1132;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MPRAPRCRAVRSLLRSHYREVLPLATFVRRLGPGQWRIVQSGDPAAPALVAQCLVCPW 60
Db 1 MPRAPRCRAVRSLLRSHYREVLPLATFVRRLGPGQWRIVQSGDPAAPALVAQCLVCPW 60
Qy 61 DARPPPAAPSPFQVSCIKELVARVLORLCERAGKNVLAFFGALLDGGGPEAFTTSVR 120
Db 61 DARPPPAAPSPFQVSCIKELVARVLORLCERAGKNVLAFFGALLDGGGPEAFTTSVR 120
Qy 121 SYLPTNTVDALRGSGAWGLLRRVGGDVLVHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180
Db 121 SYLPTNTVDALRGSGAWGLLRRVGGDVLVHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180
Qy 181 ATQARPPPHASGPRRRRLGGERAWNHSVREAGVPLGPAPGARRRGGSASRLPLPKRPRR 240
Db 181 ATQARPPPHASGPRRRRLGGERAWNHSVREAGVPLGPAPGARRRGGSASRLPLPKRPRR 240
Qy 241 GAAPEPRTPVQGSWAHPGTRGDRGFCVSPARPAEATSLGALSCTRHSHPVSG 300
Db 241 GAAPEPRTPVQGSWAHPGTRGDRGFCVSPARPAEATSLGALSCTRHSHPVSG 300
Qy 301 ROHAGPPSTSRPPRPWDTPCPVYAEKTFLYSSGDKQLRPSFLSSLRPSLTGARRL 360
Db 301 ROHAGPPSTSRPPRPWDTPCPVYAEKTFLYSSGDKQLRPSFLSSLRPSLTGARRL 360
Qy 361 VETIFLGSRRPMPGTPRRRLPQRYQMRLPFLLELGNHAQCPYGVLLKTHCPLRAAVT 420
Db 361 VETIFLGSRRPMPGTPRRRLPQRYQMRLPFLLELGNHAQCPYGVLLKTHCPLRAAVT 420
Qy 421 PAAGVCAREKPGQSVAAPEEDTDRRLVQLLRHSSPQWQYGFVACLRRLVPPGLWGS 480
Db 421 PAAGVCAREKPGQSVAAPEEDTDRRLVQLLRHSSPQWQYGFVACLRRLVPPGLWGS 480
Qy 481 RHNERRFLNRTKFIISLGHAKLSLOELTWKMSVRDCAWLRSPGVGCVPAEHLRLEE 540
Db 481 RHNERRFLNRTKFIISLGHAKLSLOELTWKMSVRDCAWLRSPGVGCVPAEHLRLEE 540
Qy 541 LAKELHLMWSVYVVELLRSFFYVTTETTFQKNRLFYKSVMSKLSQSIGIRHKLXVQLRE 600
Db 541 LAKELHLMWSVYVVELLRSFFYVTTETTFQKNRLFYKSVMSKLSQSIGIRHKLXVQLRE 600
Qy 601 LSEAEVQHQREARPAALTSRLRIFPKPDGLRPIVNMVYVVGARTFRREKRAERLTSRVKA 660
Db 601 LSEAEVQHQREARPAALTSRLRIFPKPDGLRPIVNMVYVVGARTFRREKRAERLTSRVKA 660

QY 661 LFSVLNTERARRPGLLGASVGLDDIHRARTFVLVRQAQPPPELYFVKVDVTGAYDTI 720
Db 661 LFSVLNTERARRPGLLGASVGLDDIHRARTFVLVRQAQPPPELYFVKVDVTGAYDTI 720
QY 721 PQDLTEVIASIIKPNQTYCVRRAVAVQKAAGHVRKAFKSHVSTLTDLPYMQFVAHL 780
Db 721 PQDLTEVIASIIKPNQTYCVRRAVAVQKAAGHVRKAFKSHVSTLTDLPYMQFVAHL 780
QY 781 QETSLRDAVVIQSSSLNEASSGLFDVFLRFMCHHAVIRGKSVVQCQGIPOGSILSTL 840
Db 781 QETSLRDAVVIQSSSLNEASSGLFDVFLRFMCHHAVIRGKSVVQCQGIPOGSILSTL 840
QY 841 LCSLCYGMENKLFAGIRRDGLLLRLVDDFLVTPHLTHAKTFLTRVGRVPEYGCVVNL 900
Db 841 LCSLCYGMENKLFAGIRRDGLLLRLVDDFLVTPHLTHAKTFLTRVGRVPEYGCVVNL 900
QY 901 RKTUVNFEVDEALGGTAFVQMPAHGLFPWCGLLLDTRTLEVSQDYSYARTSIRASLTF 960
Db 901 RKTUVNFEVDEALGGTAFVQMPAHGLFPWCGLLLDTRTLEVSQDYSYARTSIRASLTF 960
QY 961 NRGFKAGNMRRKLFVGLRLKCHSLFLDLQVNSLQTVCTNIYKILLQAYRFHACVLQLP 1020
Db 961 NRGFKAGNMRRKLFVGLRLKCHSLFLDLQVNSLQTVCTNIYKILLQAYRFHACVLQLP 1020
QY 1021 FHQQWKQPTFFLRVISDTASLCYSILKAKNAGMSLGAKGAGPLPSEAVQWLCHQAPLL 1080
Db 1021 FHQQWKQPTFFLRVISDTASLCYSILKAKNAGMSLGAKGAGPLPSEAVQWLCHQAPLL 1080
QY 1081 KLTHRVTVYVPLGLSLRTAQTLQSLKPLGTTTLTALEAAANPALPSDFKTILD 1132
Db 1081 KLTHRVTVYVPLGLSLRTAQTLQSLKPLGTTTLTALEAAANPALPSDFKTILD 1132

RESULT 16

ABR58045
ID ABR58045 standard; protein; 1132 AA.
XX
AC ABR58045;
XX
DT 29-AUG-2003 (first entry)
XX
DE Human telomerase reverse transcriptase.
XX
KW Enzyme; human; telomerase reverse transcriptase; adipogenic capacity;
KW primary-preadipocyte cell; adipogenesis; obesity; adipocytokine;
KW anorectic; adiponectin; insulin.
XX
OS Homo sapiens.
XX
FN WO2003031640-A2.
XX
PD 17-APR-2003.
XX
PF 07-OCT-2002; 2002WO-US031635.
XX
PR 06-OCT-2001; 2001US-0327650P.
PR 06-OCT-2001; 2001US-0327651P.
XX
PA (BOST-) BOSTON MEDICAL CENT CORP.
XX
PI Kirkland J, Tchkonja T;
XX
DR WPI; 2003-421278/39.
DR N-PSDB; ACC44482.
XX
PT New primary preadipocyte strain expressing telomerase reverse
PT transcriptase, useful in research applications, screening assays,
PT clinical applications, and in the administration of therapeutic agents,
PT particularly for obesity.
XX
PS Disclosure; Page 13; 53pp; English.
XX

CC The invention relates to the generation of primary preadipocyte cell
CC strains that expresse telomerase reverse transcriptase (TERT- the
CC catalytic subunit of telomerase), and maintain and/or enhance replicative
CC potential and maintain adipogenic capacity of the cell. This sequence
CC represents the TERT protein. The cell strain can be used in research to
CC study all aspect of adipogenesis, especially in relation to researching
CC treatments for e.g. obesity. The cell can also be used to identify
CC adipogenesis modulators for use as therapeutic agents such as hormones,
CC growth factors, cytokines, enzymes, cholesterol binding proteins,
CC cholesterol removing proteins or their combinations. Alternatively, the
CC therapeutic agent may be an adipocytokine, preferably adiponectin, or
CC insulin
XX

QY Sequence 1132 AA;

Query Match 100.0%; Score 5961; DB 6; Length 1132;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MPRAPRCRAVRSLLRSHYREVLPATFVRLPGQWRLVORGDPAAFRALVAQCLVCVPW 60
Db 1 MPRAPRCRAVRSLLRSHYREVLPATFVRLPGQWRLVORGDPAAFRALVAQCLVCVPW 60
QY 61 DARPPPAAPSPQVSCLELVARVQLCERGAQNVLAFGALDARGGPEAFTTSVR 120
Db 61 DARPPPAAPSPQVSCLELVARVQLCERGAQNVLAFGALDARGGPEAFTTSVR 120
QY 121 SYLPTNTVDALRGSGAWGLLLRRVGDVLAHLLARCALFVLVAPSCAYQVCGPLYQLGA 180
Db 121 SYLPTNTVDALRGSGAWGLLLRRVGDVLAHLLARCALFVLVAPSCAYQVCGPLYQLGA 180
QY 181 ATQARPPPHASGPRRRLGCERANWHSVREAGVPLGLPAPGARRRGGSASRSLPDKPRR 240
Db 181 ATQARPPPHASGPRRRLGCERANWHSVREAGVPLGLPAPGARRRGGSASRSLPDKPRR 240
QY 241 GAAPEPERTVGGGSAHPRGTRGSDRGCVUSPARPAEATSEALSTRSHSVG 300
Db 241 GAAPEPERTVGGGSAHPRGTRGSDRGCVUSPARPAEATSEALSTRSHSVG 300
QY 301 RQHAGPPTSRPPRPMWDTPCPPVYAEKTHFLYSSGDKQLRPSFLSSRLPSLTGARRL 360
Db 301 RQHAGPPTSRPPRPMWDTPCPPVYAEKTHFLYSSGDKQLRPSFLSSRLPSLTGARRL 360
QY 361 VETIFLGSRRPMPGTPRRLPRLPQRYWQMRPLFLELLGNHAQCPYGVLLKTHCPLRAAVT 420
Db 361 VETIFLGSRRPMPGTPRRLPRLPQRYWQMRPLFLELLGNHAQCPYGVLLKTHCPLRAAVT 420
QY 421 PAAGVCAREKPGQSVAAPEEEDTDPRLVOLLRQHSPPQVGVFVRACTRLRLVPPGLWGS 480
Db 421 PAAGVCAREKPGQSVAAPEEEDTDPRLVOLLRQHSPPQVGVFVRACTRLRLVPPGLWGS 480
QY 481 RHNERRFLRNTKPFISLGKHAQLSLQELTWKMSVRDCAWLRRSPGVGCPAAEHLREEI 540
Db 481 RHNERRFLRNTKPFISLGKHAQLSLQELTWKMSVRDCAWLRRSPGVGCPAAEHLREEI 540
QY 541 LAKFLHLMVSVYVVELLRSFFYVTTTFOKNRLLFFYRKSVMKLSQSTGIROHLKRVQURE 600
Db 541 LAKFLHLMVSVYVVELLRSFFYVTTTFOKNRLLFFYRKSVMKLSQSTGIROHLKRVQURE 600
QY 601 LSEAEVQHREARPAALLTSRLRFIPKPDGLRPIVNMMDYVVGARTFRREKRAERTLSRKA 660
Db 601 LSEAEVQHREARPAALLTSRLRFIPKPDGLRPIVNMMDYVVGARTFRREKRAERTLSRKA 660
QY 661 LFSVLNTERARRPGLLGASVGLDDIHRARTFVLVRQAQPPPELYFVKVDVTGAYDTI 720
Db 661 LFSVLNTERARRPGLLGASVGLDDIHRARTFVLVRQAQPPPELYFVKVDVTGAYDTI 720
QY 721 PQDLTEVIASIIKPNQTYCVRRAVAVQKAAGHVRKAFKSHVSTLTDLPYMQFVAHL 780
Db 721 PQDLTEVIASIIKPNQTYCVRRAVAVQKAAGHVRKAFKSHVSTLTDLPYMQFVAHL 780
QY 781 QETSLRDAVVIQSSSLNEASSGLFDVFLRFMCHHAVIRGKSVVQCQGIPOGSILSTL 840

Db 781 QETSLRDVAVIEQSSSINEASSGLFVDFLRPMCHAVIRKSVYQCGIPQGSILSTL 840
Qy LCSLCYGDWENKLPAGIRRDGLLRVDDFLLVTPHLTHAKTFLRTLVRGVPEYGCYNL 900
Db LCSLCYGDWENKLPAGIRRDGLLRVDDFLLVTPHLTHAKTFLRTLVRGVPEYGCYNL 900
Qy 901 RKTVNFVDEALGGTAFVQMPAHGLFPWCGLLDDTTLTLEVSQSYSSYARTSIRASITF 960
Db 901 RKTVNFVDEALGGTAFVQMPAHGLFPWCGLLDDTTLTLEVSQSYSSYARTSIRASITF 960
Qy 961 NRGFKAGNMRKLPGLVLRKCHSLFDLQVNSLQTVCTNLYKILLQAYRPHACVLQLP 1020
Db 961 NRGFKAGNMRKLPGLVLRKCHSLFDLQVNSLQTVCTNLYKILLQAYRPHACVLQLP 1020
Qy 1021 FHQVWKNPFTFLRVIDSTASICYSLKAKNAGMSLGAKGAGPLPSEAVQWLCHQAFLL 1080
Db 1021 FHQVWKNPFTFLRVIDSTASICYSLKAKNAGMSLGAKGAGPLPSEAVQWLCHQAFLL 1080
Qy 1081 KLTHRVTVYVPLLSRLTAQQLSRKLPGLTTLTALAAANPALPSDFKTILO 1132
Db 1081 KLTHRVTVYVPLLSRLTAQQLSRKLPGLTTLTALAAANPALPSDFKTILO 1132

RESULT 17

ADD21420
ID ADD21420 standard; protein; 1132 AA.

XX AC ADD21420;

XX DT 15-JAN-2004 (first entry)

XX DE Human TERT protein related to continual cell growth.

XX KW continual growth; cultured cell; cyclin dependent kinase; cdk4; cdk2;
KW cdk6; activating mutation; cell growth; cell division; cell cycle;
KW cancer-causing agent; continual growth-induced cell; enzyme; TERT;
KW telomerase; human.

XX OS Homo sapiens.

XX PN WO200304169-A2.

XX PD 30-MAY-2003.

XX PF 15-NOV-2002; 2002WO-US036729.

XX PR 15-NOV-2001; 2001US-0334760P.

XX PA (UTEM) UNIV TEMPLE.

XX PI Reddy PE, Rane SG, Mettus RV;

XX DR WPI; 2003-449813/42.

XX PT A composition for reversibly inducing continual growth in normal cells
comprises a cyclin dependent kinase protein (e.g. cdk4, cdk2 or cdk6) or
its active fragment, derivative, homolog or analog, having an activating
mutation.

XX PS Claim 16; Page 135-138; 77pp; English.

XX CC This invention relates to a novel composition for inducing a reversible
state of a continual growth in cultured cells and comprises at least one
compound comprising a cyclin dependent kinase (cdk)4, cdk2 or cdk6
protein having an activating mutation. Growth and division of living
cells involve a regular series of events and processes that comprise the
cell cycle. Cyclin dependent kinases cdk2, cdk4 and cdk6 are involved in
the control of G1, the point at which cells irrevocably commit to DNA
synthesis and thus enter the cell cycle. The invention is useful in
reversibly inducing continual growth in normal cells and may allow the
screening of cancer-causing agents with the continual growth-induced
cells. The present sequence is that of the human TERT protein, the
catalytic subunit of telomerase, related to the invention. Note: Due to

CC an error in the specification or sequence listing, the Seq ID numbers
given in the disclosure do not correspond to those given in the sequence
listing. It is therefore unclear which Seq ID number corresponds to which
sequence and exactly which sequence is being claimed.

XX Sequence 1132 AA;

Query Match 100.0%; Score 5961; DB 7; Length 1132;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MPAPRCRAVRSLSRSHVREVLPLATFVRRLLPGQWRVQGRDPAAPALVAQCLVCVPM 60
Db 1 MPAPRCRAVRSLSRSHVREVLPLATFVRRLLPGQWRVQGRDPAAPALVAQCLVCVPM 60
Qy 61 DARPPPAAPSQVQSLCKELVARVQLRCERAGKKNVLAFFGALLDARGGGPEAFTTSVR 120
Db 61 DARPPPAAPSQVQSLCKELVARVQLRCERAGKKNVLAFFGALLDARGGGPEAFTTSVR 120
Qy 121 SYLPTNTVDALRGSGAWGLLLRRVDDVLLVHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180
Db 121 SYLPTNTVDALRGSGAWGLLLRRVDDVLLVHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180
Qy 181 ATQARPPPHASGPRRRRLGGERAWNHSVREAGVPLGLPAGARRRGGSSASRSLPLPKRRR 240
Db 181 ATQARPPPHASGPRRRRLGGERAWNHSVREAGVPLGLPAGARRRGGSSASRSLPLPKRRR 240
Qy 241 GAAPERTPVQGGSWAHPGTRGSDRGFCVSPARPAERATSLGALSGLTRHSHPSVG 300
Db 241 GAAPERTPVQGGSWAHPGTRGSDRGFCVSPARPAERATSLGALSGLTRHSHPSVG 300
Qy 301 RQHAGPPSTSRPPMDTPCPPVYAEKHFLLYSSGDKQLRPSFLLSLRPSLTGARRL 360
Db 301 RQHAGPPSTSRPPMDTPCPPVYAEKHFLLYSSGDKQLRPSFLLSLRPSLTGARRL 360
Qy 361 VETIFLSRPMWPGTPRRLPLPQRYQWMPRLFLLELGNHACQPYGVLLKTHCPLRAAVT 420
Db 361 VETIFLSRPMWPGTPRRLPLPQRYQWMPRLFLLELGNHACQPYGVLLKTHCPLRAAVT 420
Qy 421 PAAGVCAREKPGQSVAAPEEDTPRRLVQLLRHSSPWQYVGFVACLRRLVPPGLWGS 480
Db 421 PAAGVCAREKPGQSVAAPEEDTPRRLVQLLRHSSPWQYVGFVACLRRLVPPGLWGS 480
Qy 481 RHNERRFLRNTKFIISLGKHAQLSLQELTWKMSVRDCAWLRRSPGVGCVPAEHLREBI 540
Db 481 RHNERRFLRNTKFIISLGKHAQLSLQELTWKMSVRDCAWLRRSPGVGCVPAEHLREBI 540
Qy 541 LAKFLHLMMSVYVVELLSRPFYVTTETTFQKRLFFYRKSVWSKLQSIGIRHLLKRVQRE 600
Db 541 LAKFLHLMMSVYVVELLSRPFYVTTETTFQKRLFFYRKSVWSKLQSIGIRHLLKRVQRE 600
Qy 601 LSEAEVRQREARPAALLTSRLRFIPKPDGLRPIVNMVYVVGARTFRREKRAERLTSRYKA 660
Db 601 LSEAEVRQREARPAALLTSRLRFIPKPDGLRPIVNMVYVVGARTFRREKRAERLTSRYKA 660
Qy 661 LFSVLNTERARRPGLIGASVLGLDDIHRAMRTFVLVRQAQDPPPELYFVKVDVTGAYDTI 720
Db 661 LFSVLNTERARRPGLIGASVLGLDDIHRAMRTFVLVRQAQDPPPELYFVKVDVTGAYDTI 720
Qy 721 PODRLTEVIASIIKPQNTYCVRRYAVVQKAAHGHVRKAFKSHVSTLTDLPYMRQFVAHL 780
Db 721 PODRLTEVIASIIKPQNTYCVRRYAVVQKAAHGHVRKAFKSHVSTLTDLPYMRQFVAHL 780
Qy 781 QETSPLRDADVIEQSSSINEASSGLFVDFLRPMCHAVIRKSVYQCGIPQGSILSTL 840
Db 781 QETSPLRDADVIEQSSSINEASSGLFVDFLRPMCHAVIRKSVYQCGIPQGSILSTL 840
Qy 841 LCSLCYGDWENKLPAGIRRDGLLRVDDFLLVTPHLTHAKTFLRTLVRGVPEYGCYNL 900
Db 841 LCSLCYGDWENKLPAGIRRDGLLRVDDFLLVTPHLTHAKTFLRTLVRGVPEYGCYNL 900
Qy 901 RKTVNFVDEALGGTAFVQMPAHGLFPWCGLLDDTTLTLEVSQSYSSYARTSIRASITF 960
Db 901 RKTVNFVDEALGGTAFVQMPAHGLFPWCGLLDDTTLTLEVSQSYSSYARTSIRASITF 960

Ds 901 RKTVPNPFVEDEALGGTAFVQMPAHGLFPWCGLLDTRTLEVSQSDYSYARTSRASLTF 960
Qy 961 NRGFKAGNNRRKLFVGLRLKCHSLFLDLQVNSLQTVCTNIYKILLQAYRFHACVLQLP 1020
Db 961 NRGFKAGNNRRKLFVGLRLKCHSLFLDLQVNSLQTVCTNIYKILLQAYRFHACVLQLP 1020
Qy 1021 FHQQVWKNPTFFLRVSDTASLCYSILKAKNAGSLGAKGAGPLPSEAVQWLCHQAFLL 1080
Db 1021 FHQQVWKNPTFFLRVSDTASLCYSILKAKNAGSLGAKGAGPLPSEAVQWLCHQAFLL 1080
Qy 1081 KLTHRRVTVVPLLSGLRTAQQLSKLPQTTLTALEAAANPALPSDFKTILD 1132
Db 1081 KLTHRRVTVVPLLSGLRTAQQLSKLPQTTLTALEAAANPALPSDFKTILD 1132

RESULT 18

ADH72743

ID ADH72743 standard; protein; 1132 AA.

XX AC ADH72743;

XX DT 25-MAR-2004 (first entry)

XX DE Human protein of the invention SEQ ID NO:19.

XX KW stem cell; cardiant; hepatotropic; nephrotropic; cytostatic; neurotropic;

XX KW neuroprotective; antiarthritic; antidiabetic; antiarteriosclerotic;

XX KW heart failure; leukemia; neurodegenerative disease; diabetes;

XX KW arteriosclerosis; skeletal muscle; human.

XX OS Homo sapiens.

XX FN WO2003027281-A2.

XX PD 03-APR-2003.

XX PF 20-SEP-2002; 2002WO-JP009702.

XX PR 20-SEP-2001; 2001JP-00286332.

XX PR 09-MAY-2002; 2002JP-00133575.

XX PA (KYOW) KYOWA HAKKO KOGYO KK.

XX PA (TAMA/) TAMAKI T.

XX PA (ANDO/) ANDO K.

XX PI Tamaki T, Ando K, Akatsuka A, Nakamura Y, Hotta T, Sakurada K;

XX DR WPI; 2003-371925/35.

XX PT Pluripotent stem cells originating in skeletal muscle interstitial

XX PT tissue, useful in drugs for regenerating tissues and cells e.g. in

XX PT treating heart failure, leukemia, neurodegenerative diseases, and

XX PT diabetes.

XX PS Disclosure; SEQ ID NO 19; 29pp; Japanese.

XX CC The invention relates to novel pluripotent stem cells originating from a

XX CC skeletal muscle interstitial tissue. A cell of the invention has

XX CC cardiant, hepatotropic, nephrotropic, cytostatic, neurotropic,

XX CC neuroprotective, antiarthritic, antidiabetic, and antiarteriosclerotic

XX CC activity. The cells are useful in drugs for regenerating tissues and

XX CC cells e.g. in treating heart failure, leukemia, neurodegenerative

XX CC diseases, diabetes and arteriosclerosis. The pluripotent stem cells were

XX CC isolated from rat skeletal muscles after analysis of the various

XX CC components by culturing and staining, as well as by other biochemical

XX CC analysis. The present sequence is used in the exemplification of the

XX CC invention.

XX CC Sequence 1132 AA;

XX CC Query Match 100.0%; Score 5961; DB 7; Length 1132;

XX CC Best Local Similarity 100.0%; Pred. No. 0;

XX CC Matches 1132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MPRAPRCRAVRSLLRSHYREVLPPLATFVRRLPGQWRLVQRGDPAAFRALVAQCLVCVPW 60
Db 1 MPRAPRCRAVRSLLRSHYREVLPPLATFVRRLPGQWRLVQRGDPAAFRALVAQCLVCVPW 60
Qy 61 DARRPPAAPFRQVSCIKELVARVLQRLCERGAKNVLAFGFALLDGGAGGPEAFTTSVR 120
Db 61 DARRPPAAPFRQVSCIKELVARVLQRLCERGAKNVLAFGFALLDGGAGGPEAFTTSVR 120
Qy 121 SYLPNTVTDALRGSGAWGLLLRRVGDDVLVHLLARCALFVLVAPSCAYQVCGPPLYOLGA 180
Db 121 SYLPNTVTDALRGSGAWGLLLRRVGDDVLVHLLARCALFVLVAPSCAYQVCGPPLYOLGA 180
Qy 181 ATQARPPPHASGPRRRLLGCERAMNHSVREAGVPLGLPAPGARRRGGASRSPLPKRPRR 240
Db 181 ATQARPPPHASGPRRRLLGCERAMNHSVREAGVPLGLPAPGARRRGGASRSPLPKRPRR 240
Qy 241 GAAPERTPVGOGSWAHPGRTGRGFCVVSPPAPAEATSELEGALSSTRSHPSVG 300
Db 241 GAAPERTPVGOGSWAHPGRTGRGFCVVSPPAPAEATSELEGALSSTRSHPSVG 300
Qy 301 RQHAGPSTSRPPRMDTPCPCPVYAEKHFLLSSGDKQLRPSFLLSSLRPSLTGARRL 360
Db 301 RQHAGPSTSRPPRMDTPCPCPVYAEKHFLLSSGDKQLRPSFLLSSLRPSLTGARRL 360
Qy 361 VETIFLGSRRPMPGTPRRLPRLPQRYQWMPRLFLELGNHAQCPYGVLLKTHCPLRAAVT 420
Db 361 VETIFLGSRRPMPGTPRRLPRLPQRYQWMPRLFLELGNHAQCPYGVLLKTHCPLRAAVT 420
Qy 421 PAAGVCAREKPOGSVAAPPEEDTPRRLVQLLRQHSPPQWYGVFRACLRRLVPPGLWS 480
Db 421 PAAGVCAREKPOGSVAAPPEEDTPRRLVQLLRQHSPPQWYGVFRACLRRLVPPGLWS 480
Qy 481 RHNERRFLRNTKFIKSLGKAKLSLOELTWKMSVRDCAWLRRSPGVCVPAAEHRLREEI 540
Db 481 RHNERRFLRNTKFIKSLGKAKLSLOELTWKMSVRDCAWLRRSPGVCVPAAEHRLREEI 540
Qy 541 LAKPLHLWMSVYVVELLRSFFYVTTTFQKNLFFFRKSVMSKLSQSIGIRHLKRVQVLR 600
Db 541 LAKPLHLWMSVYVVELLRSFFYVTTTFQKNLFFFRKSVMSKLSQSIGIRHLKRVQVLR 600
Qy 601 LSEAEVRQREARPPALLTSRLRTPKDGRLPIVNMDDYVVGARTFREKKAERLTSRKA 660
Db 601 LSEAEVRQREARPPALLTSRLRTPKDGRLPIVNMDDYVVGARTFREKKAERLTSRKA 660
Qy 661 LFSVLNVERARRPGLLGASVGLGLDDIHRANRTFVLVRVRAQDPPPELYFVKVDVTGAYDTI 720
Db 661 LFSVLNVERARRPGLLGASVGLGLDDIHRANRTFVLVRVRAQDPPPELYFVKVDVTGAYDTI 720
Qy 721 PQDLRTEVIASIIKPQNTYCVRRYAVVQKAAHGHVRKAFKSHVSTLTDLQPMRQFVAHL 780
Db 721 PQDLRTEVIASIIKPQNTYCVRRYAVVQKAAHGHVRKAFKSHVSTLTDLQPMRQFVAHL 780
Qy 781 QETSPLRDAVVIQSSSLNEASSGLFDVLFMRCHHAVIRGKSVYOCQIPQGSILSTL 840
Db 781 QETSPLRDAVVIQSSSLNEASSGLFDVLFMRCHHAVIRGKSVYOCQIPQGSILSTL 840
Qy 841 LCSLCYGDMMENKLFAGIRRRDGLLLRLVDDFLVTPHLLTHAKTFLRVLVRGVPYGCVVNL 900
Db 841 LCSLCYGDMMENKLFAGIRRRDGLLLRLVDDFLVTPHLLTHAKTFLRVLVRGVPYGCVVNL 900
Qy 901 RKTVPNPFVEDEALGGTAFVQMPAHGLFPWCGLLDTRTLEVSQSDYSYARTSRASLTF 960
Db 901 RKTVPNPFVEDEALGGTAFVQMPAHGLFPWCGLLDTRTLEVSQSDYSYARTSRASLTF 960
Qy 961 NRGFKAGNNRRKLFVGLRLKCHSLFLDLQVNSLQTVCTNIYKILLQAYRFHACVLQLP 1020
Db 961 NRGFKAGNNRRKLFVGLRLKCHSLFLDLQVNSLQTVCTNIYKILLQAYRFHACVLQLP 1020
Qy 1021 FHQQVWKNPTFFLRVSDTASLCYSILKAKNAGSLGAKGAGPLPSEAVQWLCHQAFLL 1080
Db 1021 FHQQVWKNPTFFLRVSDTASLCYSILKAKNAGSLGAKGAGPLPSEAVQWLCHQAFLL 1080

QY 1081 KLTHRVTVYVPLGSLRTAQOLSKRLPGTTLTALAAANPALPSDFKTIID 1132
 DB 1081 KLTHRVTVYVPLGSLRTAQOLSKRLPGTTLTALAAANPALPSDFKTIID 1132

RESULT 19
 ID ADG70114 standard; protein; 1132 AA.
 AC ADG70114;
 DT 11-MAR-2004 (first entry)
 XX HTERT protein.
 DE HTERT protein.
 KW cytosolic; gene therapy; reverse transcriptase-inhibitor; HIV-1;
 KW human telomerase reverse transcriptase; hTERT; chimeric; catalytic site;
 KW unregulated cellular growth; cancer; tumor.
 XX Homo sapiens.
 OS Homo sapiens.
 XX WO2003095605-A2.
 PN 20-NOV-2003.
 PD 14-APR-2003; 2003WO-EP003874.
 XX 08-MAY-2002; 2002US-0378820P.
 PR (PHAA) PHARMACIA ITAL SPA.
 XX Moll J, Schmichel A, Stouten P;
 PI WPI; 2004-012095/01.
 DR N-PSDB; ADG70113.
 XX New HIV-1 Reverse Transcriptase and human Telomerase Reverse
 PT Transcriptase proteins and nucleic acids, useful in gene therapy or for
 PT treating or preventing unregulated cellular growth, e.g. cancer cell or
 PT tumor growth.
 XX Example 1; SEQ ID NO 4; 141pp; English.

The invention relates to the isolation of compounds that bind and inhibit the activity of HIV-1 reverse transcriptase (RT) or human telomerase reverse transcriptase (hTERT). The method involves determining these compounds using a HIV-1 RT/hTERT chimeric construct containing these catalytic sites of each enzyme. The nucleic acid is useful for treating or preventing unregulated cellular growth, including cancer cell and tumor growth. It is also useful in gene therapy. Compounds that inhibit telomerase activity can be used to treat cancer. The vectors of the invention can be used to amplify DNA or RNA encoding HIV-1 RT/hTERT and/or express DNA which encodes HIV-RT/hTERT. This sequence corresponds to the human TERT protein.

Query Match 100.0%; Score 5961; DB 8; Length 1132;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPRAPCRAVSLRSHYREVLPATFVRRRLGPGQWRVLVQRGDPAAPRALVAQCILVCPW 60
 DB 1 MPRAPCRAVSLRSHYREVLPATFVRRRLGPGQWRVLVQRGDPAAPRALVAQCILVCPW 60

QY 61 DARPPAAPSPFQVSLKELVARVLQRLCERGAKNVLAFFGALLDARGGPEAFTTSVR 120
 DB 61 DARPPAAPSPFQVSLKELVARVLQRLCERGAKNVLAFFGALLDARGGPEAFTTSVR 120

QY 121 SYLPNTVTDALRGSGAWGLLRVGGDVLVHLLARCALFVLVAPSCAYQVCGPPLYLGA 180
 DB 121 SYLPNTVTDALRGSGAWGLLRVGGDVLVHLLARCALFVLVAPSCAYQVCGPPLYLGA 180

QY 181 ATQARPPHAGSPRRRLGECERAMNHSVREAGVPLGLPAPGARRRGGSSASRLPKRRR 240
 DB 181 ATQARPPHAGSPRRRLGECERAMNHSVREAGVPLGLPAPGARRRGGSSASRLPKRRR 240

QY 241 GAAPEPERTVPGQSWAHPGTRGPGSDRGFCVSPARPAEATSLLEGALSCTRSHPSVG 300
 DB 241 GAAPEPERTVPGQSWAHPGTRGPGSDRGFCVSPARPAEATSLLEGALSCTRSHPSVG 300

QY 301 ROHHAGPSTSRPPRPWDTPCPVYAEATKHYSGDKEQLRPSFLSSLSLPSLTGARRL 360
 DB 301 ROHHAGPSTSRPPRPWDTPCPVYAEATKHYSGDKEQLRPSFLSSLSLPSLTGARRL 360

QY 361 VETIFLGSRRPMPCTPRRLPRLPORYWQMRPLFLELLGNHAQCPYGVLLKTHCPLRAAVT 420
 DB 361 VETIFLGSRRPMPCTPRRLPRLPORYWQMRPLFLELLGNHAQCPYGVLLKTHCPLRAAVT 420

QY 421 PAAGVCAREKPGQSWAAPEEEDTPRLVOLLROHSSPWQYVGFVACLRRLVPPGLWGS 480
 DB 421 PAAGVCAREKPGQSWAAPEEEDTPRLVOLLROHSSPWQYVGFVACLRRLVPPGLWGS 480

QY 481 RHNERRFLRNTKFI SLGKIAKLSLQELTWKMSVRDCAWLRSPGVCVPAAEHRLREI 540
 DB 481 RHNERRFLRNTKFI SLGKIAKLSLQELTWKMSVRDCAWLRSPGVCVPAAEHRLREI 540

QY 541 LAKFLHLMMSVYVVELLRSFFYVTTTFQKNRFFYRKSVMKLSQSIGIRQHLKRVQURE 600
 DB 541 LAKFLHLMMSVYVVELLRSFFYVTTTFQKNRFFYRKSVMKLSQSIGIRQHLKRVQURE 600

QY 601 LSEAEVRQHRREARPAALLTSRLRFIPKDDGLRPIVNM DYVVGARTFRKRAERLTSRKA 660
 DB 601 LSEAEVRQHRREARPAALLTSRLRFIPKDDGLRPIVNM DYVVGARTFRKRAERLTSRKA 660

QY 661 LFSVLNTERARRPGLIGASVLGLDDIHRWRTFVLVRADPPPELVKVDVTGAYDTI 720
 DB 661 LFSVLNTERARRPGLIGASVLGLDDIHRWRTFVLVRADPPPELVKVDVTGAYDTI 720

QY 721 PQDLTEVIASIIKPQNTYCVRRYAVVQKAAHGHVRKAFKSHVSTLTDLQPYMRQFVAHL 780
 DB 721 PQDLTEVIASIIKPQNTYCVRRYAVVQKAAHGHVRKAFKSHVSTLTDLQPYMRQFVAHL 780

QY 781 QETSPLRDADVIEQSSSINEASSGLFDVFLRFMCHHVRIRGKSYVQCGIPQGSILSTL 840
 DB 781 QETSPLRDADVIEQSSSINEASSGLFDVFLRFMCHHVRIRGKSYVQCGIPQGSILSTL 840

QY 841 LCSLCYGDMEKLPAGTRRDGLLRLVDDFLVTPHLTHAKTFLTVRGVPEYGCVVNL 900
 DB 841 LCSLCYGDMEKLPAGTRRDGLLRLVDDFLVTPHLTHAKTFLTVRGVPEYGCVVNL 900

QY 901 RKTVVNPFVEDEALGGTAFVQMPAHGLFPWCGLLDTTLEVSQSDYSYARTSIRASLTF 960
 DB 901 RKTVVNPFVEDEALGGTAFVQMPAHGLFPWCGLLDTTLEVSQSDYSYARTSIRASLTF 960

QY 961 NRGFKAGRNMRRLFGVLRUKCHSLFLDLQVNSLQTVCTNIYKILLQVAFHACVQLP 1020
 DB 961 NRGFKAGRNMRRLFGVLRUKCHSLFLDLQVNSLQTVCTNIYKILLQVAFHACVQLP 1020

QY 1021 PHQOVWKNPTFFLRVSDTASLCYSILKAKNAGSLGAKGAAGPLPSEAVOMLCHOAFL 1080
 DB 1021 PHQOVWKNPTFFLRVSDTASLCYSILKAKNAGSLGAKGAAGPLPSEAVOMLCHOAFL 1080

QY 1081 KLTHRVTVYVPLGSLRTAQOLSKRLPGTTLTALAAANPALPSDFKTIID 1132
 DB 1081 KLTHRVTVYVPLGSLRTAQOLSKRLPGTTLTALAAANPALPSDFKTIID 1132

RESULT 20
 ID ADG90599 standard; protein; 1132 AA.
 XX ADG90599;
 AC ADG90599;
 XX 25-MAR-2004 (first entry)
 DT 25-MAR-2004 (first entry)
 XX

Human TERT SEQ ID NO:2.
DE human; immune response; telomerase reverse transcriptase; TERT;
KW cytostatic; immunostimulant; cancer; cytotoxic T cell response.
XX
XX Homo sapiens.
XX WO2004002408-A2.
XX
XX 08-JAN-2004.
XX
XX 24-JUN-2003; 2003WO-US019844.
XX
XX 27-JUN-2002; 2002US-0393295P.
XX
XX (GERO-) GERON CORP.
XX
XX Majumdar A, Ferber IA, Frolkis M, Wang Z;
XX
XX WPI; 2004-071946/07.
XX N-PSDB; ADG90598.
XX
XX Eliciting an immune response in a mammal specific for its own telomerase
PT reverse transcriptase (TERT), useful for treating or preventing cancer,
PT comprises administering a composition containing TERT of another
PT mammalian species.
XX
XX Claim 66; SEQ ID NO 2; 44pp; English.
XX
XX The invention relates to a novel method for eliciting an immune response
XX in a mammalian subject that is specific for its own telomerase reverse
XX transcriptase (TERT), comprising administering an immunogenic composition
XX containing a protein with at least 20 consecutive amino acids of TERT of
XX another mammalian species, or a nucleic acid encoding the protein. A
XX composition of the invention has cytostatic, and immunostimulant
XX activity. The protein or the nucleic acid encoding the protein is useful
XX in the manufacture of a medicament for the treatment of cancer in a human
XX or for eliciting a cytotoxic T cell response in a human.
XX
XX Query Match 100.0%; Score 5961; DB 8; Length 1132;
XX Best Local Similarity 100.0%; Pred. No. 0;
XX Matches 1132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MPRAPRCRAVRSLLRSHYREVLPATFVRRLGPGQWRLVQRGDPAAFRALVAQCLVCVPW 60
Db 1 MPRAPRCRAVRSLLRSHYREVLPATFVRRLGPGQWRLVQRGDPAAFRALVAQCLVCVPW 60
Qy 61 DARPPAPSPROVSCLELVARVLRQRCERGAKNVLAFGFALLDGGAGGPPPEAFTTSVR 120
Db 61 DARPPAPSPROVSCLELVARVLRQRCERGAKNVLAFGFALLDGGAGGPPPEAFTTSVR 120
Qy 121 SYLNTVTDALRGSGAWGLLRRVGGDDVLVHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180
Db 121 SYLNTVTDALRGSGAWGLLRRVGGDDVLVHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180
Qy 181 ATQARPPHAGPPRRRLGCERAWNHSVREAGVPLGLPAPGARRRGSGASRLPLPKRPRR 240
Db 181 ATQARPPHAGPPRRRLGCERAWNHSVREAGVPLGLPAPGARRRGSGASRLPLPKRPRR 240
Qy 241 GAAPERTPVQGSWAHPGTRGDRGFCVSPAPAEATSLGALSCTRHSFVS 300
Db 241 GAAPERTPVQGSWAHPGTRGDRGFCVSPAPAEATSLGALSCTRHSFVS 300
Qy 301 RQHAGPPSTRPRPMDTPCPVVAETKHFYSSGDKQLRPSFLSSLRPSLTGARRL 360
Db 301 RQHAGPPSTRPRPMDTPCPVVAETKHFYSSGDKQLRPSFLSSLRPSLTGARRL 360
Qy 361 VETIFLGRPWPMPGTTPRRLPRLPQRYQMRLFLLELGNHQAQCPYGVLLKTHCPRAAVT 420
Db 361 VETIFLGRPWPMPGTTPRRLPRLPQRYQMRLFLLELGNHQAQCPYGVLLKTHCPRAAVT 420

Qy 421 PAAGVCAREKPOGSSVAAPBEEDTDPRLLVOLLROHSSPWQYGVFRACLRRLVPPGLWGS 480
Db 421 PAAGVCAREKPOGSSVAAPBEEDTDPRLLVOLLROHSSPWQYGVFRACLRRLVPPGLWGS 480
Qy 481 RHNERRFLRNTKPFISLGHAKLSLOELTWKMSVRDCAWLRRSPGVGCPAAEHLRREEI 540
Db 481 RHNERRFLRNTKPFISLGHAKLSLOELTWKMSVRDCAWLRRSPGVGCPAAEHLRREEI 540
Qy 541 LAKFLHLMMSVYVVELLRSPFYVTETTFQKNRPFYFRKSVMSKLSQSIGIRHKLKRVQRE 600
Db 541 LAKFLHLMMSVYVVELLRSPFYVTETTFQKNRPFYFRKSVMSKLSQSIGIRHKLKRVQRE 600
Qy 601 LSEAEVRQHREARPALITSRLRFPKPDGLRPIVNMDDYVVGARTFREKRAERLTSRVKA 660
Db 601 LSEAEVRQHREARPALITSRLRFPKPDGLRPIVNMDDYVVGARTFREKRAERLTSRVKA 660
Qy 661 LFSVLNYERARRPGLLGASVLGLDDIHRAWRTFVLVRADPPPELYFVKVDVTGAVDTI 720
Db 661 LFSVLNYERARRPGLLGASVLGLDDIHRAWRTFVLVRADPPPELYFVKVDVTGAVDTI 720
Qy 721 PQDLRTEVIASIIKPQNTYCVRRYAVVOKAAHGHVRKAFKSHVSTLTDLQPYMQFVAHL 780
Db 721 PQDLRTEVIASIIKPQNTYCVRRYAVVOKAAHGHVRKAFKSHVSTLTDLQPYMQFVAHL 780
Qy 781 QETSPRLDADVIEQSSSINEASSGLPDVFLRFMCHHAVIRGKSYVQCQIGIPIQSILSTL 840
Db 781 QETSPRLDADVIEQSSSINEASSGLPDVFLRFMCHHAVIRGKSYVQCQIGIPIQSILSTL 840
Qy 841 LCSLCYGDMEKLFAGIRRDGLLLRLVDDFLLVTPHLTHAKTFLRTLVRGVEYGCVVNL 900
Db 841 LCSLCYGDMEKLFAGIRRDGLLLRLVDDFLLVTPHLTHAKTFLRTLVRGVEYGCVVNL 900
Qy 901 RKTWNVPFVEDEALGGTAFVQMPAHGLFPMCGLLDTRTLEVSQSDSYSSYARTSIRASLTF 960
Db 901 RKTWNVPFVEDEALGGTAFVQMPAHGLFPMCGLLDTRTLEVSQSDSYSSYARTSIRASLTF 960
Qy 961 NRGFKAGRNMRKLFGLVRLKCHSLFDLDQVNSLQTVCTNIYKILLIQAIRFHACVILQLP 1020
Db 961 NRGFKAGRNMRKLFGLVRLKCHSLFDLDQVNSLQTVCTNIYKILLIQAIRFHACVILQLP 1020
Qy 1021 FHOQVKNPFFLRVSDTASLCYSILKAKNAGMSLGAKGAAGPLPSEAVQWLCHQAFLL 1080
Db 1021 FHOQVKNPFFLRVSDTASLCYSILKAKNAGMSLGAKGAAGPLPSEAVQWLCHQAFLL 1080
Qy 1081 KLTRHRVTVYVPLGSLRTAQTSRKLPGTTLTALEAAANPALPSDFKTILD 1132
Db 1081 KLTRHRVTVYVPLGSLRTAQTSRKLPGTTLTALEAAANPALPSDFKTILD 1132
RESULT 21
ADI82172
ID ADI82172 standard; protein; 1132 AA.
XX AC ADI82172;
XX AC ADI82172;
XX DT 22-APR-2004 (first entry)
XX XX Human telomerase reverse transcriptase.
XX DE Human; embryonic stem cell; pluripotent stem cell; abnormal cell growth;
XX KW malignancy; differentiation.
XX KW Homo sapiens.
XX OS US2003224411-A1.
XX FN 04-DEC-2003.
XX PD 13-MAR-2003; 2003US-00388578.
XX PF 13-MAR-2003; 2003US-00388578.
XX PR 13-MAR-2003; 2003US-00388578.
XX XX (STAN/) STANTON L W.

Db 1081 KLTRHRTYVPLGLSLRQAOTQLSKRLPGTTLTALRAANPALPSDFKTLID 1132

RESULT 22

ADR70482

ID ADR70482 standard; protein; 1132 AA.

XX

AC ADR70482;

XX

DT 02-DEC-2004 (first entry)

XX

DE Human telomerase reverse transcriptase, TERT.

XX

KW Human; telomerase reverse transcriptase; TERT;

KW POU domain, class 5 transcription factor; POU5F1; Oct3; Oct4;

KW teratocarcinoma-derived growth factor; Cripto; podocalyxin-like; PODXL;

KW gastrin-releasing peptide receptor; GRPR; human embryonic stem cell; hES;

KW primate pluripotent stem cell; cancer; gene expression; cell separation;

KW differentiation.

XX

OS Homo sapiens.

XX

PN US2004180347-A1.

XX

PD 16-SEP-2004.

XX

PF 13-MAR-2003; 2003US-00389431.

XX

PR 13-MAR-2003; 2003US-00389431.

XX

PA (STAN//) STANTON L W.

PA (BRAN//) BRANDENBERGER R.

PA (GOLD//) GOLD J D.

PA (IRVI//) IRVING J M.

PA (MAND//) MANDALAM R.

PA (MOKM//) MOK M.

XX

PI Stanton LW, Brandenberger R, Gold JD, Irving JM, Mandalam R;

PI Mok M;

XX

DR WPI; 2004-675599/66.

DR N-PSDB; ADR70481.

XX

PT Assessing culture of undifferentiated human embryonic stem cells or their

PT progeny, by detecting Cripto, gastrin-releasing peptide (GRP) receptor

PT and podocalyxin-like protein markers, and either hTERT and/or Oct3/4, or

PT GRP receptor.

XX

PS Disclosure; SEQ ID NO 2; 57pp; English.

XX

CC The invention relates to assessing a culture of undifferentiated human

CC embryonic stem (hES) cells (undifferentiated primate pluripotent stem

CC cells) or their progeny, involves detecting or measuring a marker such as

CC Cripto (teratocarcinoma-derived growth factor), gastrin-releasing peptide

CC (GRP) receptor and podocalyxin-like protein, and either hTERT (telomerase

CC reverse transcriptase) and/or Oct3/4 (also known as POU domain, class 5,

CC transcription factor 1(POU5F1)), or GRP receptor. The method involves

CC detecting or measuring at least two markers, and detecting or measuring

CC hTERT and/or Oct3/4. The expression of the marker(s) is detected or

CC measured at mRNA level by PCR amplification. The expression of the

CC marker(s) is detected or measured at the protein level by antibody assay.

CC The method involves quantifying the proportion of undifferentiated hES

CC cells or differentiated cells in the culture from the marker expression.

CC The level of the marker is determined to be at least 100-fold higher than

CC the level of the marker in BJ fibroblasts or is determined to be no less

CC than 100-fold lower than the level of the marker in hES cells, cultured

CC on an extracellular matrix in medium conditioned with mouse embryonic

CC fibroblasts and containing 4 ng/ml basic fibroblast growth factor. The

CC method further involves modifying the culture conditions so as to cause

CC the hES cells to increase expression of the marker detected or measured

CC in the culture. The method is useful for assessing a culture of

CC undifferentiated hES cells or their progeny. The marker used in the above

CC method is useful for characterising pluripotent stem cells and their

CC differentiated progeny, for clinical diagnosis of cancer, for assessing

CC and manipulating culture conditions, regulating gene expression, cell

CC separation and purification, and to influence differentiation. The

CC present sequence is a marker protein of the invention for

CC undifferentiated stem cells.

XX

SQ Sequence 1132 AA;

Query Match 100.0%; Score 5961; DB 8; Length 1132;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MPRAPRCRAVRSLLRSHYREVLPATFVRLRGLPGQWRLVQRGDDPAARFALVAQCLVCVPW 60

Db |||||

Qy 1 MPRAPRCRAVRSLLRSHYREVLPATFVRLRGLPGQWRLVQRGDDPAARFALVAQCLVCVPW 60

Db |||||

Qy 61 DARPPPPAAPSFRVQSCLELVARVQLRCLCRGAKNVLAFGFALLDARGGPPPEAFTTSVR 120

Db |||||

Qy 61 DARPPPPAAPSFRVQSCLELVARVQLRCLCRGAKNVLAFGFALLDARGGPPPEAFTTSVR 120

Db |||||

Qy 121 SYLPNTVTDALRGSGAWGLLLRRVGGDDVLVHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180

Db |||||

Qy 121 SYLPNTVTDALRGSGAWGLLLRRVGGDDVLVHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180

Db |||||

Qy 181 ATQARPPPHASGPRRLRGCERANNHVSREAGVPLGLPAPGARRRGGASRSRLPLPKPRR 240

Db |||||

Qy 181 ATQARPPPHASGPRRLRGCERANNHVSREAGVPLGLPAPGARRRGGASRSRLPLPKPRR 240

Db |||||

Qy 241 GAAPEPERTVPGQGSWAHPGRTGPDSDRGFCVVSPPARPAEEATSELEGALSSTRHSHSVG 300

Db |||||

Qy 241 GAAPEPERTVPGQGSWAHPGRTGPDSDRGFCVVSPPARPAEEATSELEGALSSTRHSHSVG 300

Db |||||

Qy 301 RQHHAGPPSTSRPPRMDTFCPPVYAEAKHFLYSSGDKQLRPSFLSSLPSTGARRL 360

Db |||||

Qy 301 RQHHAGPPSTSRPPRMDTFCPPVYAEAKHFLYSSGDKQLRPSFLSSLPSTGARRL 360

Db |||||

Qy 361 VETIFLGSRWPMFGTPRRRLPRLPQRYWQMRPLFLELLGNHAQCPYGVLLKTHCPLRAAVT 420

Db |||||

Qy 361 VETIFLGSRWPMFGTPRRRLPRLPQRYWQMRPLFLELLGNHAQCPYGVLLKTHCPLRAAVT 420

Db |||||

Qy 421 PAAGVCAREKPGQSVAAPEEDTDPRLVOLLRQHSSPQWVYGVFVACLRRLRVPGLWGS 480

Db |||||

Qy 421 PAAGVCAREKPGQSVAAPEEDTDPRLVOLLRQHSSPQWVYGVFVACLRRLRVPGLWGS 480

Db |||||

Qy 481 RHNERFLRNTKRFISLGGHAKLSLQELTWKMSVRDCAWLRSPGVCVPAAEHRLREEI 540

Db |||||

Qy 481 RHNERFLRNTKRFISLGGHAKLSLQELTWKMSVRDCAWLRSPGVCVPAAEHRLREEI 540

Db |||||

Qy 541 LAKFLHLMSSVYVELLRSFFYVTTFTFQKNLFFYRKSVMSKLOSIGIROHLKRVQLRE 600

Db |||||

Qy 541 LAKFLHLMSSVYVELLRSFFYVTTFTFQKNLFFYRKSVMSKLOSIGIROHLKRVQLRE 600

Db |||||

Qy 601 LSAEAVRQHREARPAALLTSRLRFPKPDGLRPIVNMDDVYVVGARTFREKRAERLTSRKA 660

Db |||||

Qy 601 LSAEAVRQHREARPAALLTSRLRFPKPDGLRPIVNMDDVYVVGARTFREKRAERLTSRKA 660

Db |||||

Qy 661 LFSVLNTERARRPGLLGASVLGLDDIHRAWRTFVLVRAQDPPPELFPVKVDVTGAYDTI 720

Db |||||

Qy 661 LFSVLNTERARRPGLLGASVLGLDDIHRAWRTFVLVRAQDPPPELFPVKVDVTGAYDTI 720

Db |||||

Qy 721 PQDLTEVIASIIKPONTYCVRRYAVVQKAAHGHVKAFKSHVSTLTDLPYMQFVAHL 780

Db |||||

Qy 721 PQDLTEVIASIIKPONTYCVRRYAVVQKAAHGHVKAFKSHVSTLTDLPYMQFVAHL 780

Db |||||

Qy 781 QETSPLRDADVIEQSSSINEASSGLFDVFLRFMCHAVRIRGKSVYOCQIPQSSILSTL 840

Db |||||

Qy 781 QETSPLRDADVIEQSSSINEASSGLFDVFLRFMCHAVRIRGKSVYOCQIPQSSILSTL 840

Db |||||

Qy 841 LCSLCYGDMMENKLPAGIRRDGLLLRLVDFLLVTPHLLTHAKTFLRTLVRGVPYGCVVNL 900

Db |||||

Qy 841 LCSLCYGDMMENKLPAGIRRDGLLLRLVDFLLVTPHLLTHAKTFLRTLVRGVPYGCVVNL 900

Db |||||

Qy 901 RKTWNVPFVEDEALGGTAFVQMPAHGLFPWCGLLLDLTFRTLEVQSDYSSYARTSIRASITF 960

901 RKTVMNFFVEDEALGTAFAVMPAHGLFPWCGLLDTTRTLEVQSDYSSVARTSIRASLTF 960
 961 NRGFKAGNRMRKLGVLRLKCHSLFLDLQVNSLQVCTNIYKILLQAYRHACVLOLP 1020
 961 NRGFKAGNRMRKLGVLRLKCHSLFLDLQVNSLQVCTNIYKILLQAYRHACVLOLP 1020
 1021 FHOQVKNPTFFLRVISDTASICYSLKAKNAGMSLGAKAAGPLPSEAVOMLCHQAFLL 1080
 1021 FHOQVKNPTFFLRVISDTASICYSLKAKNAGMSLGAKAAGPLPSEAVOMLCHQAFLL 1080
 1081 KLTRHRTVYVPLLSRLTAQTLRSKLPGLTTLTALEAANPALPSDFKTILD 1132
 1081 KLTRHRTVYVPLLSRLTAQTLRSKLPGLTTLTALEAANPALPSDFKTILD 1132

RESULT 23

AAW61350 standard; protein; 1154 AA.

AAW61350;

25-MAR-2003 (revised)

12-OCT-1998 (first entry)

Human telomerase protein 2 (TP2).

TP2; human; telomerase protein 2; cancer; AIDS; ageing; therapy.

Homo sapiens.

WO9821343-A1.

22-MAY-1998.

13-NOV-1997; 97WO-US021248.

15-NOV-1996* 96US-00751189.

11-JUN-1997; 97US-00873039.

16-OCT-1997; 97US-00951733.

(AMGE-) AMGEN INC.

(AMGE-) AMGEN CANADA INC.

Harrington LA, Robinson MO;

WPI; 1998-297946/26.

N-P8DB; AAV27876.

New nucleic acid encoding human telomerase protein-2 - used for regulating telomerase activity, e.g. for treating cancer or acquired immune deficiency syndrome.

Claim 1e; Fig 9; 150pp; English.

This polypeptide comprises human telomerase protein 2 (TP2), a novel protein of the telomerase complex. Its amino acid sequence was deduced from a composite (see AAV27876) of isolated cDNA clones 32 (see AAV27872) and TP2-15 (see AAV27875), obtained from a human colon tumour cell line LIM1863 cDNA. Expressing TP2 in a cell is used to increase telomerase activity and thus proliferation for treatment of e.g. HIV infection, AIDS and ageing disorders, while expressing an inactive mutant of TP2 (or molecule antisense to the gene) is used to decrease telomerase activity, e.g. for treatment of cancer. TP2 polypeptides can also be used to screen for agents that inhibit TP2 activity or its binding to TRP1 (see AAW61347) or telomerase RNA, potentially useful therapeutically, also to raise specific antibodies useful in immunoassays and therapeutically as inhibitors. Also contemplated are transgenic animals in which the TP2 gene has been inactivated or is overexpressed. TP2 polypeptides are administered i.v., s.c. or orally, or they are delivered from engineered cells or gene therapy vectors. (Updated on 25-MAR-2003 to correct PR field.)

SQ		Sequence 1154 AA;		
Query Match		100.0%; Score 5961; DB 2; Length 1154;		
Best Local Similarity		100.0%; Pred. No. 0;		
Matches 1132; Conservative		0; Mismatches 0; Indels 0; Gaps 0;		
QY	1	MPRAPRCRAVRSLLRSHYREVLP	1	MPRPRCRAVRSLLRSHYREVLP
DB	23	MPRAPRCRAVRSLLRSHYREVLP	23	MPRAPRCRAVRSLLRSHYREVLP
QY	61	DARPPAAPSPROVSCIKELVARV	61	DARPPAAPSPROVSCIKELVARV
DB	83	DARPPAAPSPROVSCIKELVARV	83	DARPPAAPSPROVSCIKELVARV
QY	121	SYLPNTVTDALRGSGAWGLLR	121	SYLPNTVTDALRGSGAWGLLR
DB	143	SYLPNTVTDALRGSGAWGLLR	143	SYLPNTVTDALRGSGAWGLLR
QY	181	ATQARPPPHASGPRRLGGERAWN	181	ATQARPPPHASGPRRLGGERAWN
DB	203	ATQARPPPHASGPRRLGGERAWN	203	ATQARPPPHASGPRRLGGERAWN
QY	241	GAAPERTPVQGSWAHPGTRG	241	GAAPERTPVQGSWAHPGTRG
DB	263	GAAPERTPVQGSWAHPGTRG	263	GAAPERTPVQGSWAHPGTRG
QY	301	ROHAGPPTSRPPRPPMDT	301	ROHAGPPTSRPPRPPMDT
DB	323	ROHAGPPTSRPPRPPMDT	323	ROHAGPPTSRPPRPPMDT
QY	361	VETIFLGSRPMPGT	361	VETIFLGSRPMPGT
DB	383	VETIFLGSRPMPGT	383	VETIFLGSRPMPGT
QY	421	PAAGVCAREKPGQSVAAPEED	421	PAAGVCAREKPGQSVAAPEED
DB	443	PAAGVCAREKPGQSVAAPEED	443	PAAGVCAREKPGQSVAAPEED
QY	481	RHNERRFLRNTKKFISLG	481	RHNERRFLRNTKKFISLG
DB	503	RHNERRFLRNTKKFISLG	503	RHNERRFLRNTKKFISLG
QY	541	LAKFLHLMWSVYVVELLS	541	LAKFLHLMWSVYVVELLS
DB	563	LAKFLHLMWSVYVVELLS	563	LAKFLHLMWSVYVVELLS
QY	601	LSEAEVROHREARPA	601	LSEAEVROHREARPA
DB	623	LSEAEVROHREARPA	623	LSEAEVROHREARPA
QY	661	LFSVLNYERARRPGL	661	LFSVLNYERARRPGL
DB	683	LFSVLNYERARRPGL	683	LFSVLNYERARRPGL
QY	721	PODRLETVIASIIPQNT	721	PODRLETVIASIIPQNT
DB	743	PODRLETVIASIIPQNT	743	PODRLETVIASIIPQNT
QY	781	QETSPRLDAVVIQSS	781	QETSPRLDAVVIQSS
DB	803	QETSPRLDAVVIQSS	803	QETSPRLDAVVIQSS
QY	841	LCSLCYGMENKLFAG	841	LCSLCYGMENKLFAG
DB	863	LCSLCYGMENKLFAG	863	LCSLCYGMENKLFAG
QY	901	RKTVMNFFVEDEALG	901	RKTVMNFFVEDEALG
DB	923	RKTVMNFFVEDEALG	923	RKTVMNFFVEDEALG
QY	961	NRGFKAGNRMRKLG	961	NRGFKAGNRMRKLG
DB	983	NRGFKAGNRMRKLG	983	NRGFKAGNRMRKLG

QY 1021 FHQVWKNTFLRVISDTASLCYSILKAKNAGSLGAKGAGPLPSEAVQWLCHOAPLL 1080
DQ 1043 FHQVWKNTFLRVISDTASLCYSILKAKNAGSLGAKGAGPLPSEAVQWLCHOAPLL 1102
QY 1081 KLTRHRTVTVPLLSRLTAQQLSRKLPGLTTLTALEAAANPALPSDFKTIID 1132
DQ 1103 KLTRHRTVTVPLLSRLTAQQLSRKLPGLTTLTALEAAANPALPSDFKTIID 1154

RESULT 24

AAW47008
ID AAW47008 standard; protein; 1189 AA.

XX AAW47008;

DT 13-AUG-1998 (first entry)

XX Glutathione-S-transferase and hTERT fusion protein 8.

XX Human; telomerase reverse transcriptase; hTERT; TERT; diagnosis; prognosis;
KW cell proliferation; cancer; ageing; ribonucleoprotein.

XX Synthetic.

OS Homo sapiens.

XX Key Location/Qualifiers

FH Misc-difference 22..23

FT /note= "enterokinase cleavage site"

XX GB2317891-A.

XX 08-APR-1998.

XX 01-OCT-1997; 97GB-00020890.

XX 01-OCT-1996; 96US-00724643.

PR 18-APR-1997; 97US-00844419.

PR 06-MAY-1997; 97US-00846017.

PR 09-MAY-1997; 97US-00851843.

PR 14-AUG-1997; 97US-00854050.

PR 14-AUG-1997; 97US-00911312.

PR 14-AUG-1997; 97US-00912951.

PR 14-AUG-1997; 97US-00915503.

XX (GERO-) GERON CORP.

PA (UTTE-) UNIV TECHNOLOGY CORP.

XX Cech TR, Lingner J, Nakamura T, Chapman KB, Morin GB, Harley CB;

PI Andrews WH;

XX WPI; 1998-171633/16.

PT Pure and recombinant human Telomerase Reverse Transcriptase and its
PT variants - are useful in the diagnosis, prognosis and treatment of cell
PT proliferation conditions especially cancer and ageing.

XX Example 6; Page 234-235; 387pp; English.

XX The present sequence represents a fusion protein from an example of the
CC present invention which describes human telomerase reverse transcriptase
CC (hTERT). The present invention also describes the following methods: (A)
CC determining whether a test compound is a modulator of hTERT, by detecting
CC the change in hTERT recombinant protein or polynucleotide, on
CC administration of the compound; (B) preparation of recombinant telomerase
CC by contacting a protein preparation of hTERT with a telomerase RNA
CC component; (C) detection of the hTERT RNA or protein in a sample by
CC binding a relevant probe to the sample and detecting the complex formed
CC or in the case of RNA detection, amplifying the product and correlating
CC the presence of complex or amplification product with presence of hTERT in
CC the sample; and (D) increasing the proliferation of a vertebrate cell by
CC increasing hTERT expression; and (E) the use of an agent that causes an
CC increase in cell vertebrate cell proliferation to create a medicament

CC that inhibits ageing. A protein preparation of hTERT and the
CC polynucleotide encoding hTERT can be used in the manufacture of
CC medicaments for inhibiting the effect of ageing or cancer. Inhibitors of
CC telomerase activity can be used to treat conditions that are associated
CC with high telomerase activity. A protein preparation of hTERT can also be
CC used in the new methods

XX Sequence 1189 AA;

Query Match 100.0%; Score 5961; DB 2; Length 1189;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPRAPCRAVRSLLRSHYREVLPATFVRLRPGOGWRLVORGDPAAPRALVAQCLVCVPW 60

DQ 58 MPRAPCRAVRSLLRSHYREVLPATFVRLRPGOGWRLVORGDPAAPRALVAQCLVCVPW 117

QY 61 DARPPPAAPSPFVSCIKELVARVLQRLCERGANVLAFCFALDARGGPEAFTTSVR 120

DQ 118 DARPPPAAPSPFVSCIKELVARVLQRLCERGANVLAFCFALDARGGPEAFTTSVR 177

QY 121 SYLPNTVTDALRGSGAWGLLLRRVGGDDVLVHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180

DQ 178 SYLPNTVTDALRGSGAWGLLLRRVGGDDVLVHLLARCALFVLVAPSCAYQVCGPPLYQLGA 237

QY 181 ATOARPPPHASGPRRLGRCERAWNHSVREAGVPLGLPAPGARRRGGSASRSLPLPKRRR 240

DQ 238 ATOARPPPHASGPRRLGRCERAWNHSVREAGVPLGLPAPGARRRGGSASRSLPLPKRRR 297

QY 241 GAAPEPERTVGGGSAHPGRTGPGSDRGFCVSPARPABEATSLGALSCTRSHPSVG 300

DQ 298 GAAPEPERTVGGGSAHPGRTGPGSDRGFCVSPARPABEATSLGALSCTRSHPSVG 357

QY 301 RQHHAGPSTSRPPRWDTPCPVYATKHFYSSGDKQLRPSFLSSRLPSLTGARRL 360

DQ 358 RQHHAGPSTSRPPRWDTPCPVYATKHFYSSGDKQLRPSFLSSRLPSLTGARRL 417

QY 361 VETIFLGSRWPMFGTPRRRLPRLPQRYWQMRPLFLELLGNHAQCPYGVLLKTHCPLRAAVT 420

DQ 418 VETIFLGSRWPMFGTPRRRLPRLPQRYWQMRPLFLELLGNHAQCPYGVLLKTHCPLRAAVT 477

QY 421 PAAGVCAREKPOGSAVAPEEEDTDPRLLVOLLROHSSPMQVYGVFVACLRRLVPPGLWGS 480

DQ 478 PAAGVCAREKPOGSAVAPEEEDTDPRLLVOLLROHSSPMQVYGVFVACLRRLVPPGLWGS 537

QY 481 RHNERRFLRNTKPFISLGHAKLSLOELTWKMSVRDCAWLRSPGVGCPVAAEHLREEI 540

DQ 538 RHNERRFLRNTKPFISLGHAKLSLOELTWKMSVRDCAWLRSPGVGCPVAAEHLREEI 597

QY 541 LAKFLHLMVSVYVVELLSRFFYVTTTFOKNRLFYRKSVWSKLOSGIROHLKRVQLRE 600

DQ 598 LAKFLHLMVSVYVVELLSRFFYVTTTFOKNRLFYRKSVWSKLOSGIROHLKRVQLRE 657

QY 601 LSAEAVRQREARPAALTSRLRFPKPDGLRPIVNDYVVGARTFRREKRAERLTSRVKA 660

DQ 658 LSAEAVRQREARPAALTSRLRFPKPDGLRPIVNDYVVGARTFRREKRAERLTSRVKA 717

QY 661 LFSVLNRYERARRPCLLGASVGLGDDIHRWRTFVLVRAQDPPPELYFVKVDVTGAYDTI 720

DQ 718 LFSVLNRYERARRPCLLGASVGLGDDIHRWRTFVLVRAQDPPPELYFVKVDVTGAYDTI 777

QY 721 PQRLTEVIASIIKPQNTYCVRRYAVVQKAAHGHVKAFAKSHVSTLTDLPYMQFVAHL 780

DQ 778 PQRLTEVIASIIKPQNTYCVRRYAVVQKAAHGHVKAFAKSHVSTLTDLPYMQFVAHL 837

QY 781 QETSPRLDADVIBQSSSLNEASSGLFDVFLRFMCHHAVIRGKSYVOCQIPQSGISLTL 840

DQ 838 QETSPRLDADVIBQSSSLNEASSGLFDVFLRFMCHHAVIRGKSYVOCQIPQSGISLTL 897

QY 841 LCSLCYGDMMENKLFAGIRRDGLLLRLVDDFLVLTTPHLTHAKTFLRTLVRGVPYGCVVNL 900

DQ 898 LCSLCYGDMMENKLFAGIRRDGLLLRLVDDFLVLTTPHLTHAKTFLRTLVRGVPYGCVVNL 957

QY 901 RKTVVNPFVDEALGCTAFVQMPAHGLFPWCGLLLDTRTLEVSQSYSSYARTSIRASITF 960
 DB 958 RKTVVNPFVDEALGCTAFVQMPAHGLFPWCGLLLDTRTLEVSQSYSSYARTSIRASITF 1017
 QY 961 NRGPKAGNRMRKLFGLVRLKCHSLFDLQVNSLQTVCTNIYKILLQAYRPHACVQLP 1020
 DB 1018 NRGFKAGNRMRKLFGLVRLKCHSLFDLQVNSLQTVCTNIYKILLQAYRPHACVQLP 1077
 QY 1021 FHQQVWKNPTFLRVISDTASLCYSILKAKNAGMSLGAKGAGPLPSEAVQWLCHQAFLL 1080
 DB 1078 FHQQVWKNPTFLRVISDTASLCYSILKAKNAGMSLGAKGAGPLPSEAVQWLCHQAFLL 1137
 QY 1081 KLTHRVTVVPLGLSLRTAQTLRSKLPGLTTLTALEAAANPALPDSDFKTILD 1132
 DB 1138 KLTHRVTVVPLGLSLRTAQTLRSKLPGLTTLTALEAAANPALPDSDFKTILD 1189

RESULT 25

AAW47000
 ID AAW47000 standard; protein; 1285 AA.

XX
 AC AAW47000;

XX
 DT 13-AUG-1998 (first entry)

XX HIS tagged thioredoxin moiety and full length hTERT fusion protein.

DE Human; telomerase reverse transcriptase; hTERT; TRT; diagnosis; prognosis;
 KW cell proliferation; cancer; ageing; ribonucleoprotein.

XX Synthetic.

OS Homo sapiens.

XX Key Location/Qualifiers

FH Misc-difference 119..120

FT /note= "enterokinase cleavage site"

FT Region 120..1285

FT /label= hTERT

FT /note= "full length human telomerase reverse
 transcriptase"

XX GB2317891-A.

PN 08-APR-1998.

PD 01-OCT-1997; 97GB-00020890.

PF 01-OCT-1996; 96US-00724643.

PR 18-APR-1997; 97US-00844419.

PR 25-APR-1997; 97US-00846017.

PR 06-MAY-1997; 97US-00851843.

PR 09-MAY-1997; 97US-00854050.

PR 14-AUG-1997; 97US-00911312.

PR 14-AUG-1997; 97US-00912951.

PR 14-AUG-1997; 97US-00915503.

XX (GERO-) GERON CORP.

PA (UYTE-) UNIV TECHNOLOGY CORP.

XX Cech TR, Lingner J, Nakamura T, Chapman KB, Morin GB, Harley CB;
 PI Andrews WH;

XX WPI; 1998-171633/16.

XX Pure and recombinant human Telomerase Reverse Transcriptase and its
 PT variants - are useful in the diagnosis, prognosis and treatment of cell
 PT proliferation conditions especially cancer and ageing.
 XX Example 6; Page 223; 387pp; English.

XX The present sequence represents a fusion protein from an example of the
 CC present invention which describes human telomerase reverse transcriptase
 CC (hTERT). The present invention also describes the following methods: (A)

CC determining whether a test compound is a modulator of hTERT, by detecting
 CC the change in hTERT recombinant protein or polynucleotide, on
 CC administration of the compound; (B) preparation of recombinant telomerase
 CC by contacting a protein preparation of hTERT with a telomerase RNA
 CC component; (C) detection of the hTERT RNA or protein in a sample by
 CC binding a relevant probe to the sample and detecting the complex formed
 CC or in the case of RNA detection, amplifying the product and correlating
 CC the presence of complex or amplification product with presence of hTERT in
 CC the sample; and (D) increasing the proliferation of a vertebrate cell by
 CC increasing hTERT expression; and (E) the use of an agent that causes an
 CC increase in cell vertebrate cell proliferation to create a medicament
 CC that inhibits ageing. A protein preparation of hTERT and the
 CC polynucleotide encoding hTERT can be used in the manufacture of
 CC medicaments for inhibiting the effect of ageing or cancer. Inhibitors of
 CC telomerase activity can be used to treat conditions that are associated
 CC with high telomerase activity. A protein preparation of hTERT can also be
 CC used in the new methods

XX SQ Sequence 1285 AA;

Query Match 99.9%; Score 5955; DB 2; Length 1285;
 Best Local Similarity 99.9%; Pred. No. 0;
 Matches 1131; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MPRAPRCRAVRSLLRSHYREVLPATFVRRLLGPQGRWLVRQGDPAAPRALVAQCLVCVPW 60
 DB 154 MPRAPRCRAVRSLLRSHYREVLPATFVRRLLGPQGRWLVRQGDPAAPRALVAQCLVCVPW 213
 QY 61 DARPPAAPSPROVSCLELVARVLORLCERGAKNVLAFGFALLDGGAGGPEAFTTSVR 120
 DB 214 DARPPAAPSPROVSCLELVARVLORLCERGAKNVLAFGFALLDGGAGGPEAFTTSVR 273
 QY 121 SYLPNTVTDALRGSGAWGLLLRRVGDVLLHLLARCALFVLVAPSCAYQVCGPPYQLGA 180
 DB 274 SYLPNTVTDALRGSGAWGLLLRRVGDVLLHLLARCALFVLVAPSCAYQVCGPPYQLGA 333
 QY 181 ATQARPPPHASGPRRRLLGCERAWNHSVREAGVPLGLPAGARRRGGSSASRLPLPKRPRR 240
 DB 334 ATQARPPPHASGPRRRLLGCERAWNHSVREAGVPLGLPAGARRRGGSSASRLPLPKRPRR 393
 QY 241 GAAPEPERTVPGQSWAHPGTRGPDSDRGFCVSPARPAEATSLEGALSCTRHSHPVSG 300
 DB 394 GAAPEPERTVPGQSWAHPGTRGPDSDRGFCVSPARPAEATSLEGALSCTRHSHPVSG 453
 QY 301 ROEHAGPSTSRPRPMDTTPCPVYAEKTHLYSGDKEQLRPSLLSLRPSLTGARRL 360
 DB 454 ROEHAGPSTSRPRPMDTTPCPVYAEKTHLYSGDKEQLRPSLLSLRPSLTGARRL 513
 QY 361 VETIFLGSRPWMPGTTPRLPRLPQRYWQMRPLFLELLGNHAQCPYGVLLKTHCPLRAAVT 420
 DB 514 VETIFLGSRPWMPGTTPRLPRLPQRYWQMRPLFLELLGNHAQCPYGVLLKTHCPLRAAVT 573
 QY 421 PAAGVCAREKPGQSWAAPAEEDTDPRLVQLLRQHSHPWYGVFVRACLRRLRVPGLWGS 480
 DB 574 PAAGVCAREKPGQSWAAPAEEDTDPRLVQLLRQHSHPWYGVFVRACLRRLRVPGLWGS 633
 QY 481 RHNERFLRNTKTFISLCKHAKLSLOELTWKMSVRDCAWLRSQVCGVCPAAEHLRBEI 540
 DB 634 RHNERFLRNTKTFISLCKHAKLSLOELTWKMSVRDCAWLRSQVCGVCPAAEHLRBEI 693
 QY 541 LAKFLHLMMSVYVVELLSRFFVTTFQKRLFFYRKSVMKLSQSIGIRHOLKRVQURE 600
 DB 694 LAKFLHLMMSVYVVELLSRFFVTTFQKRLFFYRKSVMKLSQSIGIRHOLKRVQURE 753
 QY 601 LSEAEVRQHRARPALLTSRLRFPKPDGLRPIVNMDDYVVGARTFRREKRAERLTSRVKA 660
 DB 754 LSEAEVRQHRARPALLTSRLRFPKPDGLRPIVNMDDYVVGARTFRREKRAERLTSRVKA 813
 QY 661 LFSVLNTERARRPGLLGASVLGLDDIHRAWRTFVLVRQAQDPPPELYFVKVDVTGAYDTI 720
 DB 814 LFSVLNTERARRPGLLGASVLGLDDIHRAWRTFVLVRQAQDPPPELYFVKVDVTGAYDTI 873
 QY 721 PQDLRLTEIASIIKPQNTYCVRRVAVVQKAAHGHVRKAFKSHVSTLTLDLPYMRQFVAHL 780

Db 874 PQDLTEVIASIIKPNQTYCVRRAVVOKAAGHVRKAFKSHVSTLTDLPYMQFVNAHL 933
 Qy 781 QETSPLRDAVVEIOSSSLEASSGLFDVFLRFMCHHAVIRGKSYVQCGIPQGSII STL 840
 Db 934 QETSPLRDAVVEIOSSSLEASSGLFDVFLRFMCHHAVIRGKSYVQCGIPQGSII STL 993
 Qy 841 LCSLCYGDMEKFLAGIRDEGLLRLVDDFLVTPHLTHAKTFLRTVIRGVEYGCVVNL 900
 Db 994 LCSLCYGDMEKFLAGIRDEGLLRLVDDFLVTPHLTHAKTFLRTVIRGVEYGCVVNL 1053
 Qy 901 RKTIVNPFVEDEALGCTAFVQMPAHGLFPWCGLLDDTRTLEVQSDYSSYARTISRASLTF 960
 Db 1054 RKTIVNPFVEDEALGCTAFVQMPAHGLFPWCGLLDDTRTLEVQSDYSSYARTISRASLTF 1113
 Qy 961 NRGFKAGNMRRKLFVGLRLKCHSLFLDLQVNSLQTVCTNIYKILLQAYRFHACVLQLP 1020
 Db 1114 NRGFKAGNMRRKLFVGLRLKCHSLFLDLQVNSLQTVCTNIYKILLQAYRFHACVLQLP 1173
 Qy 1021 FHOQWKNPTFLRIVISDTASLCYSILKAKNAGSLGAKGAGPLPSEAVQWLCHOAPLL 1080
 Db 1174 FHOQWKNPTFLRIVISDTASLCYSILKAKNAGSLGAKGAGPLPSEAVQWLCHOAPLL 1233
 Qy 1081 KLTRHRVTYVPLGSLRTAQOLSKRLPGTTLTALEAAANPALSDPKTILD 1132
 Db 1234 KLTRHRVTYVPLGSLRTAQOLSKRLPGTTLTALEAAANPALSDPKTILD 1285

RESULT 26

AAW71376
 ID AAW71376 standard; protein; 1132 AA.
 XX
 AC AAW71376;
 XX
 DT 04-DEC-1998 (first entry)
 XX
 DE Human telomerase catalytic subunit referred to as hEST2.
 XX
 KW Catalytic subunit; human; telomerase; telomere maintenance; diagnosis;
 treatment; cancer.
 XX
 OS Homo sapiens.
 XX
 PN W03837181-A2.
 XX
 PD 27-AUG-1998.
 XX
 PF 20-FEB-1998; 98WO-US003404.
 XX
 PR 20-FEB-1997; 97US-0038750P.
 PR 20-MAY-1997; 97US-0047151P.
 PR 01-AUG-1997; 97US-0054549P.
 PR 14-AUG-1997; 97US-0055762P.
 PR 30-OCT-1997; 97US-0064322P.
 XX
 PA (WHED) WHITEHEAD INST BIOMEDICAL RES.
 XX
 PI Counter CM, Meyerson M, Weinberg RA;
 XX
 DR WPI; 1998-495367/42.
 DR N-PSDB; AAV60320.
 XX

XX New isolated human telomerase catalytic sub-unit gene - used to develop
 PT products for increasing or reducing the life span of cells such as cancer
 PT cells or transformed cells.
 XX
 PS Claim 5; Fig 6; 96pp; English.
 XX
 CC The present sequence represents the catalytic subunit of a human
 CC telomerase holoenzyme. Disruption of the telomerase gene alters telomere
 CC maintenance. The DNA is essential for telomerase activity, and the
 CC protein is physically associated with telomerase and a constituent of
 CC active telomerase complex. The products can be used for increasing or

CC reducing the lifespan of cells such as cancer cells or transformed cells.
 CC They can also be used in the diagnosis and treatment of malignancies. In
 CC addition, cells with a longer lifespan can be transplanted into or
 CC grafted onto an individual (e.g. as skin grafts, as systems for delivery
 CC of therapeutic proteins, such as hormones and enzymes), to whom they
 CC provide therapeutic benefit
 XX
 SQ Sequence 1132 AA;
 Query Match 99.9%; Score 5954; DB 2; Length 1132;
 Best Local Similarity 99.9%; Pred. No. 0;
 Matches 1131; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 1 MPRAPRCRAVRLSLRSHYREVLPATFVRLRPGOGWRLVQRGDPAAFRALVAQCLVCVPW 60
 Db 1 MPRAPRCRAVRLSLRSHYREVLPATFVRLRPGOGWRLVQRGDPAAFRALVAQCLVCVPW 60
 Qy 61 DARPPAPAFPROVSCLEIVARVLQRLCERGAKNVLAFGPALDARGGPEAFTTSVR 120
 Db 61 DARPPAPAFPROVSCLEIVARVLQRLCERGAKNVLAFGPALDARGGPEAFTTSVR 120
 Qy 121 SYLPTNTVDALRGSGAWGLLLRRVGDVLLHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180
 Db 121 SYLPTNTVDALRGSGAWGLLLRRVGDVLLHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180
 Qy 181 ATQARPPHAGSPRRRLGCRANVHVRAGVPLGLPAPGARRGGASRSLPLPKRPRR 240
 Db 181 ATQARPPHAGSPRRRLGCRANVHVRAGVPLGLPAPGARRGGASRSLPLPKRPRR 240
 Qy 241 GAAPEPERTVGGQSWAHPCRTGDRGFCVSPARPABEATSLGALSCTRSHSVG 300
 Db 241 GAAPEPERTVGGQSWAHPCRTGDRGFCVSPARPABEATSLGALSCTRSHSVG 300
 Qy 301 ROHHAGPSTSRPPRMDTFCPPVYAEKHFLYSSGDKQLRPSFLSSRLPSLTGARRL 360
 Db 301 ROHHAGPSTSRPPRMDTFCPPVYAEKHFLYSSGDKQLRPSFLSSRLPSLTGARRL 360
 Qy 361 VETIFLGRPMPCGTPRRLPRLPORYQWMPRLFLELLGNHAQCYPYGVLLKTHCPLRAVT 420
 Db 361 VETIFLGRPMPCGTPRRLPRLPORYQWMPRLFLELLGNHAQCYPYGVLLKTHCPLRAVT 420
 Qy 421 PAAGVCAREKPOGSVAAPPEEDTDPRLLVOLLRHSSPQWVGVFVRACLRLVPPGLWGS 480
 Db 421 PAAGVCAREKPOGSVAAPPEEDTDPRLLVOLLRHSSPQWVGVFVRACLRLVPPGLWGS 480
 Qy 481 RHNERRFLRNTKXFI SLGKHA KLSQLT WKMSVRGCAWLRSPGVGCPAAEHLRBEI 540
 Db 481 RHNERRFLRNTKXFI SLGKHA KLSQLT WKMSVRGCAWLRSPGVGCPAAEHLRBEI 540
 Qy 541 LAKFLHLMSSVYVVELLRSFFYTETTFQKNRLEFFYRKSVMWSKLSQSGIRQHLKRVQURE 600
 Db 541 LAKFLHLMSSVYVVELLRSFFYTETTFQKNRLEFFYRKSVMWSKLSQSGIRQHLKRVQURE 600
 Qy 601 LSEAEVRQHREARPAALLTSRLRFTPKDGLRPIVNMDYVVGARTFRREKRAELTSRKA 660
 Db 601 LSEAEVRQHREARPAALLTSRLRFTPKDGLRPIVNMDYVVGARTFRREKRAELTSRKA 660
 Qy 661 LFSVLYNERARRPGLLGASVLGLDDIHRWRTFVLVRVRAQDPPPELYFVKVDVTGAYDTI 720
 Db 661 LFSVLYNERARRPGLLGASVLGLDDIHRWRTFVLVRVRAQDPPPELYFVKVDVTGAYDTI 720
 Qy 721 PQDLTEVIASIIKPNQTYCVRRAVVOKAAGHVRKAFKSHVSTLTDLPYMQFVNAHL 780
 Db 721 PQDLTEVIASIIKPNQTYCVRRAVVOKAAGHVRKAFKSHVSTLTDLPYMQFVNAHL 780
 Qy 781 QETSPLRDAVVEIOSSSLEASSGLFDVFLRFMCHHAVIRGKSYVQCGIPQGSII STL 840
 Db 781 QETSPLRDAVVEIOSSSLEASSGLFDVFLRFMCHHAVIRGKSYVQCGIPQGSII STL 840
 Qy 841 LCSLCYGDMEKFLAGIRDEGLLRLVDDFLVTPHLTHAKTFLRTVIRGVEYGCVVNL 900
 Db 841 LCSLCYGDMEKFLAGIRDEGLLRLVDDFLVTPHLTHAKTFLRTVIRGVEYGCVVNL 900

Db 961 NRGFKAGNMRKLFGLVRLKCHSLFLDLQVNSLQTVCTNIYKILLQAYRFHACVQLP 1020
 Qy 1021 FHQQWKNPTTFLRVISDTASLCYSILKAKNAGMSLGAKGAAGPLPSEAVQWLCHQAFLL 1080
 Db 1021 FHQQWKNPTTFLRVISDTASLCYSILKAKNAGMSLGAKGAAGPLPSEAVQWLCHQAFLL 1080
 Qy 1081 KLTRHRVTYVPLGSLRTAQQLSRKLPGLTTLTALEAAANPALPSDFKTILD 1132
 Db 1081 KLTRHRVTYVPLGSLRTAQQLSRKLPGLTTLTALEAAANPALPSDFKTILD 1132

RESULT 28

RAY00638
 ID AAY00638 standard; protein; 1132 AA.

XX AC AAY00638;

XX DT 26-JUL-1999 (first entry)

XX DE Truncated telomerase protein sequence.

XX KW Telomerase; human; cancer; diagnosis; melanoma; skin cancer; leukaemia;
 KW neuroblastoma; breast carcinoma; colon carcinoma; lymphoma; osteosarcoma;
 KW smooth muscle cell hyperplasia; stem cell proliferation; Wilm's tumour;
 KW stem cell differentiation; organ regeneration; organ differentiation.

XX OS Homo sapiens.

XX OS Synthetic.

XX PN WO9901560-A1.

XX PD 14-JAN-1999.

XX PF 01-JUL-1998; 98WO-US013835.

XX PR 01-JUL-1997; 97US-0051410P.

XX PR 21-JUL-1997; 97US-0053018P.

XX PR 21-JUL-1997; 97US-0053329P.

XX PR 04-AUG-1997; 97US-0054642P.

XX PR 09-SEP-1997; 97US-0058287P.

XX PA (CAMB-) CAMBIA BIOSYSTEMS LLC.

XX PI Kilian A, Bowtell D;

XX DR WPI; 1999-106060/09.

XX DR N-PSDB; AAX18266.

XX PT New isolated vertebrate telomerase genes - used to develop products for
 PT treating cancers or for organ regeneration, nerve cell or brain cell
 PT growth following injury or bone marrow transplantation.

XX PS Claim 4; Fig 11f-i; 134pp; English.

XX CC This sequence is a truncated human telomerase of the invention. Primers
 CC that amplify the telomerase coding sequence can be used in a method for
 CC diagnosing cancer in a patient. The telomerase can be used for detection,
 CC diagnosis and drug screening. Inhibitors of telomerase activity can be
 CC used to treat cancers such as melanomas, other skin cancers,
 CC neuroblastomas, breast carcinomas, colon carcinomas, leukaemias,
 CC lymphomas, osteosarcomas or smooth muscle cell hyperplasias or skin
 CC growths. Enhancers of telomerase may be used to stimulate stem cell
 CC proliferation and differentiation (expansion of haematopoietic stem cells
 CC could be administered in the bone marrow transplant context). As well,
 CC many tissues have stem cells. Proliferation of these cells may be useful
 CC in wound healing, hair growth, treatment of disease such as Wilm's
 CC tumour, organ regeneration or differentiation after injury or diseases,
 CC nerve cell or brain cell growth following injury

XX SQ Sequence 1132 AA;

Query Match 99.9%; Score 5954; DB 2; Length 1132;

Best Local Similarity 99.9%; Pred. No. 0;

Matches 1131; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MPRAPRCRAVRSLLRSHYREVLPPLATEVRRLLGPGQWELVORGDPAAAFRALVAOCLVCVPM 60
 Db 1 MPRAPRCRAVRSLLRSHYREVLPPLATEVRRLLGPGQWELVORGDPAAAFRALVAOCLVCVPM 60
 Qy 61 DARPPPPAAPSFRQVSCCLKELVARVLQRLCERGAKNVLAFGFALLDARGGPPPEAFTTSVR 120
 Db 61 DARPPPPAAPSFRQVSCCLKELVARVLQRLCERGAKNVLAFGFALLDARGGPPPEAFTTSVR 120
 Qy 121 SYLPTNTVDALRGSGAWGLLLRRVGGDVLVHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180
 Db 121 SYLPTNTVDALRGSGAWGLLLRRVGGDVLVHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180
 Qy 181 ATQARPPPHASGPRRLGRCERANVHSVREAGVPLGLPAPGARRRGGASRSLSLPKPRR 240
 Db 181 ATQARPPPHASGPRRLGRCERANVHSVREAGVPLGLPAPGARRRGGASRSLSLPKPRR 240
 Qy 241 GAAPERTPTVGQSGWAHPGRTGRGSDRGFCVVSPPARPAEBEATSLGALSCTRHSHPVSG 300
 Db 241 GAAPERTPTVGQSGWAHPGRTGRGSDRGFCVVSPPARPAEBEATSLGALSCTRHSHPVSG 300
 Qy 301 ROHHAGPSTSRPRPMDTPCPVYAEKHFLYSSGDKQELRPSFLSSLRPSLTGARRL 360
 Db 301 ROHHAGPSTSRPRPMDTPCPVYAEKHFLYSSGDKQELRPSFLSSLRPSLTGARRL 360
 Qy 361 VETIFLGSRPMPGTPRRLLPRLPQRYWQMRPLFLELLGNHAQCYPYGVLLKTHCPLRAVT 420
 Db 361 VETIFLGSRPMPGTPRRLLPRLPQRYWQMRPLFLELLGNHAQCYPYGVLLKTHCPLRAVT 420
 Qy 421 PAAGVCAREXPQGSVAAPSEEDTPRLVOLLRQHSFPWQYGVFVRACLRLVPPGLWGS 480
 Db 421 PAAGVCAREXPQGSVAAPSEEDTPRLVOLLRQHSFPWQYGVFVRACLRLVPPGLWGS 480
 Qy 481 RHNERFLRNTKKFISLGKAKLSLOELTWKMSVRDCAWLRRSPGVGCVAAEHLREEI 540
 Db 481 RHNERFLRNTKKFISLGKAKLSLOELTWKMSVRDCAWLRRSPGVGCVAAEHLREEI 540
 Qy 541 LAKFLHLMWSVYVVELLSRFYVTTTFFQKNRLFYFKRSVMSKLSQIGIRQLKRVQLRE 600
 Db 541 LAKFLHLMWSVYVVELLSRFYVTTTFFQKNRLFYFKRSVMSKLSQIGIRQLKRVQLRE 600
 Qy 601 LSEAEVRQHREARPAALLTSRLRPIKPDGLRPIVNM DYVVGARTFREKRAERLTSRKA 660
 Db 601 LSEAEVRQHREARPAALLTSRLRPIKPDGLRPIVNM DYVVGARTFREKRAERLTSRKA 660
 Qy 661 LFSVLNVERARRPGLLGASVLGLDDIHRWRTFVLVRADPPPELYFVKVDVTGADTI 720
 Db 661 LFSVLNVERARRPGLLGASVLGLDDIHRWRTFVLVRADPPPELYFVKVDVTGADTI 720
 Qy 721 PQDLRTEVIASIIKPQNTYCVRRYAVVOKAAHGHVRKAFKSHVSTLTDLQPMRQFVAHL 780
 Db 721 PQDLRTEVIASIIKPQNTYCVRRYAVVOKAAHGHVRKAFKSHVSTLTDLQPMRQFVAHL 780
 Qy 781 QETSPLRDVAVIEQSSSLNEASSGLFDVFLRFMCHAVIRGSKSVOCGIPQGSILSTL 840
 Db 781 QETSPLRDVAVIEQSSSLNEASSGLFDVFLRFMCHAVIRGSKSVOCGIPQGSILSTL 840
 Qy 841 LCSLCYGDMMENKLPAGIRRRDGLLLRLVDDFLLVTPHLLTHAKTFLRTLVRGVEYGCVVNL 900
 Db 841 LCSLCYGDMMENKLPAGIRRRDGLLLRLVDDFLLVTPHLLTHAKTFLRTLVRGVEYGCVVNL 900
 Qy 901 RKTVMNFPVEDEALGGTAFTQMPAHGLFPWCGLLLDTRTLEVSQSDYSYARTSIRASLTF 960
 Db 901 RKTVMNFPVEDEALGGTAFTQMPAHGLFPWCGLLLDTRTLEVSQSDYSYARTSIRASLTF 960
 Qy 961 NRGFKAGNMRKLFGLVRLKCHSLFLDLQVNSLQTVCTNIYKILLQAYRFHACVQLP 1020
 Db 961 NRGFKAGNMRKLFGLVRLKCHSLFLDLQVNSLQTVCTNIYKILLQAYRFHACVQLP 1020
 Qy 1021 FHQQWKNPTTFLRVISDTASLCYSILKAKNAGMSLGAKGAAGPLPSEAVQWLCHQAFLL 1080
 Db 1021 FHQQWKNPTTFLRVISDTASLCYSILKAKNAGMSLGAKGAAGPLPSEAVQWLCHQAFLL 1080

QY 1081 KLTRHRTVTVPLGLSLRTAQTLQSLKRLPGTTLTALAAANPALPDSDFKTILD 1132
 DB 1081 KLTRHRTVTVPLGLSLRTAQTLQSLKRLPGTTLTALAAANPALPDSDFKTILD 1132

RESULT 29
 AAY28401
 ID AAY28401 standard; protein; 1132 AA.
 AC AAY28401;
 DT 22-SEP-1999 (first entry)
 XX
 XX Human EST2 protein sequence.
 DE
 XX EST2; proliferative capacity; cellular proliferation; decubitus ulcer;
 KW telomerase-activating therapeutic agent; cell life-span extension;
 KW venous disease; venous stasis ulcer; excessive pressure; arterial ulcer;
 KW tissue regeneration enhancer; atherosclerosis; therapy.
 XX
 OS Homo sapiens.
 XX
 PN W09935243-A2.
 XX
 PD 15-JUL-1999.
 XX
 PF 12-JAN-1999; 99WO-US000682.
 XX
 PR 12-JAN-1998; 98US-0071220P.
 PR 13-JAN-1998; 98US-0071455P.
 PR 21-APR-1998; 98US-00063657.
 XX
 PA (COLD-) COLD SPRING HARBOR LAB.
 XX
 PI Hannon GJ, Wang J, Beach DH;
 XX N-PSDB; AAX89424.
 DR WPI; 1999-444196/37.
 DR N-PSDB; AAX89424.
 XX
 PT Increasing proliferative capacity of cells useful for promoting wound
 PT healing.
 XX
 PS Claim 3; Page 65-70; 73pp; English.
 CC
 CC This sequence is the human EST2 protein, and can be used in the method of
 CC the invention. The method is for increasing the proliferative capacity of
 CC cells, and comprises contacting the cell with a telomerase-activating
 CC therapeutic agent (TATA). The method can be used for extending the life-
 CC span of cells, e.g. by increasing the number of mitotic divisions. They
 CC can be used for e.g. the extension of skin or other epithelial cell
 CC cultures or grafts, the expansion of mesenchymal cell cultures or grafts,
 CC and the expansion of chondrocyte or osteocyte cultures or grafts. They
 CC can be applied to e.g. neuronal, haematopoietic, epithelial, pancreatic,
 CC hepatic, chondrocytic and osteocytic stem and progenitor cells in in
 CC vivo, in vitro or ex vivo protocols. The methods can be used for
 CC promoting the healing of wounds resulting from e.g. surgery, burns,
 CC inflammation or irritation or ulcers resulting from e.g. venous disease
 CC (venous stasis ulcers), excessive pressure (decubitus ulcers) or arterial
 CC ulcers. They can also be used to enhance tissue regeneration processes,
 CC e.g. of the skin, hair and/or fingernails. They can also be used for
 CC treating age-related conditions, e.g. atrophy of the skin through loss of
 CC extracellular matrix homeostasis in dermal fibroblasts, age-related
 CC macular degeneration caused by accumulation of lipofuscin and
 CC downregulation of a neuronal survival factor in retinal pigmented
 CC epithelial (RPE) cells, and atherosclerosis caused by loss of
 CC proliferative capacity and overexpression of hypertensive and thrombotic
 CC factors in endothelial cells. Expanded populations of normal or
 CC genetically engineered rejuvenated cells could be used for autologous or
 CC allogeneic cell and gene therapy. They can also be used for prolonging
 CC the lifespan of a culture of normal cells or tissue being used to secrete
 CC therapeutic or other commercially significant proteins and products

SQ Sequence 1132 AA;		Query Match	99.9%; Score 5954; DB 2; Length 1132;
		Best Local Similarity	99.9%; Pred. No. 0;
		Matches 1131; Conservative	0; Mismatches 1; Indels 0; Gaps 0;
QY	1	MPRAPRCRAVRSLLRSHYREVLP	PLATFVRRLLPGQWRLLVQRGDPAAFPALVAQCILVCPW 60
DB	1	MPRAPRCRAVRSLLRSHYREVLP	PLATFVRRLLPGQWRLLVQRGDPAAFPALVAQCILVCPW 60
QY	61	DARPPAPSPROVSCUKELVARVL	ORLCERGAKNVLAFFGALLDARGGPEAFTTSVR 120
DB	61	DARPPAPSPROVSCUKELVARVL	ORLCERGAKNVLAFFGALLDARGGPEAFTTSVR 120
QY	121	SYLPNTVTDALRGSGAWGLLRR	VGGDDVLVHLLARCALFVLVAPSCAQVCGPPLYQLGA 180
DB	121	SYLPNTVTDALRGSGAWGLLRR	VGGDDVLVHLLARCALFVLVAPSCAQVCGPPLYQLGA 180
QY	181	ATQARPPPHASGPRRLRGCE	RAMNHSVREAGVPLGPAPGARRRGGSASRSLPLPKRR 240
DB	181	ATQARPPPHASGPRRLRGCE	RAMNHSVREAGVPLGPAPGARRRGGSASRSLPLPKRR 240
QY	241	GAAPERTPVQSGSWAHPGTR	CGSDRGFCVSPARPAEATSLEGALSGRHSPVSG 300
DB	241	GAAPERTPVQSGSWAHPGTR	CGSDRGFCVSPARPAEATSLEGALSGRHSPVSG 300
QY	301	ROHAGPPSTRPPRWDTPCP	PVYAETKHFLYSSGDKQLRPSFLSSLPSTGARRL 360
DB	301	ROHAGPPSTRPPRWDTPCP	PVYAETKHFLYSSGDKQLRPSFLSSLPSTGARRL 360
QY	361	VETIFLGSRRPMPCTPRRL	PRLPQRYQMRLPFLLELGNHAOCPPYGVLLKTHCPLRAAVT 420
DB	361	VETIFLGSRRPMPCTPRRL	PRLPQRYQMRLPFLLELGNHAOCPPYGVLLKTHCPLRAAVT 420
QY	421	PAAGVCAREKPGQSVAAPE	EEDTDPRLVQLLRHSSPWQYVGFVACLRRLVPPGLWGS 480
DB	421	PAAGVCAREKPGQSVAAPE	EEDTDPRLVQLLRHSSPWQYVGFVACLRRLVPPGLWGS 480
QY	481	RHNERRFLRNTKFI	SIGKHAKLSLOELTWKMSVRDCAWLRSPGVCVPAEHLRBEI 540
DB	481	RHNERRFLRNTKFI	SIGKHAKLSLOELTWKMSVRDCAWLRSPGVCVPAEHLRBEI 540
QY	541	LAKFLHLMMSVYVVELLS	RFYVTTETTFQKNRLFFYRKSVMSKLSQSIGIRHKLKVQLRE 600
DB	541	LAKFLHLMMSVYVVELLS	RFYVTTETTFQKNRLFFYRKSVMSKLSQSIGIRHKLKVQLRE 600
QY	601	LSEAEVQHRREARPA	LTSRLRFPKPDGLRPIVNMVYVGARTFRREKRAERLTSRYKA 660
DB	601	LSEAEVQHRREARPA	LTSRLRFPKPDGLRPIVNMVYVGARTFRREKRAERLTSRYKA 660
QY	661	LFSVLNYERARRPCL	LASVLGLDDIHRWRTFVLVRAQDPPPELYFVKVDVTGAYDTI 720
DB	661	LFSVLNYERARRPCL	LASVLGLDDIHRWRTFVLVRAQDPPPELYFVKVDVTGAYDTI 720
QY	721	PQDRLTEVIASII	KPQNTYCVRRYAVVQKAHGHVRKAFKSHVSTLTDLPYMRQFVAHL 780
DB	721	PQDRLTEVIASII	KPQNTYCVRRYAVVQKAHGHVRKAFKSHVSTLTDLPYMRQFVAHL 780
QY	781	QETSPLRDADVIE	QSSSINEASSGLFDVFLRFMCHHAVIRGKSYVQCQIPQSSILSTL 840
DB	781	QETSPLRDADVIE	QSSSINEASSGLFDVFLRFMCHHAVIRGKSYVQCQIPQSSILSTL 840
QY	841	LCSCYCGDMENKLF	AGTRRDLGLLRLLVDDFLVTPHLLTHAKTFTLTVRGVPEYGCVVNL 900
DB	841	LCSCYCGDMENKLF	AGTRRDLGLLRLLVDDFLVTPHLLTHAKTFTLTVRGVPEYGCVVNL 900
QY	901	RKTVVNPVEDEAL	GGTAFTVQMPAHGLFPWCGLLDTRTLEVSQSDYSYARTSIRASLTF 960
DB	901	RKTVVNPVEDEAL	GGTAFTVQMPAHGLFPWCGLLDTRTLEVSQSDYSYARTSIRASLTF 960
QY	961	NRGFKAGNNRRKL	FGVLRKCHSLFLDLQVNSLQTVCTNIYKILLQAYRHFACVLQLP 1020
DB	961	NRGFKAGNNRRKL	FGVLRKCHSLFLDLQVNSLQTVCTNIYKILLQAYRHFACVLQLP 1020

QY 1021 FHQWKNPTFFLRVISTASLCYSILKAKNAGMSLGAKGAGPLPSEAVOWLCHQAPLL 1080
 Db FHQWKNPTFFLRVISTASLCYSILKAKNAGMSLGAKGAGPLPSEAVOWLCHQAPLL 1080
 QY 1081 KLTRHRVTYVPLGLSLRTAQQLSKPLPGTTLTALAAANPALPSDFKTILD 1132
 Db KLTRHRVTYVPLGLSLRTAQQLSKPLPGTTLTALAAANPALPSDFKTILD 1132

RESULT 30

AA96566

ID AA96566 standard; protein; 1132 AA.

XX AA96566;

AC 12-SEP-2000 (first entry)

DT hEST2, a human telomerase catalytic subunit homologue.

DE hEST2; telomerase; catalytic subunit; reverse transcriptase; life-span;
 XX retinoblastoma; p53; tumour suppressor; inhibitor; arteriosclerosis;
 KW proliferation; immortal; tumour therapy; macular degeneration;
 KW activator. INK4.

XX Homo sapiens.

XX WO200031238-A2.

XX 02-JUN-2000.

XX 24-NOV-1999; 99WO-US027907.

XX 25-NOV-1998; 98US-0109891P.

PR 17-FEB-1999; 98US-0120549P.

XX (GENE-) GENETICA INC.

XX Hannon GJ, Beach DH;

XX WPI; 2000-400055/34.

DR N-PSDB; AAA29388.

XX New method for increasing the proliferative capacity of cell lines
 PT comprises administering agents reversibly activating telomerase activity
 PT and reversibly inactivating Rb/INK4 and/or p53 pathways useful in
 PT treating age related diseases.

XX Claim 14; Page 116-119; 123pp; English.

XX This protein, designated hEST2, is a human telomerase catalytic subunit
 CC homologue of yeast Est2p and Euploetes p123. hEST2 is a member of the
 CC reverse transcriptase family of enzymes. The invention concerns methods
 CC and reagents for extending the life-span, e.g. the number of mitotic
 CC divisions, of a cell. The method relies on activation of a telomerase
 CC activity and inhibition of one or both of a retinoblastoma (Rb)/INK4
 CC pathway or a p53 pathway. Phosphorylation of Rb by cyclin-dependent
 CC kinases, cdk4 and cdk6, releases the cells into the division cycle.
 CC Binding of INK4 family members, e.g. the tumour suppressor p16INK4a,
 CC inhibits kinase activity and results in growth arrest. Rb inactivators
 CC can selectively and reversibly inactivate an Rb/INK4 pathway, especially
 CC an Rb/p16INK4a pathway. The oncoprotein MDM2 is a cellular inhibitor of
 CC Rb/E2F function and the p53 tumour suppressor and can also be used in the
 CC methods. Other molecules which can be used include cdk4 or cdk6 mutants.
 CC In particular, a cdk4 mutant is one which differs from at one or more of
 CC residues K22, R24, H95 and/or D97. Additional constructs include a
 CC papilloma virus E7 protein, or other viral oncoprotein which bypasses Rb
 CC and/or p53. Antisense constructs of the Rb and p16INK4a genes may also be
 CC used. The methods are useful for increasing the proliferative capacity of
 CC cells. The cells are subsequently of use in pharmaceutical and cosmetic
 CC preparations used to treat conditions related to (premature) ageing, e.g.
 CC macular degeneration and arteriosclerosis. The cells can also be used to
 CC replace tumour cell lines in vitro and for studies on biochemical and

CC physiological aspects of growth and differentiation. Long lived
 CC (immortal) cells could also be of use in the production of normal or
 CC genetically engineered biotechnology products

SQ Sequence 1132 AA;

Query Match 99.9%; Score 5954; DB 3; Length 1132;

Best Local Similarity 99.9%; Pred. No. 0;

Matches 1131; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MPRAPRCRAVRSLLRSHYREVLPLATFVRRLPGOGWRLVORGDDPAAFALVAQCILVCVPW 60

Db 1 MPRAPRCRAVRSLLRSHYREVLPLATFVRRLPGOGWRLVORGDDPAAFALVAQCILVCVPW 60

QY 61 DARPPPAAPSFROVSCLELVARVQLRCERGANVLAFGFALLDARGGPPPEAFTTSVR 120

Db 61 DARPPPAAPSFROVSCLELVARVQLRCERGANVLAFGFALLDARGGPPPEAFTTSVR 120

QY 121 SYLPNTVTDLRGSGAWGLLLRRVGGDDVLVHLLARCALFVLVAPSCAYQVCGPPLYOLGA 180

Db 121 SYLPNTVTDLRGSGAWGLLLRRVGGDDVLVHLLARCALFVLVAPSCAYQVCGPPLYOLGA 180

QY 181 ATQARPPPHASGPRRLGCCRANWHSVREAGVPLGLPAGARRRGSGASRLPLPKPRR 240

Db 181 ATQARPPPHASGPRRLGCCRANWHSVREAGVPLGLPAGARRRGSGASRLPLPKPRR 240

QY 241 GAAPEPERTVGGSGWAHPGRTGRGSDRGFCVVSPPARPAEEATSLGALSSTRHSHPVG 300

Db 241 GAAPEPERTVGGSGWAHPGRTGRGSDRGFCVVSPPARPAEEATSLGALSSTRHSHPVG 300

QY 301 ROHHAGPSTSRPPRWDTPCPVYATKIFLVSSGDKQOLRPSFLSSLRPSLTGARRL 360

Db 301 ROHHAGPSTSRPPRWDTPCPVYATKIFLVSSGDKQOLRPSFLSSLRPSLTGARRL 360

QY 361 VETIFGSRPMPGTPRRLPRLPQRYWQMPPLFLELGNHAQCPYGVLLKTHCPLRAVT 420

Db 361 VETIFGSRPMPGTPRRLPRLPQRYWQMPPLFLELGNHAQCPYGVLLKTHCPLRAVT 420

QY 421 PAAGVCAREKPGQSVAAPEEEDTPRLVQLLRQHSPPQVYGFVRACLRLVPPGLWGS 480

Db 421 PAAGVCAREKPGQSVAAPEEEDTPRLVQLLRQHSPPQVYGFVRACLRLVPPGLWGS 480

QY 481 RHNERFLRNTKFIISLGKIAKLSQLBLTWKMSVRDCAWLRRSPGVCVCPAAEHLRBEI 540

Db 481 RHNERFLRNTKFIISLGKIAKLSQLBLTWKMSVRDCAWLRRSPGVCVCPAAEHLRBEI 540

QY 541 LAKFLHLMWSVYVVELLSRFPYVTTTFQKNRLFYFKSVMSKQSIGIRQHLKRVQURE 600

Db 541 LAKFLHLMWSVYVVELLSRFPYVTTTFQKNRLFYFKSVMSKQSIGIRQHLKRVQURE 600

QY 601 LSAEVRQHREARPALTSRLRFPKPDGLRPIVNMDDYVVGARTFRREKRAERLTSRKA 660

Db 601 LSAEVRQHREARPALTSRLRFPKPDGLRPIVNMDDYVVGARTFRREKRAERLTSRKA 660

QY 661 LFSVLNVERARRPCLLGASVLGDDIHRNWRFLVLRADQDPPPELFPVKVDVTGADTI 720

Db 661 LFSVLNVERARRPCLLGASVLGDDIHRNWRFLVLRADQDPPPELFPVKVDVTGADTI 720

QY 721 PQRLTEVIASIIKPQNTYCVRRYAVVQKAHGHVRKAFKSHVSTLTDLOPYMQFVAHL 780

Db 721 PQRLTEVIASIIKPQNTYCVRRYAVVQKAHGHVRKAFKSHVSTLTDLOPYMQFVAHL 780

QY 781 QETSPLDADVVIQSSSLNEASSGLFDVFLRFMCHHAVIRGKSVYQCGIPQGSILSTL 840

Db 781 QETSPLDADVVIQSSSLNEASSGLFDVFLRFMCHHAVIRGKSVYQCGIPQGSILSTL 840

QY 841 LCSLCYGDMEKULFAGIRRDGLLLRLVDDFLVTPHLLTHAKTFLRTVVRGPEYGCVVNL 900

Db 841 LCSLCYGDMEKULFAGIRRDGLLLRLVDDFLVTPHLLTHAKTFLRTVVRGPEYGCVVNL 900

QY 901 RKTWNFPVDEALGGTAFVQMPAHGLFPWCGLLDTRTLEVDSDYSYARTSIRASLTF 960

Db 901 RKTWNFPVDEALGGTAFVQMPAHGLFPWCGLLDTRTLEVDSDYSYARTSIRASLTF 960

```

QY 961 NRGFAGNRNRRLFGVLRKCHSLFLDLQVNSLQTVCTNIYKILLQAYRFHACVLQLP 1020
DB 961 NRGFAGNRNRRLFGVLRKCHSLFLDLQVNSLQTVCTNIYKILLQAYRFHACVLQLP 1020
QY 1021 FHQQVWKNPTFFLRVLTSDTASLCYSTLKAKNAGMSLGAKGAGPLPSEAVQWLCHOAELL 1080
DB 1021 FHQQVWKNPTFFLRVLTSDTASLCYSTLKAKNAGMSLGAKGAGPLPSEAVQWLCHOAELL 1080
QY 1081 KLTHRVTVVPLLSRLTAQTOLSRKLPCTTLTALAAANPALPSDFKTILD 1132
DB 1081 KLTHRVTVVPLLSRLTAQTOLSRKLPCTTLTALAAANPALPSDFKTILD 1132

RESULT 31
ADC47061
ID ADC47061 standard; protein; 1132 AA.
XX
AC ADC47061;
XX
DT 18-DEC-2003 (first entry)
XX
DE Human TERT amino acid sequence #SEQ ID 2.
XX
KW Human; TERT; telomerase; antibody; reverse transcriptase; tumour;
KW autoimmune disease; liver cancer.
XX
OS Homo sapiens.
XX
PN WO2003054545-A1.
XX
PD 03-JUL-2003.
XX
PF 19-DEC-2002; 2002WO-JP013310.
XX
PR 21-DEC-2001; 2001JP-00390050.
XX
PA (MITS-) MITSUBISHI KAGAKU MEDICAL INC.
PA (MURA/) MURAKAMI S.
PA (KANE/) KANEKO S.
XX
PI Murakami S, Kaneko S, Masutomi K;
XX
DR WPI; 2003-569289/53.
DR N-PSDB; ADC47060.
XX
PT Detecting anti-telomerase antibody for detecting tumors and autoimmune
PT disease.
XX
PS Example Examples; Page 36-41; 45pp; Japanese.
XX
CC The invention relates to a method for detecting an anti-telomerase
CC antibody. The method of the invention comprises reacting telomerase
CC producing protein and a fragment or complex of template RNA with anti-
CC telomerase antibody in a sample, and analysing the product. The
CC telomerase producing protein is preferably telomerase reverse
CC transcriptase, and the analysis method is preferably western blot. The
CC method can be used to detect for tumours and autoimmune disease. The
CC method can also be used for detecting liver cancer. The current sequence
CC represents the human TERT amino acid sequence.
XX
SQ Sequence 1132 AA;

Query Match 99.9%; Score 5954; DB 7; Length 1132;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1131; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MPRAPRCRAVRSLLSHREVLPPLATFVRRLGPGQWRVLVQRGDPAAFRALVAQCLVCPW 60
DB 1 MPRAPRCRAVRSLLSHREVLPPLATFVRRLGPGQWRVLVQRGDPAAFRALVAQCLVCPW 60
QY 61 DARPPPAAPSPRQVSLKELVARVLQRLCERGAKNVLAFGFALLDGAAGGPPPEAFTTSVR 120

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RESULT 32
ADE40482

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DB 61 DARPPPAAPSPRQVSLKELVARVLQRLCERGAKNVLAFGFALLDGAAGGPPPEAFTTSVR 120
QY 121 SYLPTNTVDALRGSGAWGLLRRVGDVLLHLLARCALFVLVAPSCAYQVCPPPLYQLGA 180
DB 121 SYLPTNTVDALRGSGAWGLLRRVGDVLLHLLARCALFVLVAPSCAYQVCPPPLYQLGA 180
QY 181 ATQARPPPHASGPRRLRCERAWNHSVREAGVPLGLPAPGARRRGSGASRSRLPKRPRR 240
DB 181 ATQARPPPHASGPRRLRCERAWNHSVREAGVPLGLPAPGARRRGSGASRSRLPKRPRR 240
QY 241 GAAPPERTPVQCGSWAHPGTRGSPDRGFCVSPARPAEATSLEGALSGRHSHPSVG 300
DB 241 GAAPPERTPVQCGSWAHPGTRGSPDRGFCVSPARPAEATSLEGALSGRHSHPSVG 300
QY 301 ROHAGAPSTSRPPRMDTPCPVYAETKHFYSSGDKQLRPSFLLSRLPSLTGARRL 360
DB 301 ROHAGAPSTSRPPRMDTPCPVYAETKHFYSSGDKQLRPSFLLSRLPSLTGARRL 360
QY 361 VETIFLGSRPWMPGTTPRLPRLPQRYWQMRPLFLELLGNHAQCPYGVLLKTHCPLRAAVT 420
DB 361 VETIFLGSRPWMPGTTPRLPRLPQRYWQMRPLFLELLGNHAQCPYGVLLKTHCPLRAAVT 420
QY 421 PAAGVCAREKPGQSVAAPEEEDTDRRLVOLLROHSSPMQVYGFVACLRRLVPLGWS 480
DB 421 PAAGVCAREKPGQSVAAPEEEDTDRRLVOLLROHSSPMQVYGFVACLRRLVPLGWS 480
QY 481 RHNERFLRNTKFTISLGKHAKLSQLTWMKVRDCAWLRRSPGVGCVPAAEHRLREI 540
DB 481 RHNERFLRNTKFTISLGKHAKLSQLTWMKVRDCAWLRRSPGVGCVPAAEHRLREI 540
QY 541 LAKFLHLMWSVYVVELLSFFYVTTTFOKNRLFYRKSVMSKLSQIGIRQHLKRVQURE 600
DB 541 LAKFLHLMWSVYVVELLSFFYVTTTFOKNRLFYRKSVMSKLSQIGIRQHLKRVQURE 600
QY 601 LSEAEVRQREARPAALLTSRLRFTPKDGLRPIVNMVYVVGARTFRREKRAERLTSRKA 660
DB 601 LSEAEVRQREARPAALLTSRLRFTPKDGLRPIVNMVYVVGARTFRREKRAERLTSRKA 660
QY 661 LFSVLNTERARRPGLLGASVLGLDDIHRAWTFVLVRVRAQDPPPELYFVKVDVTGAYDTI 720
DB 661 LFSVLNTERARRPGLLGASVLGLDDIHRAWTFVLVRVRAQDPPPELYFVKVDVTGAYDTI 720
QY 721 PDRLTEVIASIIKPQNTYCVRRYAVVQAAHGHVKAFKSHVSTLTDLQPTMRQFVAHL 780
DB 721 PDRLTEVIASIIKPQNTYCVRRYAVVQAAHGHVKAFKSHVSTLTDLQPTMRQFVAHL 780
QY 781 QETSPLRDAVIEQSSSLNEASSGLFDVFLRFMCHHAVIRKSKSVQCGIPQGSILSTL 840
DB 781 QETSPLRDAVIEQSSSLNEASSGLFDVFLRFMCHHAVIRKSKSVQCGIPQGSILSTL 840
QY 841 LCSLCYGMENKLFAGIRRDGLLLRLVDDFLLVTPHLTHAKTFLTLVRGVEYCVNVL 900
DB 841 LCSLCYGMENKLFAGIRRDGLLLRLVDDFLLVTPHLTHAKTFLTLVRGVEYCVNVL 900
QY 901 RKTVNVFEDEALGGTAFVQMPAHGLFPWPCGLLDDTTLTLEVSQSYSSYARTSIRASLTF 960
DB 901 RKTVNVFEDEALGGTAFVQMPAHGLFPWPCGLLDDTTLTLEVSQSYSSYARTSIRASLTF 960
QY 961 NRGFAGNRNRRLFGVLRKCHSLFLDLQVNSLQTVCTNIYKILLQAYRFHACVLQLP 1020
DB 961 NRGFAGNRNRRLFGVLRKCHSLFLDLQVNSLQTVCTNIYKILLQAYRFHACVLQLP 1020
QY 1021 FHQQVWKNPTFFLRVLTSDTASLCYSTLKAKNAGMSLGAKGAGPLPSEAVQWLCHOAELL 1080
DB 1021 FHQQVWKNPTFFLRVLTSDTASLCYSTLKAKNAGMSLGAKGAGPLPSEAVQWLCHOAELL 1080
QY 1081 KLTHRVTVVPLLSRLTAQTOLSRKLPCTTLTALAAANPALPSDFKTILD 1132
DB 1081 KLTHRVTVVPLLSRLTAQTOLSRKLPCTTLTALAAANPALPSDFKTILD 1132

```

ID ADE40482 standard; protein; 1132 AA.
XX
AC ADE40482;
XX
DT 29-JAN-2004 (first entry)
XX
DE Human telomerase reverse transcriptase (hTERT).
XX
KW Immortal porcine cell; telomerase reverse transcriptase; epithelial cell;
KW uterine endometrial glandular tissue; virus quantification;
KW virus production; porcine reproductive and respiratory syndrome virus;
KW PRRSV; toxicity evaluation; human; hTERT; enzyme.
XX
OS Homo sapiens.
XX
PN WO2003077853-A2.
XX
PD 25-SEP-2003.
XX
PF 11-MAR-2003; 2003WO-US007526.
XX
PR 11-MAR-2002; 2002US-0363129P.
XX
PA (MINU) UNIV MINNESOTA.
XX
PI Farris JA, Foster DN, O'grady SM;
XX
DR WPI; 2003-779075/73.
DR N-PSDB; ADE40481.
XX
PT New immortal porcine cell comprising a polynucleotide encoding an
PT exogenous telomerase reverse transcriptase polypeptide, useful for
PT measuring the amount of virus in a sample or for evaluating toxicity of a
PT compound.
XX
PS Claim 4; SEQ ID NO 2; 42pp; English.
XX
CC The invention relates to immortal porcine cells comprising a
CC polynucleotide encoding an exogenous telomerase reverse transcriptase
CC (TERT). The invention also encompasses the method of making immortal
CC porcine cells, and the use of the immortal porcine cells for measuring
CC the amount of virus in a sample, producing a virus, and evaluating the
CC toxicity of a compound. The cells of the invention may be diploid or
CC aneuploid, and may be an epithelial cell obtained from uterine
CC endometrial glandular tissue. The exogenous telomerase reverse
CC transcriptase expressed by the cells of the invention is preferably human
CC telomerase reverse transcriptase (ADE40482). The immortal porcine cells
CC are useful for measuring an amount of a virus in a sample, producing a
CC virus (especially porcine reproductive and respiratory syndrome virus
CC (PRRSV)), or for evaluating toxicity of a compound. The present sequence
CC represents human telomerase reverse transcriptase (hTERT), which is
CC claimed for use in the immortal cells of the invention.
XX
SQ Sequence 1132 AA;

Query Match 99.9%; Score 5954; DB 7; Length 1132;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1131; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MPRAPCRAVRLSLRSHYREVLPATFVRRLLGPGQWRVLVQRGDPAAFRALVAQCCLVCVPW 60
DB 1 MPRAPCRAVRLSLRSHYREVLPATFVRRLLGPGQWRVLVQRGDPAAFRALVAQCCLVCVPW 60

QY 61 DARPPPAAPSPQVSCLELVARVLQRLCERGAKNVLAFGFALLDGGAGGPEAFTTSVR 120
DB 61 DARPPPAAPSPQVSCLELVARVLQRLCERGAKNVLAFGFALLDGGAGGPEAFTTSVR 120

QY 121 SYLPTNTVDALRGSGAWGALLRRVGDVVLVHLLARCALFVLVAPSCAYQVCGPELYQLGA 180
DB 121 SYLPTNTVDALRGSGAWGALLRRVGDVVLVHLLARCALFVLVAPSCAYQVCGPELYQLGA 180

QY 181 ATOARPPPHASGPRRLRCERAWNHSVREAGVPLGLPAPGARRRGGSASRSLLPLPKPRR 240
XX

DB 181 ATOARPPPHASGPRRLRCERAWNHSVREAGVPLGLPAPGARRRGGSASRSLLPLPKPRR 240
QY 241 GAAPEPERTVPGQSGWAHPGRTGRGSDRGFCVVPSPARPAEATSLEGALSGTRHSHPSVG 300
DB 241 GAAPEPERTVPGQSGWAHPGRTGRGSDRGFCVVPSPARPAEATSLEGALSGTRHSHPSVG 300
QY 301 ROHHAGPSTSRPRRWDTPCPVYAEKHFVLYSSGDKQLRPSFLSSLRPSLTGARRL 360
DB 301 ROHHAGPSTSRPRRWDTPCPVYAEKHFVLYSSGDKQLRPSFLSSLRPSLTGARRL 360
QY 361 VETIFLGSRRPMPGTPRRLPRLPQRYWQMPLEFLLELGNHAQCPYGVLLKTHCPLRAAVT 420
DB 361 VETIFLGSRRPMPGTPRRLPRLPQRYWQMPLEFLLELGNHAQCPYGVLLKTHCPLRAAVT 420
QY 421 PAAGVCAREKPOGSVAAPPEEDTPRRLVQLLRQHSSPWQYVGFVRACTLRRLVPPGLWGS 480
DB 421 PAAGVCAREKPOGSVAAPPEEDTPRRLVQLLRQHSSPWQYVGFVRACTLRRLVPPGLWGS 480
QY 481 RHNERFLRNTKKFISLGKHAQLSLOELTWKMSVRDCAMLRSSPGVGCVPAAEHRLREEI 540
DB 481 RHNERFLRNTKKFISLGKHAQLSLOELTWKMSVRDCAMLRSSPGVGCVPAAEHRLREEI 540
QY 541 LAKFLHLMMSVYVVELLRSFFYVTETTFQKNRLFYFRKSVMSKLSQSIGIQLKRVQLRE 600
DB 541 LAKFLHLMMSVYVVELLRSFFYVTETTFQKNRLFYFRKSVMSKLSQSIGIQLKRVQLRE 600
QY 601 LSEAEVQHQREARPAALLTSRLRFPKPDGLRPIVNMVYVVGARTFRREKRAERLTSRVKA 660
DB 601 LSEAEVQHQREARPAALLTSRLRFPKPDGLRPIVNMVYVVGARTFRREKRAERLTSRVKA 660
QY 661 LFSVLNVRARRPCLIGASVLGLDDIHRARWTFVLVRAQDPPPELYFVKVDVTGAYDTI 720
DB 661 LFSVLNVRARRPCLIGASVLGLDDIHRARWTFVLVRAQDPPPELYFVKVDVTGAYDTI 720
QY 721 PQDLTEVIAIIPONTYCVRRYAVVQKAAHGHRKAFKSHVSTLTDLOPYMRQFVAHL 780
DB 721 PQDLTEVIAIIPONTYCVRRYAVVQKAAHGHRKAFKSHVSTLTDLOPYMRQFVAHL 780
QY 781 QETSPLRDADVIRBQSSSLNEASSGLFDVFLRFMCHHAVRIRGKSYVQCQGIPOGSIILSTL 840
DB 781 QETSPLRDADVIRBQSSSLNEASSGLFDVFLRFMCHHAVRIRGKSYVQCQGIPOGSIILSTL 840
QY 841 LCSLCYGDMEKMLFAGIRRDGLLLRLVDDFLLVTPHLTHAKTFLRTLVRGVPYGCVVNL 900
DB 841 LCSLCYGDMEKMLFAGIRRDGLLLRLVDDFLLVTPHLTHAKTFLRTLVRGVPYGCVVNL 900
QY 901 RKTVMNFPVEDEALGGTAFVQMPAHGLFPWCGLLLDTRTLEVSQSDYSYARTSIRASLTF 960
DB 901 RKTVMNFPVEDEALGGTAFVQMPAHGLFPWCGLLLDTRTLEVSQSDYSYARTSIRASLTF 960
QY 961 NRGFKAQRNNRRKLFVGLRLKCHSLFLDLQVNSLQTVCTWYIKILLQAVRFHACVILQLP 1020
DB 961 NRGFKAQRNNRRKLFVGLRLKCHSLFLDLQVNSLQTVCTWYIKILLQAVRFHACVILQLP 1020
QY 1021 FHOQVKNPTFFLRVSDTASLCYSILKAKNAGSLGAKGAAGPLPSEAWMLCHQAPLL 1080
DB 1021 FHOQVKNPTFFLRVSDTASLCYSILKAKNAGSLGAKGAAGPLPSEAWMLCHQAPLL 1080
QY 1081 KLTRHRYVYVPLGLSLRTAQTLQRKLPGLTTLTALEAAANPALPSPDFKTILD 1132
DB 1081 KLTRHRYVYVPLGLSLRTAQTLQRKLPGLTTLTALEAAANPALPSPDFKTILD 1132

RESULT 33
AAW56113
ID AAW56113 standard; protein; 1132 AA.
XX
AC AAW56113;
XX
DT 13-AUG-1998 (first entry)
XX
DE Human telomerase reverse transcriptase protein refined sequence.
XX

KW Human; telomerase reverse transcriptase; hTERT; TRT; diagnosis; prognosis;
KW cell proliferation; cancer; ageing; ribonucleoprotein.
XX
OS Homo sapiens.
XX GB2317891-A.
XX
XX
XX 08-APR-1998.
XX
XX 01-OCT-1997; 97GB-00020890.
XX
XX 01-OCT-1996; 96US-00724643.
XX 18-APR-1997; 97US-00844419.
XX 25-APR-1997; 97US-00846017.
XX 06-MAY-1997; 97US-00851843.
XX 09-MAY-1997; 97US-00854050.
XX 14-AUG-1997; 97US-00911312.
XX 14-AUG-1997; 97US-00912951.
XX 14-AUG-1997; 97US-00915503.
XX
XX (GERO-) GERON CORP.
XX (UYTE-) UNIV TECHNOLOGY CORP.
XX
XX Cech TR, Lingner J, Nakamura T, Chapman KB, Morin GB, Harley CB;
XX Andrews WH;
XX
XX WPI; 1998-171633/16.
XX N-PSDB; AA22428.
XX
XX Pure and recombinant human Telomerase Reverse Transcriptase and its
XX variants - are useful in the diagnosis, prognosis and treatment of cell
XX proliferation conditions especially cancer and ageing.
XX
XX Example 1; Fig 74; 387pp; English.
XX
XX The present sequence represents human telomerase reverse transcriptase
XX (hTERT), which is a ribonucleoprotein. The present invention also
XX describes the following methods: (A) determining whether a test compound
XX is a modulator of hTERT, by detecting the change in hTERT recombinant
XX protein or polynucleotide, on administration of the compound; (B)
XX preparation of recombinant telomerase by contacting a protein preparation
XX of hTERT with a telomerase RNA component; (C) detection of the hTERT RNA or
XX protein in a sample by binding a relevant probe to the sample and
XX detecting the complex formed or in the case of RNA detection, amplifying
XX the product and correlating the presence of complex or amplification
XX product with presence of hTERT in the sample; and (D) increasing the
XX proliferation of a vertebrate cell by increasing hTERT expression; and (E)
XX the use of an agent that causes an increase in cell vertebrate cell
XX proliferation to create a medicament that inhibits ageing. A protein
XX preparation of hTERT and the polynucleotide encoding hTERT can be used in
XX the manufacture of medicaments for inhibiting the effect of ageing or
XX cancer. Inhibitors of telomerase activity can be used to treat conditions
XX that are associated with high telomerase activity. A protein preparation
XX of hTERT can also be used in the new methods
XX
XX Sequence 1132 AA;
Query Match 99.8%; Score 5952; DB 2; Length 1132;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1130; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 MPRAPRCVRSLLSHRYEVLPATFVRRLPQCGWRLVQRGDPAAFRALVAQCLVCPW 60
DB 1 MPRAPRCVRSLLSHRYEVLPATFVRRLPQCGWRLVQRGDPAAFRALVAQCLVCPW 60
QY 61 DARPPPAAPSFQVSCLELVARVLQRLCERCAKNVLAFGFALLDGAAGGPEAFTTSVR 120
DB 61 DARPPPAAPSFQVSCLELVARVLQRLCERCAKNVLAFGFALLDGAAGGPEAFTTSVR 120
QY 121 SYLPTNTVTDALGSGAWGILLRRVGDVLLVHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180
DB 121 SYLPTNTVTDALGSGAWGILLRRVGDVLLVHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180

QY 181 ATQARPPPHASGPRRRRLGCERAWNHSVREAGVPLGAPAGARRRGGSSASRSLPLPKRPRR 240
DB 181 ATQARPPPHASGPRRRRLGCERAWNHSVREAGVPLGAPAGARRRGGSSASRSLPLPKRPRR 240
QY 241 GAAPERTPVGQGSWAHPGTRGSPDRGFCVVSAPARPAEATSLLEGALSCTRHHSPSVG 300
DB 241 GAAPERTPVGQGSWAHPGTRGSPDRGFCVVSAPARPAEATSLLEGALSCTRHHSPSVG 300
QY 301 RQHAGAPPSTSRPPRPMDTPCPVVAETKHFYSSGDKQLRPSFLLSRLPSLTGARRL 360
DB 301 RQHAGAPPSTSRPPRPMDTPCPVVAETKHFYSSGDKQLRPSFLLSRLPSLTGARRL 360
QY 361 VETIFLGSRPMPGTPRRRLPRLPQRYQWMLFLELLGNHQAQCPYGVLLKTHCPRAAAT 420
DB 361 VETIFLGSRPMPGTPRRRLPRLPQRYQWMLFLELLGNHQAQCPYGVLLKTHCPRAAAT 420
QY 421 PAAGVCAREKPOGSAVAPEEEDTPRRLLVOLLROHSSPMQVYGFVRACLRLVPPGLMGS 480
DB 421 PAAGVCAREKPOGSAVAPEEEDTPRRLLVOLLROHSSPMQVYGFVRACLRLVPPGLMGS 480
QY 481 RHNERRLNTKFTISLGKHAKLSLOELTWKMSVRDCAWLRRSPGVGCVPAAEHRLRBEI 540
DB 481 RHNERRLNTKFTISLGKHAKLSLOELTWKMSVRDCAWLRRSPGVGCVPAAEHRLRBEI 540
QY 541 LAKFLHLMMSVYVVELLRSFFVTETTPQKNRLFYRPSVMSKLSQSIGIRQHLKRVQLRE 600
DB 541 LAKFLHLMMSVYVVELLRSFFVTETTPQKNRLFYRPSVMSKLSQSIGIRQHLKRVQLRE 600
QY 601 LSEAEVRQHREARPAALLTSRLRFIPKPDGLRPIVNMDDYVVGARTFRREKRAERLTSRVA 660
DB 601 LSEAEVRQHREARPAALLTSRLRFIPKPDGLRPIVNMDDYVVGARTFRREKRAERLTSRVA 660
QY 661 LFSVLNTERARRPGLLGASVLGLDDIHRAMTFVLVRQAQPPPELYFVKVDVTGAYDTI 720
DB 661 LFSVLNTERARRPGLLGASVLGLDDIHRAMTFVLVRQAQPPPELYFVKVDVTGAYDTI 720
QY 721 PODRLTEVIASIIKPQNTYCVRRYAVVQAAHGHVRAKFKSHVSTLTDLQPMRQFVAHL 780
DB 721 PODRLTEVIASIIKPQNTYCVRRYAVVQAAHGHVRAKFKSHVSTLTDLQPMRQFVAHL 780
QY 781 QETSPLRDVAVIEOSSLSNEASSGLFDVFLRFMCHHVRIRGKSVVQCGIPQGSILSTL 840
DB 781 QETSPLRDVAVIEOSSLSNEASSGLFDVFLRFMCHHVRIRGKSVVQCGIPQGSILSTL 840
QY 841 LCSLCYGDMEKNLFGIRRDGLLLRLVDDFLLVTPHLTHAKTFLRTLVRGPEYGCNNL 900
DB 841 LCSLCYGDMEKNLFGIRRDGLLLRLVDDFLLVTPHLTHAKTFLRTLVRGPEYGCNNL 900
QY 901 RKTVVNPFVEDEALGGTAFVQMPAHGLFPWCGLLDDTRTLEVSQSDYSYARTSIRASLTF 960
DB 901 RKTVVNPFVEDEALGGTAFVQMPAHGLFPWCGLLDDTRTLEVSQSDYSYARTSIRASLTF 960
QY 961 NRGFKAGNMRRKLFGLVRLKCHSLFDLQVNSLQTVCTNIYKILLLOAYRPHACVQLQP 1020
DB 961 NRGFKAGNMRRKLFGLVRLKCHSLFDLQVNSLQTVCTNIYKILLLOAYRPHACVQLQP 1020
QY 1021 FHOQWKNPTFFLRVISDTASLCYSILKAKNAGSLGAKGAGPLPSSAVOWLCHOAFLL 1080
DB 1021 FHOQWKNPTFFLRVISDTASLCYSILKAKNAGSLGAKGAGPLPSSAVOWLCHOAFLL 1080
QY 1081 KLTRHRTVYVPLLSGLRTAQQLSRKLPGLTTLTALAAANPALPSDFKTILD 1132
DB 1081 KLTRHRTVYVPLLSGLRTAQQLSRKLPGLTTLTALAAANPALPSDFKTILD 1132
RESULT 34
AA00647
ID AA00647 standard; protein; 1166 AA.
XX
XX AC AA00647;
XX
XX DT 26-JUL-1999 (first entry)
XX


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DE Telomerase (ver. 2) protein sequence.
XX
KW Telomerase; human; cancer; diagnosis; melanoma; skin cancer; leukaemia;
KW neuroblastoma; breast carcinoma; colon carcinoma; lymphoma; osteosarcoma;
KW smooth muscle cell hyperplasia; stem cell proliferation; Wilm's tumour;
KW stem cell differentiation; organ regeneration; organ differentiation.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO9901560-A1.
XX
PD 14-JAN-1999.
XX
PF 01-JUL-1998; 98WO-US013835.
XX
PR 01-JUL-1997; 97US-0051410P.
PR 21-JUL-1997; 97US-0053018P.
PR 21-JUL-1997; 97US-0053329P.
PR 04-AUG-1997; 97US-0054642P.
PR 09-SEP-1997; 97US-0056287P.
XX
PA (CAMB-) CAMBIA BIOSYSTEMS LLC.
PI Kilian A, Bowtell D;
XX
XX WPI, 1999-106060/09.
DR N-PSDB; AAX18275.
XX
XX New isolated vertebrate telomerase genes - used to develop products for
PT treating cancers or for organ regeneration, nerve cell or brain cell
PT growth following injury or bone marrow transplantation.
XX
PS Claim 4; Fig 11z-ac; 134pp; English.
XX
XX This sequence is a truncated human telomerase of the invention. Primers
CC that amplify the telomerase coding sequence can be used in a method for
CC diagnosing cancer in a patient. The telomerase can be used for detection,
CC diagnosis and drug screening. Inhibitors of telomerase activity can be
CC used to treat cancers such as melanomas, other skin cancers,
CC neuroblastomas, breast carcinomas, colon carcinomas, leukemias,
CC lymphomas, osteosarcomas or smooth muscle cell hyperplasias or skin
CC growths. Enhancers of telomerase may be used to stimulate stem cell
CC proliferation and differentiation (expansion of haematopoietic stem cells
CC could be administered in the bone marrow transplant context). As well,
CC many tissues have stem cells. Proliferation of these cells may be useful
CC in wound healing, hair growth, treatment of disease such as Wilm's
CC tumour, organ regeneration or differentiation after injury or diseases,
CC nerve cell or brain cell growth following injury
XX
SQ Sequence 1166 AA;
Query Match 99.4%; Score 5927; DB 2; Length 1166;
Best Local Similarity 97.0%; Pred. No. 0;
Matches 1131; Conservative 0; Mismatches 1; Indels 34; Gaps 1;
QY 1 MPRAPRCRAVRSLLRSHRYEVLPLATFVRRLGPGQWRILVQRGDPAAFRALVAQCLVCVPW 60
DB 1 MPRAPRCRAVRSLLRSHRYEVLPLATFVRRLGPGQWRILVQRGDPAAFRALVAQCLVCVPW 60
QY 61 DARPPPAAPSFRV-----SCLKELVARVLQ 86
DB 61 DARPPPAAPSPQVGLPGVRLGLRAAGGNORUAESSAGSGRPPRSCUKELVARVLQ 120
QY 87 RLCERGAKNVLAFGFALLDARGGPPPEAFTTSVRSYLPNTVTDALRGSGAGWLLLRVGD 146
DB 121 RLCERGAKNVLAFGFALLDARGGPPPEAFTTSVRSYLPNTVTDALRGSGAGWLLLRVGD 180
QY 147 DVLVHLLARCALFVLVAPSCAYQVCGPPLYQLGAATQARPPPHASGPPRRRLGCRANWHS 206
DB 181 DVLVHLLARCALFVLVAPSCAYQVCGPPLYQLGAATQARPPPHASGPPRRRLGCRANWHS 240
QY 207 VREAGVPLGLPAPGARRRRGGSASRSLLPKRPRRGAAPERTPVGGQSWAHPGRTGRPS 266

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DB 241 VREAGVPLGLPAPGARRRRGGSASRSLLPKRPRRGAAPERTPVGGQSWAHPGRTGRPS 300
QY 267 DRGFCVVSPARPAAEATSLGALSGRSHSPVGRQHHAGPPSTSRPPRWDTCPPVYA 326
DB 301 DRGFCVVSPARPAAEATSLGALSGRSHSPVGRQHHAGPPSTSRPPRWDTCPPVYA 360
QY 327 ETKEFLYSSGDKEQLRPSFLLSLSRLTGARRLVETIFLGSRRPMPGTPRRLPRLPQRY 386
DB 361 ETKEFLYSSGDKEQLRPSFLLSLSRLTGARRLVETIFLGSRRPMPGTPRRLPRLPQRY 420
QY 387 WQMRPLFLELLGNHAQCPYGVLLKTHCPRAAATPAAGVCAREKPOGQSVAAPEEDTDP 446
DB 421 WQMRPLFLELLGNHAQCPYGVLLKTHCPRAAATPAAGVCAREKPOGQSVAAPEEDTDP 480
QY 447 RLVQLLRQHSHPQVYGFVRACLRLRLLVPPGLWGSRRHNRRLNTRKFKFISLGKIAKLSLQ 506
DB 481 RLVQLLRQHSHPQVYGFVRACLRLRLLVPPGLWGSRRHNRRLNTRKFKFISLGKIAKLSLQ 540
QY 507 ELTWKMSVRDCAMLRSPGVCVPAABHRLREEILAKFLHWMMSVYVVELLSRSPFYVTE 566
DB 541 ELTWKMSVRDCAMLRSPGVCVPAABHRLREEILAKFLHWMMSVYVVELLSRSPFYVTE 600
QY 567 TFOKNRLFYRKSVWSKLSQSIGIRQHLKRVQLRSEAEVROHREARPALITSRLRFPK 626
DB 601 TFOKNRLFYRKSVWSKLSQSIGIRQHLKRVQLRSEAEVROHREARPALITSRLRFPK 660
QY 627 PDGLRPIVNMDDYVVGARTFRREKRAERLTSRKALFSVLNVERARRPGLLGASVLGDDI 686
DB 661 PDGLRPIVNMDDYVVGARTFRREKRAERLTSRKALFSVLNVERARRPGLLGASVLGDDI 720
QY 687 HRAWRTPVLVRAQDPPPELYFVKVDVTGAYDTIPQDRLTEVIASIIKQNTYCVRRYAV 746
DB 721 HRAWRTPVLVRAQDPPPELYFVKVDVTGAYDTIPQDRLTEVIASIIKQNTYCVRRYAV 780
QY 747 VQKAAHGHVRKAFKSHVSTLTDLPQYMRQFVAHLQETSPLRDAVVIQSSSLNEASSGLF 806
DB 781 VQKAAHGHVRKAFKSHVSTLTDLPQYMRQFVAHLQETSPLRDAVVIQSSSLNEASSGLF 840
QY 807 DVFLRFMCHHAVIRGKSVYQCGIPQGSILSTLCSLCYGDMENTKLFAGIRRDGLLRL 866
DB 841 DVFLRFMCHHAVIRGKSVYQCGIPQGSILSTLCSLCYGDMENTKLFAGIRRDGLLRL 900
QY 867 VDFLLVTPHLLTHAKTFLRLVRGVPYCGVNLKTVNFPFVEDEALGGTAFVQMPAHG 926
DB 901 VDDFLLVTPHLLTHAKTFLRLVRGVPYCGVNLKTVNFPFVEDEALGGTAFVQMPAHG 960
QY 927 LFPWCGLLDTRTLEVQSDYSSYARTSIRASLTFNRGFKAGRNRRKLFGLRLKCHSLF 986
DB 961 LFPWCGLLDTRTLEVQSDYSSYARTSIRASLTFNRGFKAGRNRRKLFGLRLKCHSLF 1020
QY 987 LDQVNSLQTVCTNIYKILLQAYRFHACVQLQLPFHQQVWKNPTFFLRVISTASLCYSI 1046
DB 1021 LDQVNSLQTVCTNIYKILLQAYRFHACVQLQLPFHQQVWKNPTFFLRVISTASLCYSI 1080
QY 1047 LKAKNAGMSLGAKGAGPLPSEAVQWILCHOAFLLKLTNRHVTVYVPLGLSLRTATQLSRK 1106
DB 1081 LKAKNAGMSLGAKGAGPLPSEAVQWILCHOAFLLKLTNRHVTVYVPLGLSLRTATQLSRK 1140
QY 1107 LPGTTLTALAAANPALPSDFKTILD 1132
DB 1141 LPGTTLTALAAANPALPSDFKTILD 1166

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RESULT 35

AAW56101

ID AAW56101 standard; protein; 1405 AA.

XX AAW56101;

AC AAW56101;

XX 13-AUG-1998 (first entry)

XX Enhanced green fluorescent protein and hTERT fusion protein.

XX Human; telomerase reverse transcriptase; hTERT; TERT; diagnosis; prognosis;
 KW cell proliferation; cancer; ageing; ribonucleoprotein.
 XX Synthetic.
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Region 1..250
 FT /note= "enhanced green fluorescent protein fragment"
 FT Region 276..1405
 FT /note= "hTERT protein fragment"
 XX
 PN GB2317891-A.
 XX
 PN 08-APR-1998.
 PD
 XX 01-OCT-1997; 97GB-00020890.
 XX
 PR 01-OCT-1996; 96US-00724643.
 PR 18-APR-1997; 97US-00844419.
 PR 25-APR-1997; 97US-00846017.
 PR 06-MAY-1997; 97US-00851843.
 PR 09-MAY-1997; 97US-00854050.
 PR 14-AUG-1997; 97US-00911312.
 PR 14-AUG-1997; 97US-00912951.
 PR 14-AUG-1997; 97US-00915503.
 XX
 PA (GERO-) GERON CORP.
 PA (UYTE-) UNIV TECHNOLOGY CORP.
 XX
 PI Cech TR, Lingner J, Nakamura T, Chapman KB, Morin GB, Harley CB;
 PI Andrews WH;
 XX
 DR WPI; 1998-171633/16.
 XX
 PT Pure and recombinant human Telomerase Reverse Transcriptase and its
 PT variants - are useful in the diagnosis, prognosis and treatment of cell
 PT proliferation conditions especially cancer and ageing.
 XX
 PS Example 15; Page 269-270; 387pp; English.
 XX
 CC The present sequence represents a fusion protein from an example of the
 CC present invention which describes human telomerase reverse transcriptase
 CC (hTERT). The present invention also describes the following methods: (A)
 CC determining whether a test compound is a modulator of hTERT, by detecting
 CC the change in hTERT recombinant protein or polynucleotide, on
 CC administration of the compound; (B) preparation of recombinant telomerase
 CC by contacting a protein preparation of hTERT with a telomerase RNA
 CC component; (C) detection of the hTERT RNA or protein in a sample by
 CC binding a relevant probe to the sample and detecting the complex formed
 CC or in the case of RNA detection, amplifying the product and correlating
 CC the presence of complex or amplification product with presence of hTERT in
 CC the sample; and (D) increasing the proliferation of a vertebrate cell by
 CC increasing hTERT expression; and (E) the use of an agent that causes an
 CC increase in cell vertebrate cell proliferation to create a medicament
 CC that inhibits ageing. A protein preparation of hTERT and the
 CC polynucleotide encoding hTERT can be used in the manufacture of
 CC medicaments for inhibiting the effect of ageing or cancer. Inhibitors of
 CC telomerase activity can be used to treat conditions that are associated
 CC with high telomerase activity. A protein preparation of hTERT can also be
 CC used in the new methods
 XX
 SQ Sequence 1405 AA;
 Query Match 99.3%; Score 5918; DB 2; Length 1405;
 Best Local Similarity 99.6%; Pred. No. 0;
 Matches 1128; Conservative 1; Mismatches 1; Indels 2; Gaps 2;
 QY 1 MPAPRCRAVRSLLSHRYEVLPATFVRRILGPGQWRVLVQRGDDPAAFRALVAQCLVCPW 60
 DB 276 MPAPRCRAVRSLLSHRYEVLPATFVRRILGPGQWRVLVQRGDDPAAFRALVAQCLVCPW 335

QY 61 DARPPAAPSPQVSCSLKELVARVLQRLCERGAKNVLAFGFALLDAGRGPEAFTTSVR 120
 DB 336 DARPPAAPSPQVSCSLKELVARVLQRLCERGAKNVLAFGFALLDAGRGPEAFTTSVR 395
 QY 121 SYLNTVTDALRGSGAWGLLRRVDDVLVHLARCALFVLVAPSCAVQVCGPPYQLGA 180
 DB 396 SYLNTVTDALRGSGAWGLLRRVDDVLVHLARCALFVLVAPSCAVQVCGPPYQLGA 455
 QY 181 ATOARPPPHASGPRRRRLGCERAWNHSVREAGVPLGPAAGARRRGSGASRSLLPKRRR 240
 DB 456 ATOARPPPHASGPRRRRLGCERAWNHSVREAGVPLGPAAGARRRGSGASRSLLPKRRR 515
 QY 241 GAAPERTPVQGSWAHPGTRGSDRGFCVSPARPAEATSLEGALSGRHSHPSVG 300
 DB 516 GAAPERTPVQGSWAHPGTRGSDRGFCVSPARPAEATSLEGALSGRHSHPSVG 575
 QY 301 ROHAGBPSTSRPPRMDTPCPVVAETKFLYSAGDKEQLRPSFLLSLSPSLTGARRL 360
 DB 576 ROHAGBPSTSRPPRMDTPCPVVAETKFLYSAGDKEQLRPSFLLSLSPSLTGARRL 634
 QY 361 VETIFLAGSRPWPMPGTTPRLPRLPQRYWQMRPLFLELLGNHAQCPYGVLLKTHCPLRAAVT 420
 DB 635 VETIFLAGSRPWPMPGTTPRLPRLPQRYWQMRPLFLELLGNHAQCPYGVLLKTHCPLRAAVT 694
 QY 421 PAAGVCAREKPGQSVAAPEEEDTPRRLVQLLRHSSPWQYGVFVRACLRRLVPPGLWGS 480
 DB 695 PAAGVCAREKPGQSVAAPEEEDTPRRLVQLLRHSSPWQYGVFVRACLRRLVPPGLWGS 754
 QY 481 RHNERRLRNNTKFTSLGKHAKLSLOELTWKMSVRDCAWLRSBQVGCVAEHLRREI 540
 DB 755 RHNERRLRNNTKFTSLGKHAKLSLOELTWKMSVRDCAWLRSBQVGCVAEHLRREI 814
 QY 541 LAKFLHLMMSVYVVELLSRFPYVTTETTPQKRLFFYRSKSVMSKLSQSIGRQHLKXVQRE 600
 DB 815 LAKFLHLMMSVYVVELLSRFPYVTTETTPQKRLFFYRSKSVMSKLSQSIGRQHLKXVQRE 874
 QY 601 LSEAEVQHRERARPAALTSRLRFPKPDGLRPIVNMDDYVVGARTFRREKRAERLTSRVKA 660
 DB 875 LSEAEVQHRERARPAALTSRLRFPKPDGLRPIVNMDDYVVGARTFRREKRAERLTSRVKA 934
 QY 661 LFSVLNTERARRPGLGASVGLDDIHRAMTFFVLVRAQDPPPELYFVKVDVTGAYDTI 720
 DB 935 LFSVLNTERARRPGLGASVGLDDIHRAMTFFVLVRAQDPPPELYFVKVDVTGAYDTI 994
 QY 721 PODRLTEVIASIIKPNQTYCVRRYAVVQKAAGHVRKAFKSHVSTLTDLQPMRQFVAHL 780
 DB 995 PODRLTEVIASIIKPNQTYCVRRYAVVQKAAGHVRKAFKSHVSTLTDLQPMRQFVAHL 1054
 QY 781 QETSPLRDAVVIEQSSSLNEASSGLFDVFLRFMCHHAVIRGKSYVQCGIPQGSILSTL 840
 DB 1055 QETSPLRDAVVIEQSSSLNEASSGLFDVFLRFMCHHAVIRGKSYVQCGIPQGSILSTL 1114
 QY 841 LCSLCYGDMEKNLFGIRRDGLLRLVDDFLVLTPLTHAKTFLTLVRGPEYCVNL 900
 DB 1115 LCSLCYGDMEKNLFGIRRDGLLRLVDDFLVLTPLTHAKTFLTLVRGPEYCVNL 1174
 QY 901 RKTVNPVEDEALGGTAFVQMPAHGLFPWCGLLDITLTVQSDYSYVARTSTRASLTF 960
 DB 1175 RKTVNPVEDEALGGTAFVQMPAHGLFPWCGLLDITLTVQSDYSYVARTSTRASLTF 1234
 QY 961 NRGFKAGNMRKLFVGLRLKCHSLFLDLQVNSLQTVCTNIYKILLQAYRFHACVLQUP 1020
 DB 1235 NRGFKAGNMRKLFVGLRLKCHSLFLDLQVNSLQTVCTNIYKILLQAYRFHACVLQUP 1294
 QY 1021 FHOQWKNPTFPLRVISDTASLCYSILKAKVAGMSLGAKGAAGPLPSBAVOMLCHQAFLL 1080
 DB 1295 FHOQWKNPTFPLRVISDTASLCYSILKAKVAGMSLGAKGAAGPLPSBAVOMLCHQAFLL 1354
 QY 1081 KLTRHRYTVYVLLGSLRTAOTOLSRKLPCTTLTALAAANPALPSDFKTILD 1132
 DB 1355 KLTRHRYTVYVLLGSLRTAOTOLSRKLPCTTLTALAAANPALPSDFKTILD 1405

Db 1088 PFHQVWKNPTFFLRVISTASLCYSILKAKNAGMSLGAKGAGPLPSEAVQWLCHQAPL 1147
 QY 1080 LKLTTHRVTVYVLLGSLRTAQOLSKPLPGTTLTALAAANPALPSDFKTILD 1132
 Db 1148 LKLTTHRVTVYVLLGSLRTAQOLSKPLPGTTLTALAAANPALPSDFKTILD 1199

RESULT 37
 ID AAY00641
 AC AAY00641; standard; protein; 1120 AA.
 XX AAY00641;
 DT 26-JUL-1999 (first entry)
 XX Telomerase protein sequence lacking motif A.

DE Telomerase; human; cancer; diagnosis; melanoma; skin cancer; leukaemia;
 KW neuroblastoma; breast carcinoma; colon carcinoma; lymphoma; osteosarcoma;
 KW smooth muscle cell hyperplasia; stem cell proliferation; Wilm's tumour;
 KW stem cell differentiation; organ regeneration; organ differentiation.

OS Homo sapiens.
 OS Synthetic.
 XX WO9901560-A1.
 XX 14-JAN-1999.
 XX 01-JUL-1998; 98WO-US013835.
 XX 01-JUL-1997; 97US-0051410P.
 PR 21-JUL-1997; 97US-0053018P.
 PR 21-JUL-1997; 97US-0053329P.
 PR 04-AUG-1997; 97US-0054642P.
 PR 09-SEP-1997; 97US-0058287P.
 XX (CAMB-) CAMBIA BIOSYSTEMS LLC.
 XX Kilian A, Bowtell D;
 DR WPI; 1999-106060/09.
 DR N-PSDB; AAX18269.
 XX New isolated vertebrate telomerase genes - used to develop products for
 PT treating cancers or for organ regeneration, nerve cell or brain cell
 PT growth following injury or bone marrow transplantation.
 XX Claim 4; Fig 11n-o; 134pp; English.

XX This sequence is a truncated human telomerase of the invention. Primers
 CC that amplify the telomerase coding sequence can be used in a method for
 CC diagnosing cancer in a patient. The telomerase can be used for detection,
 CC diagnosis and drug screening. Inhibitors of telomerase activity can be
 CC used to treat cancers such as melanomas, other skin cancers,
 CC neuroblastomas, breast carcinomas, colon carcinomas, leukaemias,
 CC lymphomas, osteosarcomas or smooth muscle cell hyperplasias or skin
 CC growths. Enhancers of telomerase may be used to stimulate stem cell
 CC proliferation and differentiation (expansion of haematopoietic stem cells
 CC could be administered in the bone marrow transplant context). As well,
 CC many tissues have stem cells. Proliferation of these cells may be useful
 CC in wound healing, hair growth, treatment of disease such as Wilm's
 CC tumour, organ regeneration or differentiation after injury or diseases,
 CC nerve cell or brain cell growth following injury

XX Sequence 1120 AA;
 Query Match 98.7%; Score 5882; DB 2; Length 1120;
 Beat Local Similarity 98.9%; Pred No. 0;
 Matches 1120; Conservative 0; Mismatches 0; Indels 12; Gaps 1;

QY 1 MPRAPRCRAVRSLLRSHYREVLPATFVRRLGPOGWRLVQRGDPAAFRALVAQCLVCPW 60
 |||

Db 1 MPRAPRCRAVRSLLRSHYREVLPATFVRRLGPOGWRLVQRGDPAAFRALVAQCLVCPW 60
 QY 61 DARPPAAPSPROVSCLEKELVARVLRQRCERAKNVLAFGPALLDAGRGPPPEAFTTSVR 120
 |||
 Db 61 DARPPAAPSPROVSCLEKELVARVLRQRCERAKNVLAFGPALLDAGRGPPPEAFTTSVR 120
 |||
 QY 121 SYLPNTVTDALRGSGAWGLLRVGGDDVLVHLLARCALFVLVAPSCAVQVCGPPYQLGA 180
 |||
 Db 121 SYLPNTVTDALRGSGAWGLLRVGGDDVLVHLLARCALFVLVAPSCAVQVCGPPYQLGA 180
 |||
 QY 181 ATOARPPPHASGPRRLGCRANWHSVREAGVPLGLPAPGARRRGGSSASRSILPKRPRR 240
 |||
 Db 181 ATOARPPPHASGPRRLGCRANWHSVREAGVPLGLPAPGARRRGGSSASRSILPKRPRR 240
 |||
 QY 241 GAAPEPERTVQGSWAHPGTRGSPDRGFCVWSPARPAEATSLEGALSGRHSHPSVG 300
 |||
 Db 241 GAAPEPERTVQGSWAHPGTRGSPDRGFCVWSPARPAEATSLEGALSGRHSHPSVG 300
 |||
 QY 301 RQHAGPPSTSRPPRPPWDTPCPPVYAEYKHFILYSSGDEQURPSPFLLSLRSLTGARRL 360
 |||
 Db 301 RQHAGPPSTSRPPRPPWDTPCPPVYAEYKHFILYSSGDEQURPSPFLLSLRSLTGARRL 360
 |||
 QY 361 VETIFLGSPPMPCPTPRRLPRLPQRYWQMRPLFLELLGNHQAQCPYGVLLKTHCPRAAVT 420
 |||
 Db 361 VETIFLGSPPMPCPTPRRLPRLPQRYWQMRPLFLELLGNHQAQCPYGVLLKTHCPRAAVT 420
 |||
 QY 421 PAAGVCAREKPGQGSVAAPPEEDTDPRRLVQLLRHSSPWQVYGFVRACLRLRVPGLWGS 480
 |||
 Db 421 PAAGVCAREKPGQGSVAAPPEEDTDPRRLVQLLRHSSPWQVYGFVRACLRLRVPGLWGS 480
 |||
 QY 481 RHNERRFLRNTKCFISLGHAKLSLOELTWKMSVRDCAWLRRSPGVCGVPAEHLRBEI 540
 |||
 Db 481 RHNERRFLRNTKCFISLGHAKLSLOELTWKMSVRDCAWLRRSPGVCGVPAEHLRBEI 540
 |||
 QY 541 LAKFLHLMWSYVVELLSRFYVTTTFFQKRLFFYKRSVMSKLOSIGIRQHLKAVOLRE 600
 |||
 Db 541 LAKFLHLMWSYVVELLSRFYVTTTFFQKRLFFYKRSVMSKLOSIGIRQHLKAVOLRE 600
 |||
 QY 601 LSEAEVROHREARPAALLTSRLRFPKPDGLRPIVNMDDYVVGARTFRREKRAELTSRVKA 660
 |||
 Db 601 LSEAEVROHREARPAALLTSRLRFPKPDGLRPIVNMDDYVVGARTFRREKRAELTSRVKA 660
 |||
 QY 661 LFSVLNTERARRRPGLLGASVLGLDDIHRARTFVLVRVAQDPPPELYFVKVVDVTGAYDTI 720
 |||
 Db 661 LFSVLNTERARRRPGLLGASVLGLDDIHRARTFVLVRVAQDPPPELYFVKVVDVTGAYDTI 720
 |||
 QY 721 PQDRLETVIASIIRPONTYCVRRYAVQKAAHGVKAFKSHVSTLTDLQPMRQFVAHL 780
 |||
 Db 721 PQDRLETVIASIIRPONTYCVRRYAVQKAAHGVKAFKSHVSTLTDLQPMRQFVAHL 780
 |||
 QY 711 --DLRTEVIAIIIPONTYCVRRYAVQKAAHGVKAFKSHVSTLTDLQPMRQFVAHL 768
 |||
 Db 711 --DLRTEVIAIIIPONTYCVRRYAVQKAAHGVKAFKSHVSTLTDLQPMRQFVAHL 768
 |||
 QY 781 QETSPLRDAVVIQSSSLNEASSGLFDVFLRPMCHHAVIRGKSVQCGIPQGSILSTL 840
 |||
 Db 781 QETSPLRDAVVIQSSSLNEASSGLFDVFLRPMCHHAVIRGKSVQCGIPQGSILSTL 840
 |||
 QY 841 LCSLCYGMENKLFAGIRRDGLLRVDDFLVTPHLLTHAKTFLRTLVRGPEYGCNVNL 900
 |||
 Db 841 LCSLCYGMENKLFAGIRRDGLLRVDDFLVTPHLLTHAKTFLRTLVRGPEYGCNVNL 900
 |||
 QY 901 RKTVMNPFVEALGCTAFVQMPAHGLPPWCGLLDTRTLEVSQSYSSYARTSIRASLTF 960
 |||
 Db 901 RKTVMNPFVEALGCTAFVQMPAHGLPPWCGLLDTRTLEVSQSYSSYARTSIRASLTF 960
 |||
 QY 889 RKTVMNPFVEALGCTAFVQMPAHGLPPWCGLLDTRTLEVSQSYSSYARTSIRASLTF 948
 |||
 Db 889 RKTVMNPFVEALGCTAFVQMPAHGLPPWCGLLDTRTLEVSQSYSSYARTSIRASLTF 948
 |||
 QY 961 NRGFKAGNMRKLFGLVLRKCHSIFLDQVNSLQTVCTNLYKILLQAYRFHACVLQLP 1020
 |||
 Db 961 NRGFKAGNMRKLFGLVLRKCHSIFLDQVNSLQTVCTNLYKILLQAYRFHACVLQLP 1020
 |||
 QY 949 NRGFKAGNMRKLFGLVLRKCHSIFLDQVNSLQTVCTNLYKILLQAYRFHACVLQLP 1008
 |||
 Db 949 NRGFKAGNMRKLFGLVLRKCHSIFLDQVNSLQTVCTNLYKILLQAYRFHACVLQLP 1008
 |||
 QY 1021 FHQVWKNPTFFLRVISTASLCYSILKAKNAGMSLGAKGAGPLPSEAVQWLCHQAPL 1080
 |||
 Db 1009 FHQVWKNPTFFLRVISTASLCYSILKAKNAGMSLGAKGAGPLPSEAVQWLCHQAPL 1068
 |||
 QY 1081 KLTHRVTVYVLLGSLRTAQOLSKPLPGTTLTALAAANPALPSDFKTILD 1132
 |||
 Db 1069 KLTHRVTVYVLLGSLRTAQOLSKPLPGTTLTALAAANPALPSDFKTILD 1120
 |||

RESULT 38
 AAY00650
 ID AAY00650 standard; protein; 1120 AA.
 XX
 AC AAY00650;
 XX
 DT 26-JUL-1999 (first entry)
 XX
 DE Telomerase (ver. 2) protein sequence lacking motif A.
 XX
 KW Telomerase; human; cancer; diagnosis; melanoma; skin cancer; leukaemia;
 KW neuroblastoma; breast carcinoma; colon carcinoma; lymphoma; osteosarcoma;
 KW smooth muscle cell hyperplasia; stem cell proliferation; Wilms' tumour;
 KW stem cell differentiation; organ regeneration; organ differentiation.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 PN WO9901560-A1.
 XX
 XX 14-JAN-1999.
 PD
 XX 01-JUL-1998; 98WO-US013835.
 PF
 XX 01-JUL-1997; 97US-0051410P.
 PR 21-JUL-1997; 97US-0053018P.
 PR 21-JUL-1997; 97US-0053329P.
 PR 04-AUG-1997; 97US-0054642P.
 PR 09-SEP-1997; 97US-0058287P.
 XX
 PA (CAMB-) CAMBIA BIOSYSTEMS LLC.
 XX
 PI Kilian A, Bowtell D;
 XX
 DR WPI: 1999-106060/09.
 DR N-PSDB; AX18278.
 XX
 PT New isolated vertebrate telomerase genes - used to develop products for
 PT treating cancers or for organ regeneration, nerve cell or brain cell
 PT growth following injury or bone marrow transplantation.
 XX
 PS Claim 4; Fig 11ah-aj; 134pp; English.
 XX
 CC This sequence is a truncated human telomerase of the invention. Primers
 CC that amplify the telomerase coding sequence can be used in a method for
 CC diagnosing cancer in a patient. The telomerase can be used for detection,
 CC diagnosis and drug screening. Inhibitors of telomerase activity can be
 CC used to treat cancers such as melanomas, other skin cancers,
 CC neuroblastomas, breast carcinomas, colon carcinomas, leukemias,
 CC lymphomas, osteosarcomas or smooth muscle cell hyperplasias or skin
 CC growths. Enhancers of telomerase may be used to stimulate stem cell
 CC proliferation and differentiation (expansion of haematopoietic stem cells
 CC could be administered in the bone marrow transplant context). As well,
 CC many tissues have stem cells. Proliferation of these cells may be useful
 CC in wound healing, hair growth, treatment of disease such as Wilms'
 CC tumour, organ regeneration or differentiation after injury or diseases,
 CC nerve cell or brain cell growth following injury. Note: The N-terminus of
 CC this sequence can be replaced by the sequences shown in AAY00656-Y00658
 XX
 SQ Sequence 1120 AA;
 Query Match 98.5%; Score 5873; DB 2; Length 1120;
 Best Local Similarity 98.9%; Pred. No. 0;
 Matches 1119; Conservative 0; Mismatches 1; Indels 12; Gaps 1;
 QY 1 MPRAPRCVAVRSLLSHREVULPLATFVRRLGPQQRVLVQRGDPAAFRALVAQCLVCPW 60
 DB 1 MPRAPRCVAVRSLLSHREVULPLATFVRRLGPQQRVLVQRGDPAAFRALVAQCLVCPW 60
 QY 61 DARPPPAAPSPRQVSCLELVARVLQRLCERGAKNVLAFGFALLDARGGPPPEAFTTSVR 120

Db 61 DARPPPAAPSPRQVSCLELVARVLQRLCERGAKNVLAFGFALLDARGGPPPEAFTTSVR 120
 QY 121 SYLPNTVTDALRGSGAWGLLLRRVGDVVLVHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180
 Db 121 SYLPNTVTDALRGSGAWGLLLRRVGDVVLVHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180
 QY 181 ATQARPPPHASGPRRLGRCERAMNHSVREAGVPLGLPAPGARRRRGGASRSLLPKPRR 240
 Db 181 ATQARPPPHASGPRRLGRCERAMNHSVREAGVPLGLPAPGARRRRGGASRSLLPKPRR 240
 QY 241 GAPEPERTVGGQSWAHPGRTGRPSDRGFCVSPARPABEATSLGALSSTRHSHSVG 300
 Db 241 GAPEPERTVGGQSWAHPGRTGRPSDRGFCVSPARPABEATSLGALSSTRHSHSVG 300
 QY 301 RQHHAGPSTSRPPWDTPCPVYATKTHFLYSSGDKQLRPSFLSSLRPSLTGAPRL 360
 Db 301 RQHHAGPSTSRPPWDTPCPVYATKTHFLYSSGDKQLRPSFLSSLRPSLTGAPRL 360
 QY 361 VETIFGSRPMPGTPRRLPRLPQRYQWMPRLFLELLGNHAOCYPYGVLLKTHCPLRAVT 420
 Db 361 VETIFGSRPMPGTPRRLPRLPQRYQWMPRLFLELLGNHAOCYPYGVLLKTHCPLRAVT 420
 QY 421 PAAGVCAREKPOGSAVAPEEEDTPRLVOLLROHSSPWQVYGFVRACLRRLVPPGLWGS 480
 Db 421 PAAGVCAREKPOGSAVAPEEEDTPRLVOLLROHSSPWQVYGFVRACLRRLVPPGLWGS 480
 QY 481 RHNERFLRNTKTFISLGKHAQLSLOELTWKMSVRDCAWLRSPGVCVPAAEHRLREPI 540
 Db 481 RHNERFLRNTKTFISLGKHAQLSLOELTWKMSVRDCAWLRSPGVCVPAAEHRLREPI 540
 QY 541 LAKFLHLMMSVYVVELLSRFYVTTETTFQKRLFFYKSVMSKLOSGIQRHLKRVQLRE 600
 Db 541 LAKFLHLMMSVYVVELLSRFYVTTETTFQKRLFFYKSVMSKLOSGIQRHLKRVQLRE 600
 QY 601 LSEAEVQHQREARPAALLTSRLRPIKPDGLRPIVMDYVVGARTFREKRAERLTSRKA 660
 Db 601 LSEAEVQHQREARPAALLTSRLRPIKPDGLRPIVMDYVVGARTFREKRAERLTSRKA 660
 QY 661 LFSVLYNERARRPGLLGASVLGLDDIHRWRTFVLVRAQDPPPELVFVKVDVTGAVDTI 720
 Db 661 LFSVLYNERARRPGLLGASVLGLDDIHRWRTFVLVRAQDPPPELVFVKVDVTGAVDTI 720
 QY 721 PQDLTEVIASIIKPQNTYCVRRYAVVQKAAGHVRKAFKSHVSTLTDLOPMRQFVAHL 780
 Db 711 --DRLTEVIASIIKPQNTYCVRRYAVVQKAAGHVRKAFKSHVSTLTDLOPMRQFVAHL 768
 QY 781 QETSPDRDAVIEQSSSINEASSGLFDVFLRFMCHHAVIRGKSYVQCGIPQGSILSTL 840
 Db 769 QETSPDRDAVIEQSSSINEASSGLFDVFLRFMCHHAVIRGKSYVQCGIPQGSILSTL 828
 QY 841 LCSLCYGDMMENKLPAGIRRDGLLLRLVDDFLVTPHLLTHAKTFLRVLVRGVPYGCVVNL 900
 Db 829 LCSLCYGDMMENKLPAGIRRDGLLLRLVDDFLVTPHLLTHAKTFLRVLVRGVPYGCVVNL 888
 QY 901 RKTVVNPEDEALGCTAFVQMPAHGLFPWCGLLDTRTLEVSQSDYSYARTSIRASLTF 960
 Db 889 RKTVVNPEDEALGCTAFVQMPAHGLFPWCGLLDTRTLEVSQSDYSYARTSIRASLTF 948
 QY 961 NRGFKAGNNRRKLFVGLRLKCHSLFLDLQVNSLQTVCTNIYKILLQAYRFHACVLQLP 1020
 Db 949 NRGFKAGNNRRKLFVGLRLKCHSLFLDLQVNSLQTVCTNIYKILLQAYRFHACVLQLP 1008
 QY 1021 FHQQVWKNPTFFLRVSDTASLCYSILKAKNAGMSLGAKGAAGPLPSEAVWLCHQAFLL 1080
 Db 1009 FHQQVWKNPTFFLRVSDTASLCYSILKAKNAGMSLGAKGAAGPLPSEAVWLCHQAFLL 1068
 QY 1081 KLTEHRVTYVPLIGSLRTACTOLSRKLPGLTTLTALEAAANPALPSDEKTLTD 1132
 Db 1069 KLTEHRVTYVPLIGSLRTACTOLSRKLPGLTTLTALEAAANPALPSDEKTLTD 1120
 RESULT 39
 AAW47006

ID	AAW47006 standard; protein; 1150 AA.	QY	61	DAREPPAAPSPROVSKELVARVQLRCERAKNVLAFGFALLDARGGPPPEAFTTSVR	120
AC	AAW47006;	Db	61	DAREPPAAPSPROVSKELVARVQLRCERAKNVLAFGFALLDARGGPPPEAFTTSVR	120
XX					
DT	13-AUG-1998 (first entry)	QY	121	SYLPTNTVDALRGSGANGLLLRVDDVVLHLLARCALFVLVAPSCAYQVCGPPLYQGA	180
XX		Db	121	SYLPTNTVDALRGSGANGLLLRVDDVVLHLLARCALFVLVAPSCAYQVCGPPLYQGA	180
DE	Glutathione-S-transferase and hTERT fusion protein 6.	QY	181	ATQARPPPHAGSPRRRLGCERAWNHSVREAGVPLGLPAPGARRRGSGASRSLPLPKRPRR	240
XX		Db	181	ATQARPPPHAGSPRRRLGCERAWNHSVREAGVPLGLPAPGARRRGSGASRSLPLPKRPRR	240
KW	Human; telomerase reverse transcriptase; hTERT; TRT; diagnosis; prognosis; cell proliferation; cancer; ageing; ribonucleoprotein.	QY	241	GAPEPERTVPGQSGWAHPGTRGSDRGFCVSPARPAEBATSLGALSSTRHSPSVG	300
XX		Db	241	GAPEPERTVPGQSGWAHPGTRGSDRGFCVSPARPAEBATSLGALSSTRHSPSVG	300
OS	Synthetic.	QY	301	ROHAGPPSTSRPRPMDTTPCPVYAEYTKHFLYSSGDEQLRPSFLSSLSPLTGARRL	360
OS	Homo sapiens.	Db	301	ROHAGPPSTSRPRPMDTTPCPVYAEYTKHFLYSSGDEQLRPSFLSSLSPLTGARRL	360
XX		QY	361	VETIFLGSRRPMPGTPRRRLPRLPORYWQMRPLFLLELGNHAQCPVGLLTKHCPRAAVT	420
XX		Db	361	VETIFLGSRRPMPGTPRRRLPRLPORYWQMRPLFLLELGNHAQCPVGLLTKHCPRAAVT	420
PN	GB2317891-A.	QY	421	PAAGVCAREKPGQSVAAPEEEDTDPRLVQLLRQHSSFPWQYVGFVRACLRLVPPGL-WG	479
XX		Db	421	PAAGVCAREKPGQSVAAPEEEDTDPRLVQLLRQHSSFPWQYVGFVRACLRLVPPGL-WG	479
PD	08-APR-1998.	QY	480	SRHNERFLNNTKXFI SLGKHAKLSLOELTWKMSVRDCAWLRRSPGVCVPAAEHRLREE	539
XX		Db	480	SRHNERFLNNTKXFI SLGKHAKLSLOELTWKMSVRDCAWLRRSPGVCVPAAEHRLREE	539
XX		QY	540	ILAKFLHLMVSVVVELLSRFPFYTTETFOKNRLLFFYRKSVWSKLOSTIGIQHLKRVQLR	599
XX		Db	540	ILAKFLHLMVSVVVELLSRFPFYTTETFOKNRLLFFYRKSVWSKLOSTIGIQHLKRVQLR	599
PT	Pure and recombinant human Telomerase Reverse Transcriptase and its variants - are useful in the diagnosis, prognosis and treatment of cell proliferation conditions especially cancer and ageing.	QY	600	ELSEAEVRQHRARPALLTSRLRPIPKPDGLRPIVN-MDYVVGARTFREREKRAERLTSRV	658
PT		Db	599	ELSEAEVRQHRARPALLTSRLRPIPKPDGLRPIVN-MDYVVGARTFREREKRAERLTSRV	657
XX		QY	659	KALFSLVNYERARRPGLLGASVLGDDIHRARWTFVLRAQDPPPELYFKVDVTGAYD	718
PS	Example 6; Page 231-232; 387pp; English.	Db	658	KALFSLVNYERARRPGLLGASVLGDDIHRARWTFVLRAQDPPPELYFKVDVTGAYD	717
CC	The present sequence represents a fusion protein from an example of the present invention which describes human telomerase reverse transcriptase (hTERT). The present invention also describes the following methods: (A) determining whether a test compound is a modulator of hTERT, by detecting the change in hTERT recombinant protein or polynucleotide, on administration of the compound; (B) preparation of recombinant telomerase by contacting a protein preparation of hTERT with a telomerase RNA component; (C) detection of the hTERT RNA or protein in a sample by binding a relevant probe to the sample and detecting the complex formed or in the case of RNA detection, amplifying the product and correlating the presence of complex or amplification product with presence of hTERT in the sample; and (D) increasing the proliferation of a vertebrate cell by increasing hTERT expression; and (E) the use of an agent that causes an increase in cell vertebrate cell proliferation to create a medicament that inhibits ageing. A protein preparation of hTERT and the polynucleotide encoding hTERT can be used in the manufacture of medicaments for inhibiting the effect of ageing or cancer. Inhibitors of telomerase activity can be used to treat conditions that are associated with high telomerase activity. A protein preparation of hTERT can also be used in the new methods	QY	719	TIPODRLTEVIASIIKQNTYCVRRYAVVQAAHGHVRKAFKSHVSTLTDLPYMRQFVA	778
CC		Db	718	TIPODRLTEVIASIIKQNTYCVRRYAVVQAAHGHVRKAFKSHVSTLTDLPYMRQFVA	777
CC		QY	779	HLOETSPDRDAVVIQSSSL-NEASSGLFDVFLRFMCHHVRIRGKSVYQCGIPOQSIL	837
CC		Db	778	HLOETSPDRDAVVIQSSSL-NEASSGLFDVFLRFMCHHVRIRGKSVYQCGIPOQSIL	835
CC		QY	838	STLLCSLCYGDWENKLPAGIRRDGLLLRLVDDPDLVTLTHLTHAKTFLTLVRGVEYGCV	897
CC		Db	836	STLLCSLCYGDWENKLPAGIRRDGLLLRLVDDPDLVTLTHLTHAKTFLTLVRGVEYGCV	894
CC		QY	898	VNLBKTWVNPVEDEALGGTAFVQMPAHGLFPW-CGLLDDTTELEVQSDSYSSARTSIRA	956
CC		Db	895	VNLBKTWVNPVEDEALGGTAFVQMPAHGLFPW-CGLLDDTTELEVQSDSYSSARTSIRA	952
CC		QY	957	SLTNRNGFKAGR-NWRRKLFGLVLRKCHSLFLDLQVNSLQVCTNIVYKILLQYRPHAC	1015
CC		Db	953	SLTNRNGFKAGR-NWRRKLFGLVLRKCHSLFLDLQVNSLQVCTNIVYKILLQYRPHAC	1012
XX		QY	1016	VLQPLFHQQVWKNPTFFLRVISTASLCYSILKAKNAGMSLGAKGAPLPSEAVQWLCH	1075
XX		Db	1013	VLQPLFHQQVWKNPTFFLRVISTASLCYSILKAKNAGMSLGAKGAPLPSEAVQWLCH	1072
QY	1 MPAPRCRAVRSLLRSHYREVLPATFVRRLLGPOQWRLLVQRGDPAAFRALVAQCLVCPW	QY	1076	QAFLLKLTTRHVTYVPLLGSLRTAQTSRLKPGTTLTALAAANPALPSDFKTLTD	1132
Db	1 MPAPRCRAVRSLLRSHYREVLPATFVRRLLGPOQWRLLVQRGDPAAFRALVAQCLVCPW	Db	1073	QAFLLKLTTRHVTYVPLLGSLRTAQTSRLKPGTTLTALAAANPAL-SDFKTLTD	1128

Sequence 1150 AA;

Query Match 96.0%; Score 5721; DB 2; Length 1150;

Best Local Similarity 97.8%; Pred. No. 0;

Matches 1112; Conservative 6; Mismatches 5; Indels 14; Gaps 13;

QY 1 MPAPRCRAVRSLLRSHYREVLPATFVRRLLGPOQWRLLVQRGDPAAFRALVAQCLVCPW 60

Db 1 MPAPRCRAVRSLLRSHYREVLPATFVRRLLGPOQWRLLVQRGDPAAFRALVAQCLVCPW 60

XX DE Altered C-terminus telomerase (ver. 2) protein sequence.

XX Telomerase; human; cancer; diagnosis; melanoma; skin cancer; leukaemia;

KW neuroblastoma; breast carcinoma; colon carcinoma; lymphoma; osteosarcoma;

KW smooth muscle cell hyperplasia; stem cell proliferation; Wilms' tumor;

KW stem cell differentiation; organ regeneration; organ differentiation.

OS Homo sapiens.

OS Synthetic.

XX WO9901560-A1.

XX 14-JAN-1999.

XX 01-JUL-1998; 98WO-US013835.

XX 01-JUL-1997; 97US-0051410P.

PR 21-JUL-1997; 97US-0053018P.

PR 21-JUL-1997; 97US-0053329P.

PR 04-AUG-1997; 97US-0054642P.

PR 09-SEP-1997; 97US-0058287P.

XX (CAMP-) CAMBIA BIOSYSTEMS LLC.

PA Kilian A, Bowtell D;

XX WPI; 1999-106060/09.

DR N-PSDB; AX18277.

DR New isolated vertebrate telomerase genes - used to develop products for

PT treating cancers or for organ regeneration, nerve cell or brain cell

PT growth following injury or bone marrow transplantation.

XX Claim 4; Fig 11af-ag; 134pp; English.

XX This sequence is a truncated human telomerase of the invention. Primers

CC that amplify the telomerase coding sequence can be used in a method for

CC diagnosing cancer in a patient. The telomerase can be used for detection,

CC diagnosis and drug screening. Inhibitors of telomerase activity can be

CC used to treat cancers such as melanomas, other skin cancers,

CC neuroblastomas, breast carcinomas, colon carcinomas, leukaemias,

CC lymphomas, osteosarcomas or smooth muscle cell hyperplasias or skin

CC growths. Enhancers of telomerase may be used to stimulate stem cell

CC proliferation and differentiation (expansion of haematopoietic stem cells

CC could be administered in the bone marrow transplant context). As well,

CC many tissues have stem cells. Proliferation of these cells may be useful

CC in wound healing, hair growth, treatment of disease such as Wilms'

CC tumour, organ regeneration or differentiation after injury or diseases,

CC nerve cell or brain cell growth following injury. Note: The N-terminus of

CC this sequence can be replaced by the sequences shown in AAY00656-Y00658,

CC and the C-terminus can be replaced by the sequence shown in AAY00654

XX Sequence 1093 AA;

Query Match 92.5%; Score 5516; DB 2; Length 1093;

Best Local Similarity 96.2%; Pred No. 0;

Matches 1051; Conservative 0; Mismatches 1; Indels 40; Gaps 1;

QY 1 MPAPRCRAVRSLLSHRYEVLPLATFVRRLLPGQWRLLVQRGDPAAFRALVAQCILVCVPW 60

Db 1 MPAPRCRAVRSLLSHRYEVLPLATFVRRLLPGQWRLLVQRGDPAAFRALVAQCILVCVPW 60

QY 61 DARPPPAAPRSQVSLKELVARVLQRLCERGAKNVLAFFGALLDAGRGPPPEAFTTSVR 120

Db 61 DARPPPAAPRSQVSLKELVARVLQRLCERGAKNVLAFFGALLDAGRGPPPEAFTTSVR 120

QY 121 SYLPTNTVDALRGSGAWGLLRVDDVLLHLLARCALFVLVAPSCAYQVCGPPYQLGA 180

Db 121 SYLPTNTVDALRGSGAWGLLRVDDVLLHLLARCALFVLVAPSCAYQVCGPPYQLGA 180

QY 181 ATQARPPPHASGPRRRRLGRCERAMNHSVREAGVPLGLPAPGARRRGGASRSRLPLPKRRR 240

Db 181 ATQARPPPHASGPRRRRLGRCERAMNHSVREAGVPLGLPAPGARRRGGASRSRLPLPKRRR 240

QY 241 GAAPEPRTPVGQGSWAHPGRTGRCFVSWPAPAEATSLGALSGLTRHSHPSVG 300

Db 241 GAAPEPRTPVGQGSWAHPGRTGRCFVSWPAPAEATSLGALSGLTRHSHPSVG 300

QY 301 ROHAGPSTSRPPRPMWDTPCPPVYAEKTHFLYSGDKQELRPSFLSSLSPLTGARRL 360

Db 301 ROHAGPSTSRPPRPMWDTPCPPVYAEKTHFLYSGDKQELRPSFLSSLSPLTGARRL 360

QY 361 VETIFLSRPMWPGTPRRLPELPORYWOMRPLFLELLGNHAQCPVGLLTKHCPRAAVT 420

Db 361 VETIFLSRPMWPGTPRRLPELPORYWOMRPLFLELLGNHAQCPVGLLTKHCPRAAVT 420

QY 421 PAAGVCAREKPGQGSVAAPAEEDTDPRLVQLLRQHSSPWQVYGFVRACLRLVPPGLWGS 480

Db 421 PAAGVCAREKPGQGSVAAPAEEDTDPRLVQLLRQHSSPWQVYGFVRACLRLVPPGLWGS 480

QY 481 RHNERRRFLRNTKTFISLGKHAHKLISLQ----- 507

Db 481 RHNERRRFLRNTKTFISLGKHAHKLISLQ----- 507

QY 508 -----LTKMSVRDCAWLRSPGVCVPAAEHRLREEILAKFLHLMVSVVVELLSRF 560

Db 541 LAKFLHMLTWKMSVRDCAWLRSPGVCVPAAEHRLREEILAKFLHLMVSVVVELLSRF 600

QY 561 FYVTETTFQKRLFFYRKSVMKLSQIGIRHKLKRVOLRELSEAEVROHREARPAALLTSR 620

Db 601 FYVTETTFQKRLFFYRKSVMKLSQIGIRHKLKRVOLRELSEAEVROHREARPAALLTSR 660

QY 621 LRFIPKPDGLRPIVNDYVVGARTFRREKRAERLTSRVKALFSLVNYERARRPGLLGASV 680

Db 661 LRFIPKPDGLRPIVNDYVVGARTFRREKRAERLTSRVKALFSLVNYERARRPGLLGASV 720

QY 681 LGLDDIHRARTFVLVRQAQDPPPELYFVKVDVTGAYDTIPQDRLTEVIASIIKPONTYC 740

Db 721 LGLDDIHRARTFVLVRQAQDPPPELYFVKVDVTGAYDTIPQDRLTEVIASIIKPONTYC 780

QY 741 VRRVAVVQKAAGHVRKAFKSHVSTLTDLQPYMQFVAHLQETSPRLDVAVIEQSSSLNE 800

Db 781 VRRVAVVQKAAGHVRKAFKSHVSTLTDLQPYMQFVAHLQETSPRLDVAVIEQSSSLNE 840

QY 801 ASSGLPDLVFLRFMCHAVRINGKSYVQCQIPQGSIIISLTLCSLCYGDENKLFAGIRRD 860

Db 841 ASSGLPDLVFLRFMCHAVRINGKSYVQCQIPQGSIIISLTLCSLCYGDENKLFAGIRRD 900

QY 861 GLLRLVDDFLVPLTHLTHAKTFLRTLVRGVPEYGCVVNLKRTVWNPFEDEALGGTAFV 920

Db 901 GLLRLVDDFLVPLTHLTHAKTFLRTLVRGVPEYGCVVNLKRTVWNPFEDEALGGTAFV 960

QY 921 QMPAHLGFPWCGLLLDTRTLEVSQSDYSYARTSIRASLTFRNGFKAGRMRRKLFGLVRL 980

Db 961 QMPAHLGFPWCGLLLDTRTLEVSQSDYSYARTSIRASLTFRNGFKAGRMRRKLFGLVRL 1020

QY 981 KCHSLFLDLQVNSLQVCTNIIYKILLQAVRFHACVQLQLPFPHQWKNKPTFFLRVISDTA 1040

Db 1021 KCHSLFLDLQVNSLQVCTNIIYKILLQAVRFHACVQLQLPFPHQWKNKPTFFLRVISDTA 1080

QY 1041 SLCSYILKAKNA 1052

Db 1081 SLCSYILKAKNA 1092

RESULT 42

AAY00652

ID AAY00652 standard; protein; 1041 AA.

XX AC AAY00652;

XX AC AAY00652;

XX AC AAY00652;

DT 26-JUL-1999 (first entry)

XX DE Altered C-terminus telomerase lacking motif A (ver. 2) protein sequence.

XX XX

KW Telomerase; human; cancer; diagnosis; melanoma; skin cancer; leukaemia;
 KW neuroblastoma; breast carcinoma; colon carcinoma; lymphoma; osteosarcoma;
 KW smooth muscle cell hyperplasia; stem cell proliferation; Wilm's tumour;
 KW stem cell differentiation; organ regeneration; organ differentiation.
 XX Homo sapiens.
 OS Synthetic.
 XX WO9901560-A1.
 FN 14-JAN-1999.
 PD 01-JUL-1998; 98WO-US013835.
 PF 01-JUL-1997; 97US-0051410P.
 XX 21-JUL-1997; 97US-0053018P.
 PR 21-JUL-1997; 97US-0053329P.
 PR 04-AUG-1997; 97US-0054642P.
 PR 09-SEP-1997; 97US-0058287P.
 XX (CAMB-) CAMBIA BIOSYSTEMS LLC.
 FA Kilian A, Bowtell D;
 XX WPI; 1999-106060/09.
 DR N-PSDB; AAX18280.
 XX
 PT New isolated vertebrate telomerase genes - used to develop products for
 PT treating cancers or for organ regeneration, nerve cell or brain cell
 PT growth following injury or bone marrow transplantation.
 XX
 PS Claim 4; Fig 11am-an; 134pp; English.
 XX
 CC This sequence is a truncated human telomerase of the invention. Primers
 CC that amplify the telomerase coding sequence can be used in a method for
 CC diagnosing cancer in a patient. The telomerase can be used for detection,
 CC diagnosis and drug screening. Inhibitors of telomerase activity can be
 CC used to treat cancers such as melanomas, other skin cancers,
 CC neuroblastomas, breast carcinomas, colon carcinomas, leukaemias,
 CC lymphomas, osteosarcomas or smooth muscle cell hyperplasias or skin
 CC growths. Enhancers of telomerase may be used to stimulate stem cell
 CC proliferation and differentiation (expansion of haematopoietic stem cells
 CC could be administered in the bone marrow transplant context). As well,
 CC many tissues have stem cells. Proliferation of these cells may be useful
 CC in wound healing, hair growth, treatment of disease such as Wilm's
 CC tumour, organ regeneration or differentiation after injury or diseases,
 CC nerve cell or brain cell growth following injury. Note: The N-terminus of
 CC this sequence can be replaced by the sequences shown in AAY00656-Y00658,
 CC and the C-terminus can be replaced by the sequence shown in AAY00654
 XX Sequence 1041 AA;
 SQ

Query Match 91.7%; Score 5467; DB 2; Length 1041;
 Best Local Similarity 98.8%; Pred. No. 0;
 Matches 1039; Conservative 0; Mismatches 1; Indels 12; Gaps 1;

QY 1 MPRAPCRVRSLRSHRVREVLPLATFVRRLGPGQWRLVQRGDPAAFRALVAQCLVCVPW 60
 DB 1 MPRAPCRVRSLRSHRVREVLPLATFVRRLGPGQWRLVQRGDPAAFRALVAQCLVCVPW 60
 QY 61 DARPPPAAPSPROVSCLELVARVLORLCERGANVLAFFGALLDGGGPPPEAFTTSVR 120
 DB 61 DARPPPAAPSPROVSCLELVARVLORLCERGANVLAFFGALLDGGGPPPEAFTTSVR 120
 QY 121 SYLNTVNTDALRGSGAWGLLLRRVGDVLLVHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180
 DB 121 SYLNTVNTDALRGSGAWGLLLRRVGDVLLVHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180
 QY 181 ATQARPPPHASPPRRRLCERAWNHSVREAGVPLGAPAGARRGGGASRSLPLPKPRRR 240
 DB 181 ATQARPPPHASPPRRRLCERAWNHSVREAGVPLGAPAGARRGGGASRSLPLPKPRRR 240
 QY 241 GAAPEPERTVPGQSWAHPGRTGRPSDRGFCVWSPARPAEATSLEGALSGTRHSHPSVG 300

DB 241 GAAPEPERTVPGQSWAHPGRTGRPSDRGFCVWSPARPAEATSLEGALSGTRHSHPSVG 300
 QY 301 RQHHAGPPSTSRPPRMDTPCPPVYAEHTKHFLYSSGDKQELRPSFLSSLRPSLTGARRL 360
 DB 301 RQHHAGPPSTSRPPRMDTPCPPVYAEHTKHFLYSSGDKQELRPSFLSSLRPSLTGARRL 360
 QY 361 VETIFLGSRRPMPGTPRRRLPRLPQRYWQTRPFLFELIIGNHAQCPYGVLLKTHCPLRAAVT 420
 DB 361 VETIFLGSRRPMPGTPRRRLPRLPQRYWQTRPFLFELIIGNHAQCPYGVLLKTHCPLRAAVT 420
 QY 421 PAAGVCAREKPOGSAVAPEEEDTPRELVLLOLHSSPQWVGVFVACLRRLVPPGLWGS 480
 DB 421 PAAGVCAREKPOGSAVAPEEEDTPRELVLLOLHSSPQWVGVFVACLRRLVPPGLWGS 480
 QY 481 RHNERRFLRNTKKFISLGKHAQLSLOBLTWKMSVRDCAWLRRSPGVGCVPAAEHRLREEI 540
 DB 481 RHNERRFLRNTKKFISLGKHAQLSLOBLTWKMSVRDCAWLRRSPGVGCVPAAEHRLREEI 540
 QY 541 LAKFLHLMMSVYVELLRSPFYVTETTFQKNRLFVYRKSVMSKLSIGIRQHLKRVOLRE 600
 DB 541 LAKFLHLMMSVYVELLRSPFYVTETTFQKNRLFVYRKSVMSKLSIGIRQHLKRVOLRE 600
 QY 601 LSAEVRQHREARPAALLTSRLRFTPKDGLRPIVNMDDYVVGARTFREKRAERLTSRVKA 660
 DB 601 LSAEVRQHREARPAALLTSRLRFTPKDGLRPIVNMDDYVVGARTFREKRAERLTSRVKA 660
 QY 661 LFSVLNVERARRPGLLGASVLGLDDIHRAMRTFVLVRAQDPPPELVFVVDVTGAYDTI 720
 DB 661 LFSVLNVERARRPGLLGASVLGLDDIHRAMRTFVLVRAQDPPPELVFVVDVTGAYDTI 720
 QY 721 PQRLTEVIASIIKPQNTYCVRRYAVVQKAAGHVRKAFKSHVSTLTDLQPYMRQFVAHL 780
 DB 721 --DLTEVIASIIKPQNTYCVRRYAVVQKAAGHVRKAFKSHVSTLTDLQPYMRQFVAHL 780
 QY 781 QETSPURDAVVIQSSSLNEASSGLPDLRFMCHHAVIRGKSVYVOCQIGPOGSIILSTL 840
 DB 769 QETSPURDAVVIQSSSLNEASSGLPDLRFMCHHAVIRGKSVYVOCQIGPOGSIILSTL 828
 QY 841 LCSLCYGDMMENKLFAGIRRRDGLLLRLVDDFLVTPHLLTHAKTFLRTLVRGVPYGCVVNL 900
 DB 829 LCSLCYGDMMENKLFAGIRRRDGLLLRLVDDFLVTPHLLTHAKTFLRTLVRGVPYGCVVNL 888
 QY 901 RKTVPNPVDEALGGTAFVQMPAHGLFPWCGLLLDTRTLEVDQSDYSSYARTSIRASLTFF 960
 DB 889 RKTVPNPVDEALGGTAFVQMPAHGLFPWCGLLLDTRTLEVDQSDYSSYARTSIRASLTFF 948
 QY 961 NRGFKAGRNRRKLFGLRLKCHSLPDLQVNSIQTVCTNIYKILLQAYRFHACVLQLP 1020
 DB 949 NRGFKAGRNRRKLFGLRLKCHSLPDLQVNSIQTVCTNIYKILLQAYRFHACVLQLP 1008
 QY 1021 FHQQVWKNPTFFLRVISDTSALCYSLKAKNA 1052
 DB 1009 FHQQVWKNPTFFLRVISDTSALCYSLKAKNA 1040
 XX AAY00643 standard; protein; 1041 AA.
 XX AC AAY00643;
 XX DT 26-JUL-1999 (first entry)
 XX DE Altered C-terminus telomerase protein sequence lacking motif A.
 KW Telomerase; human; cancer; diagnosis; melanoma; skin cancer; leukaemia;
 KW neuroblastoma; breast carcinoma; colon carcinoma; lymphoma; osteosarcoma;
 KW smooth muscle cell hyperplasia; stem cell proliferation; Wilm's tumour;
 KW stem cell differentiation; organ regeneration; organ differentiation.
 OS Homo sapiens.
 OS Synthetic.

XX WO901560-A1.
 XX 14-JAN-1999.
 XX 01-JUL-1998; 98WO-US013835.
 XX 01-JUL-1997; 97US-0051410P.
 PR 21-JUL-1997; 97US-0053018P.
 PR 21-JUL-1997; 97US-0053018P.
 PR 04-AUG-1997; 97US-0054642P.
 PR 09-SEP-1997; 97US-0058287P.
 XX (CMB-) CAMBIA BIOSYSTEMS LLC.
 XX Kilian A, Bowtell D;
 XX WPI: 1999-106060/09.
 DR N-PSDB; AAX18271.
 XX New isolated vertebrate telomerase genes - used to develop products for
 PT treating cancers or for organ regeneration, nerve cell or brain cell
 PT growth following injury or bone marrow transplantation.
 XX Claim 4; Fig 11r-s; 134pp; English.
 XX This sequence is a truncated human telomerase of the invention. Primers
 CC that amplify the telomerase coding sequence can be used in a method for
 CC diagnosing cancer in a patient. The telomerase can be used for detection,
 CC diagnosis and drug screening. Inhibitors of telomerase activity can be
 CC used to treat cancers such as melanomas, other skin cancers,
 CC neuroblastomas, breast carcinomas, colon carcinomas, leukemias,
 CC lymphomas, osteosarcomas or smooth muscle cell hyperplasias or skin
 CC growths. Enhancers of telomerase may be used to stimulate stem cell
 CC proliferation and differentiation (expansion of haematopoietic stem cells
 CC could be administered in the bone marrow transplant context). As well,
 CC many tissues have stem cells. Proliferation of these cells may be useful
 CC in wound healing, hair growth, treatment of disease such as Wilm's
 CC tumour, organ regeneration or differentiation after injury or diseases,
 CC nerve cell or brain cell growth following injury. Note: The C-terminus of
 CC this sequence can be replaced by the sequence shown in AAY00654
 XX Sequence 1041 AA;
 Query Match 91.7%; Score 5467; DB 2; Length 1041;
 Best Local Similarity 98.8%; Pred No. 0;
 Matches 1039; Conservative 0; Mismatches 1; Indels 12; Gaps 1;
 QY 1 MPRAPCRRAVRSLLSHYREVLPATFVRRGPOQWRLVQRGDPAAPRALVAQCLVCPW 60
 DB 1 MPRAPCRRAVRSLLSHYREVLPATFVRRGPOQWRLVQRGDPAAPRALVAQCLVCPW 60
 QY 61 DARPPPAAPSPQNSCLKELVARVLRQICERGAKNVLAFFGALLDAGRGPPPEATTSVR 120
 DB 61 DARPPPAAPSPQNSCLKELVARVLRQICERGAKNVLAFFGALLDAGRGPPPEATTSVR 120
 QY 121 SYLPTNTVDALRGSGAWGLLRVGDVLLVHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180
 DB 121 SYLPTNTVDALRGSGAWGLLRVGDVLLVHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180
 QY 181 ATQARPPPHASGPRRLGGERAWNHSVREAGVPLGLPAPGARRRGGASRSILPKRPRR 240
 DB 181 ATQARPPPHASGPRRLGGERAWNHSVREAGVPLGLPAPGARRRGGASRSILPKRPRR 240
 QY 241 GAAPPERTPVQGSWAHPGRTRGSDRGFCVVSPPAPAEATSLLEGALSGTRHSHPSVG 300
 DB 241 GAAPPERTPVQGSWAHPGRTRGSDRGFCVVSPPAPAEATSLLEGALSGTRHSHPSVG 300
 QY 301 RQHAGPSTSPRPDPWTPCPVVAETKHFLYSSGDKQLRPSLLSLRPSLTGARRL 360
 DB 301 RQHAGPSTSPRPDPWTPCPVVAETKHFLYSSGDKQLRPSLLSLRPSLTGARRL 360
 QY 361 VETIFLGRPWPMPGTTPRLPRLPQRYWQMRPLFLELLGNHAQCPYGVLLKTHCPLRAAVT 420

DB 361 VETIFLGRPWPMPGTTPRLPRLPQRYWQMRPLFLELLGNHAQCPYGVLLKTHCPLRAAVT 420
 QY 421 PAAGVCAREKPGQSVAAPEEEDTDPRLVQLLRHSSPWQVYGFVRACLRRLVPPGLNGS 480
 DB 421 PAAGVCAREKPGQSVAAPEEEDTDPRLVQLLRHSSPWQVYGFVRACLRRLVPPGLNGS 480
 QY 481 RHNERRFLRNTKFTISLGKHAQLSLQELTWKMSVRDCAWLRSPGVCVPAAEHLRREI 540
 DB 481 RHNERRFLRNTKFTISLGKHAQLSLQELTWKMSVRDCAWLRSPGVCVPAAEHLRREI 540
 QY 541 LAKFLHLMMSVYVVELLSFPYVTTTQKRLFPYKSVMSKLOSIGIRQHLKRVQLRE 600
 DB 541 LAKFLHLMMSVYVVELLSFPYVTTTQKRLFPYKSVMSKLOSIGIRQHLKRVQLRE 600
 QY 601 LSEAEVROHREARPAALLTSRLRFPKPDGLRPIVNDYVVGARTFRREKRAERLTSRVKA 660
 DB 601 LSEAEVROHREARPAALLTSRLRFPKPDGLRPIVNDYVVGARTFRREKRAERLTSRVKA 660
 QY 661 LFSVLNTERARRPGLLGASVLGLDDIHRAMRTFVLVRAQDPPPELYFVKVVDVTGAYDTI 720
 DB 661 LFSVLNTERARRPGLLGASVLGLDDIHRAMRTFVLVRAQDPPPELYFVKVVDVTGAYDTI 720
 QY 721 PODRLTEVIASIIKPONTYCVRRYAVVQKAAGHVRAKAFKSHVSTLTDLQPMRQFVAHL 780
 DB 721 PODRLTEVIASIIKPONTYCVRRYAVVQKAAGHVRAKAFKSHVSTLTDLQPMRQFVAHL 780
 QY 781 QETSPRLDAVVEIOSSSINEASSGLFDVFLRFMCHHVRIRGKSVQCGIPQGSILSTL 840
 DB 781 QETSPRLDAVVEIOSSSINEASSGLFDVFLRFMCHHVRIRGKSVQCGIPQGSILSTL 840
 QY 841 LCSLCYGMENKLFAGIRRDGLLRLVDDFLVTPHLLTHAKTFLRTLVRGVPEYGVVNL 900
 DB 841 LCSLCYGMENKLFAGIRRDGLLRLVDDFLVTPHLLTHAKTFLRTLVRGVPEYGVVNL 900
 QY 901 RKTVPVPEDEALGGTAFAVOMPAHGLPPWCGLLDTRTLEVSQSYSSYARTSIRASLTF 960
 DB 901 RKTVPVPEDEALGGTAFAVOMPAHGLPPWCGLLDTRTLEVSQSYSSYARTSIRASLTF 960
 QY 961 NRGPKAGNMRKLPGLVLRKCHSLFDLVNSLQVCTNLYKILLQAYRPHACVQLP 1020
 DB 961 NRGPKAGNMRKLPGLVLRKCHSLFDLVNSLQVCTNLYKILLQAYRPHACVQLP 1020
 QY 1021 FHQWKNPTFFLRVISDTASLCYSILKAKNA 1052
 DB 1009 FHQWKNPTFFLRVISDTASLCYSILKAKNA 1040
 RESULT 44
 AAY00639
 ID AAY00639 standard; protein; 948 AA.
 AC AAY00639;
 XX 26-JUL-1999 (first entry)
 XX N-terminal truncated telomerase protein sequence.
 XX Telomerase; human; cancer; diagnosis; melanoma; skin cancer; leukaemia;
 KW neuroblastoma; breast carcinoma; colon carcinoma; lymphoma; osteosarcoma;
 KW smooth muscle cell hyperplasia; stem cell proliferation; Wilm's tumour;
 KW stem cell differentiation; organ regeneration; organ differentiation.
 OS Homo sapiens.
 OS Synthetic.
 XX WO901560-A1.
 XX 14-JAN-1999.
 XX 01-JUL-1998; 98WO-US013835.
 XX 01-JUL-1997; 97US-0051410P.

PR 21-JUL-1997; 97US-0053018P.
 PR 21-JUL-1997; 97US-0053322P.
 PR 04-AUG-1997; 97US-0054642P.
 PR 09-SEP-1997; 97US-0058287P.
 XX
 PA (CAMB-) CAMBIA BIOSYSTEMS LLC.
 XX
 XX
 PI Kilian A, Bowtell D;
 XX WPI; 1999-106060/09.
 DR N-PSDB; AAY00648.
 XX
 XX New isolated vertebrate telomerase genes - used to develop products for
 PT treating cancers or for organ regeneration, nerve cell or brain cell
 PT growth following injury or bone marrow transplantation.
 XX
 PS Claim 4; Fig 11j-k; 134pp; English.
 XX
 CC This sequence is a truncated human telomerase of the invention. Primers
 CC that amplify the telomerase coding sequence can be used in a method for
 CC diagnosing cancer in a patient. The telomerase can be used for detection,
 CC diagnosis and drug screening. Inhibitors of telomerase activity can be
 CC used to treat cancers such as melanomas, other skin cancers,
 CC neuroblastomas, breast carcinomas, colon carcinomas, leukemias,
 CC lymphomas, osteosarcomas or smooth muscle cell hyperplasias or skin
 CC growths. Enhancers of telomerase may be used to stimulate stem cell
 CC proliferation and differentiation (expansion of haematopoietic stem cells
 CC could be administered in the bone marrow transplant context). As well,
 CC many tissues have stem cells. Proliferation of these cells may be useful
 CC in wound healing, hair growth, treatment of disease such as Wilms
 CC tumour, organ regeneration or differentiation after injury or diseases,
 CC nerve cell or brain cell growth following injury
 XX
 SQ Sequence 948 AA;
 Query Match 84.0%; Score 5008; DB 2; Length 948;
 Best Local Similarity 99.9%; Pred. No. 0;
 Matches 946; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MPRAPCRAVSLRLSHRYEVLPLATFVRRLGPGQWRLVQRGDPAAFPALVAQCLVCVPW 60
 DB 1 MPRAPCRAVSLRLSHRYEVLPLATFVRRLGPGQWRLVQRGDPAAFPALVAQCLVCVPW 60
 QY 61 DARPPAAPSPROVSCLELVARVLQRLCERGAKNVLAFGALLDGAAGGPEAFTTSVR 120
 DB 61 DARPPAAPSPROVSCLELVARVLQRLCERGAKNVLAFGALLDGAAGGPEAFTTSVR 120
 QY 121 SYLPTNTVDALRGSGAWGLLRLRRVGGDDVLVHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180
 DB 121 SYLPTNTVDALRGSGAWGLLRLRRVGGDDVLVHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180
 QY 181 ATQARPPHAGSPRRRLGCEAWNHSVREAGVPLGLPAGARRRGGSASRLPLPKRPRR 240
 DB 181 ATQARPPHAGSPRRRLGCEAWNHSVREAGVPLGLPAGARRRGGSASRLPLPKRPRR 240
 QY 241 GAAPERTPVQGSWAHPGTRGSDRGFCVSPAPAEATSLGALSSTRHSHSVG 300
 DB 241 GAAPERTPVQGSWAHPGTRGSDRGFCVSPAPAEATSLGALSSTRHSHSVG 300
 QY 301 RQHAGPSTSRPRPMDTPCPVVAETKHFLYSSGDKQLRPSFLSSLRPSLTGARRL 360
 DB 301 RQHAGPSTSRPRPMDTPCPVVAETKHFLYSSGDKQLRPSFLSSLRPSLTGARRL 360
 QY 361 VETIFLGRPMWPGTFRRLPLPQRYWQMRPLFLELGNHAQCPYGVLLKTHCPLRAAVT 420
 DB 361 VETIFLGRPMWPGTFRRLPLPQRYWQMRPLFLELGNHAQCPYGVLLKTHCPLRAAVT 420
 QY 421 PAAGVCAREKPGQSVAAPEEDTPRRLVQLLRHSSPWQYGVFRACLRRLVPPGLWS 480
 DB 421 PAAGVCAREKPGQSVAAPEEDTPRRLVQLLRHSSPWQYGVFRACLRRLVPPGLWS 480
 QY 481 RHNERRFLRNTKFTISLGKHAKLISQELTWKMSVRDCAWLRRSPGVCVPAAEHRLREEI 540

DB 481 RHNERRFLRNTKFTISLGKHAKLISQELTWKMSVRDCAWLRRSPGVCVPAAEHRLREEI 540
 QY 541 LAKFLHLMSSVYVELLRSFFYYTETTFQKNRLFYRKSVMKLSQSIGIRHKLKRVQLRE 600
 DB 541 LAKFLHLMSSVYVELLRSFFYYTETTFQKNRLFYRKSVMKLSQSIGIRHKLKRVQLRE 600
 QY 601 LSEAEVQHQREARPAALLTSRLRFPKPDGLRPIVNMNDYVVGARTFREKRAERLTSRYKA 660
 DB 601 LSEAEVQHQREARPAALLTSRLRFPKPDGLRPIVNMNDYVVGARTFREKRAERLTSRYKA 660
 QY 661 LFSVLNVERARRPGLLGASVLGLDDIHRWRTFVLVRAQDPPPELFFVKVDVTGAYDTI 720
 DB 661 LFSVLNVERARRPGLLGASVLGLDDIHRWRTFVLVRAQDPPPELFFVKVDVTGAYDTI 720
 QY 721 PQDLTEVIASIIKPNQTYCVRRYAVVQKAAHGVKAFKSHVSTLTDLQPMYQFVAHL 780
 DB 721 PQDLTEVIASIIKPNQTYCVRRYAVVQKAAHGVKAFKSHVSTLTDLQPMYQFVAHL 780
 QY 781 QETSPDLDAVIBQSSSLNEASSGLFDVFLRFMCHHVRIRGKSYVOCGIPQGSILSTL 840
 DB 781 QETSPDLDAVIBQSSSLNEASSGLFDVFLRFMCHHVRIRGKSYVOCGIPQGSILSTL 840
 QY 841 LCSLCYGDMMENKLPAGIRRDGLLRLVDDFLLVTPHLLTHAKTFLRTLVRGVEYGCVVNL 900
 DB 841 LCSLCYGDMMENKLPAGIRRDGLLRLVDDFLLVTPHLLTHAKTFLRTLVRGVEYGCVVNL 900
 QY 901 RKTVPNPFVEDEALGGTAFVQMPAHGLFPMCGLLDTRTLEVSQSDYS 947
 DB 901 RKTVPNPFVEDEALGGTAFVQMPAHGLFPMCGLLDTRTLEVSQSDYS 947
 RESULT 45
 AAY00648
 ID AAY00648 standard; protein; 948 AA.
 XX
 AC AAY00648;
 XX
 DT 26-JUL-1999 (first entry)
 XX
 DE Truncated telomerase 3 protein sequence.
 XX
 KW Telomerase; human; cancer; diagnosis; melanoma; skin cancer; leukaemia;
 KW neuroblastoma; breast carcinoma; colon carcinoma; lymphoma; osteosarcoma;
 KW smooth muscle cell hyperplasia; stem cell proliferation; Wilms' tumour;
 KW stem cell differentiation; organ regeneration; organ differentiation.
 OS Homo sapiens.
 OS Synthetic.
 XX W09901560-A1.
 XX
 PD 14-JAN-1999.
 XX
 PF 01-JUL-1998; 98WO-US013835.
 XX
 PR 01-JUL-1997; 97US-0051410P.
 PR 21-JUL-1997; 97US-0053018P.
 PR 21-JUL-1997; 97US-0053322P.
 PR 04-AUG-1997; 97US-0054642P.
 PR 09-SEP-1997; 97US-0058287P.
 XX
 PA (CAMB-) CAMBIA BIOSYSTEMS LLC.
 XX
 PI Kilian A, Bowtell D;
 XX WPI; 1999-106060/09.
 DR N-PSDB; AAX18276.
 DR
 XX New isolated vertebrate telomerase genes - used to develop products for
 PT treating cancers or for organ regeneration, nerve cell or brain cell
 PT growth following injury or bone marrow transplantation.
 XX
 PS Claim 4; Fig 11ad-ae; 134pp; English.

XX CC This sequence is a truncated human telomerase of the invention. Primers
CC CC that amplify the telomerase coding sequence can be used in a method for
CC CC diagnosing cancer in a patient. The telomerase can be used for detection,
CC CC diagnosis and drug screening. Inhibitors of telomerase activity can be
CC CC used to treat cancers such as melanomas, other skin cancers,
CC CC neuroblastomas, breast carcinomas, colon carcinomas, leukemias,
CC CC lymphomas, osteosarcomas or smooth muscle cell hyperplasias or skin
CC CC growths. Enhancers of telomerase may be used to stimulate stem cell
CC CC proliferation and differentiation (expansion of haematopoietic stem cells
CC CC could be administered in the bone marrow transplant context). As well
CC CC many tissues have stem cells. Proliferation of these cells may be useful
CC CC in wound healing, hair growth, treatment of disease such as Wilms'
CC CC tumour, organ regeneration or differentiation after injury or diseases,
CC CC nerve cell or brain cell growth following injury. Note: The N-terminus of
CC CC this sequence can be replaced by the sequences shown in AAY00656-Y00658
XX CC Sequence 948 AA:
XX CC

Query Match	83.9%;	Score 5004;	DB 2;	Length 948;	
Best Local Similarity	99.9%;	Pred. No. 0;			
Matches	946;	Conservative 0;	Mismatches 1;	Indels 0;	Gaps 0;
QY	1	MPRAPRCRAVRSLLRSHYREVLP	PLATFVRRLLGPOGWR	LVOQGDPAAPFALVAQCLVCPW	60
DB	1	MPRAPRCRAVPSLLRSHYREVLP	PLATFVRRLLGPOGWR	LVOQGDPAAPFALVAQCLVCPW	60
QY	61	DARPPPAAPGFRQVSCLEKELVAR	VLORLCERGAKNVLA	FGFALLDARGGPEAFTTSR	120
DB	61	DARPPPAAPGFRQVSCLEKELVAR	VLORLCERGAKNVLA	FGFALLDARGGPEAFTTSR	120
QY	121	SYLPNTVTDALRGSGAWGLLR	RVGGDVLVHLLARCALFVL	VAPSCAYQVCGPPLYQLGA	180
DB	121	SYLPNTVTDALRGSGAWGLLR	RVGGDVLVHLLARCALFVL	VAPSCAYQVCGPPLYQLGA	180
QY	181	ATOARPPPHASGPRRLRCERAW	HSVREAGVPLG	PAPGARRRGGSASRSLPLPKRPR	240
DB	181	ATOARPPPHASGPRRLRCERAW	HSVREAGVPLG	PAPGARRRGGSASRSLPLPKRPR	240
QY	241	GAAPERTPVQGSWAHPGTRG	PSDRGFCVSPARPAEBATS	LEGALSGTRHSHPSVG	300
DB	241	GAAPERTPVQGSWAHPGTRG	PSDRGFCVSPARPAEBATS	LEGALSGTRHSHPSVG	300
QY	301	ROHHAGPSTSRPPRPMDT	PCPPVYAETKHF	LYSSGDKQOLRPSFLLSSLRPSLTGARRL	360
DB	301	ROHHAGPSTSRPPRPMDT	PCPPVYAETKHF	LYSSGDKQOLRPSFLLSSLRPSLTGARRL	360
QY	361	VFETFLGSRPWPMPGT	PRRLPLRPORYQWMP	PLFELIGNHAQCPYGVLLKTHCP	420
DB	361	VFETFLGSRPWPMPGT	PRRLPLRPORYQWMP	PLFELIGNHAQCPYGVLLKTHCP	420
QY	421	PAAGVCAREKPGQSVAAPEED	TPRRLVOLLRQHS	SPWQVYGFVRACLRLLVPPLGWS	480
DB	421	PAAGVCAREKPGQSVAAPEED	TPRRLVOLLRQHS	SPWQVYGFVRACLRLLVPPLGWS	480
QY	481	RHNERRFLRNTKFI	SLGKGAKLSIQEL	TKWVSVDCAWLRSPCVGCPVAAEHRLREI	540
DB	481	RHNERRFLRNTKFI	SLGKGAKLSIQEL	TKWVSVDCAWLRSPCVGCPVAAEHRLREI	540
QY	541	LAKPLHWMMSVYVVELLR	SPFYVTTTQKNR	LFPYRKSVMSKLQSIGIROHLKR	600
DB	541	LAKPLHWMMSVYVVELLR	SPFYVTTTQKNR	LFPYRKSVMSKLQSIGIROHLKR	600
QY	601	LSEAEVQREAR	PALLTSRLRF	IPKPDGLRPIVNM DYVVGARTFRREKRAERLTSRVKA	660
DB	601	LSEAEVQREAR	PALLTSRLRF	IPKPDGLRPIVNM DYVVGARTFRREKRAERLTSRVKA	660
QY	661	LFSVLNTERARRPGL	LGASVLGLDD	IHRAWTFFVLVRQAQDPPPELYFKVDVTGAYDTI	720
DB	661	LFSVLNTERARRPGL	LGASVLGLDD	IHRAWTFFVLVRQAQDPPPELYFKVDVTGAYDTI	720
QY	721	QDRLTEVIASII	KPQNTYCVRRYAV	VQAAHGVKRAFKSHVSTLTDLQYPMRQFAHL	780

SQ	Sequence 936 AA;	
	Query Match 82.7%; Score 4932; DB 2; Length 936;	
	Best Local Similarity 98.7%; Pred. No. 0;	
	Matches 935; Conservative 0; Mismatches 0; Indels 12; Gaps 1;	
Qy	1 MPRAPRCRAVRSLLRSHYREVLPVPLATFVRRLLGPGQWRVLVQRGDPAAPRALVAQCLVCVPW 60	
Db	1 MPRAPRCRAVRSLLRSHYREVLPVPLATFVRRLLGPGQWRVLVQRGDPAAPRALVAQCLVCVPW 60	
Qy	61 DARPPPAAPSPRQVSKLXELVARVLQRLCERGAKNVLAFGFALLDARGGGPEAFTTSVR 120	
Db	61 DARPPPAAPSPRQVSKLXELVARVLQRLCERGAKNVLAFGFALLDARGGGPEAFTTSVR 120	
Qy	121 SYLPNTVTDALRGSGAWGLLRVGGDVLVHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180	
Db	121 SYLPNTVTDALRGSGAWGLLRVGGDVLVHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180	
Qy	181 ATOARPPPHASGPRRLRCERAWNHSVREAGVPLGLPAPGARRRGGASRSRLPLPKRPR 240	
Db	181 ATOARPPPHASGPRRLRCERAWNHSVREAGVPLGLPAPGARRRGGASRSRLPLPKRPR 240	
Qy	241 GAAPEPERTVPGQSWAHPGRTGRPSDRGFCVSPARPAEAEATSLGALSCTRHSHPSVG 300	
Db	241 GAAPEPERTVPGQSWAHPGRTGRPSDRGFCVSPARPAEAEATSLGALSCTRHSHPSVG 300	
Qy	301 RQHAGPSTSRPRPMDTPCPVVAETKHFYLSGDKQELRPSFLSSLRPSLTGARRL 360	
Db	301 RQHAGPSTSRPRPMDTPCPVVAETKHFYLSGDKQELRPSFLSSLRPSLTGARRL 360	
Qy	361 VETIFLGSRPWMPGTPRRLPRLPQRYWQMRPLFLELLGNHAQCPVGLLTKHCPRAAVT 420	
Db	361 VETIFLGSRPWMPGTPRRLPRLPQRYWQMRPLFLELLGNHAQCPVGLLTKHCPRAAVT 420	
Qy	421 PAAGVCAREKPGQSWAHPGRTGRPSDRGFCVSPARPAEAEATSLGALSCTRHSHPSVG 480	
Db	421 PAAGVCAREKPGQSWAHPGRTGRPSDRGFCVSPARPAEAEATSLGALSCTRHSHPSVG 480	
Qy	481 RHNERFRLNKKFISLGHAKLSLOELTWKMSVRDCAWLRSPGVCVPAAEHRLRBEI 540	
Db	481 RHNERFRLNKKFISLGHAKLSLOELTWKMSVRDCAWLRSPGVCVPAAEHRLRBEI 540	
Qy	541 LAKFLHLMWSVYVVELLSRFFVTETTFQKRLFFYKSVMSKLSQIGIROHLKRVOLRE 600	
Db	541 LAKFLHLMWSVYVVELLSRFFVTETTFQKRLFFYKSVMSKLSQIGIROHLKRVOLRE 600	
Qy	601 LSEAEVRQHREARPAALLTSRLRFIPKPDGLRPIVNM DYVVGARTFRREKRAERLTSRYKA 660	
Db	601 LSEAEVRQHREARPAALLTSRLRFIPKPDGLRPIVNM DYVVGARTFRREKRAERLTSRYKA 660	
Qy	661 LFSVLNYERARRPGLLGASVLGLDDIHRAWRTFVLVRQAQDPPPELIPVVKVDVTGAYDTI 720	
Db	661 LFSVLNYERARRPGLLGASVLGLDDIHRAWRTFVLVRQAQDPPPELIPVVKVDVTGAYDTI 720	
Qy	721 PQDRLETVIASLIKPNQTYCYVRRYAVVQKAAHGHVRKAFKSHVSTLTLDQPYMRFQVAHL 780	
Db	711 --DRUTEVIASTLIKPNQTYCYVRRYAVVQKAAHGHVRKAFKSHVSTLTLDQPYMRFQVAHL 768	
Qy	781 QETSPLRDAVTEIQSSSLEASSGLFDVFLRFMCHHAVIRKSVVQCGIPIQGSILSTL 840	
Db	769 QETSPLRDAVTEIQSSSLEASSGLFDVFLRFMCHHAVIRKSVVQCGIPIQGSILSTL 828	
Qy	841 LCSLCYGMENKLFAGIRRDGLLLRLVDDFLVTPHLLTHAKTFURLTVRGVPEYGCVVNL 900	
Db	829 LCSLCYGMENKLFAGIRRDGLLLRLVDDFLVTPHLLTHAKTFURLTVRGVPEYGCVVNL 888	
Qy	901 RKTUVNFFVEALGGTAVQMPAHLFPWCGLLDTRTLEVSQSDYS 947	
Db	889 RKTUVNFFVEALGGTAVQMPAHLFPWCGLLDTRTLEVSQSDYS 935	
	Query Match 82.6%; Score 4923; DB 2; Length 936;	
	Best Local Similarity 98.6%; Pred. No. 0;	
	Matches 934; Conservative 0; Mismatches 1; Indels 12; Gaps 1;	
Qy	1 MPRAPRCRAVRSLLRSHYREVLPVPLATFVRRLLGPGQWRVLVQRGDPAAPRALVAQCLVCVPW 60	
Db	1 MPRAPRCRAVRSLLRSHYREVLPVPLATFVRRLLGPGQWRVLVQRGDPAAPRALVAQCLVCVPW 60	
Qy	61 DARPPPAAPSPRQVSKLXELVARVLQRLCERGAKNVLAFGFALLDARGGGPEAFTTSVR 120	
Db	61 DARPPPAAPSPRQVSKLXELVARVLQRLCERGAKNVLAFGFALLDARGGGPEAFTTSVR 120	
Qy	121 SYLPNTVTDALRGSGAWGLLRVGGDVLVHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180	
	Sequence 936 AA;	

Db 121 SYLNTVTTDALRGSGAWGLLLRRVGDVLLVHLLARCALFVLVAPSCAVQVCGPPLYQLGA 180
QY 181 ATOARPPPHASGRRRLGRCERAWNHSVREAGVPLGLPAPGARRRGSGASRSLLPKRPRR 240
Db 181 ATOARPPPHASGRRRLGRCERAWNHSVREAGVPLGLPAPGARRRGSGASRSLLPKRPRR 240
QY 241 GAAPERTPVCGSWAHPCRTGSDRGFCVVSAPAPAEATSLGALSCTRHSHPVSG 300
Db 241 GAAPERTPVCGSWAHPCRTGSDRGFCVVSAPAPAEATSLGALSCTRHSHPVSG 300
QY 301 RQHAGPSTSPRPPTWPCPPVVAETHFLYSYSGDKQLRPSFLLSRLPSLTGARRL 360
Db 301 RQHAGPSTSPRPPTWPCPPVVAETHFLYSYSGDKQLRPSFLLSRLPSLTGARRL 360
QY 361 VETIFLGSPPWPGTTPRLPRLPQRYQWRPLFLELLGNHAQCXYGLLKTHCPLRAAVT 420
Db 361 VETIFLGSPPWPGTTPRLPRLPQRYQWRPLFLELLGNHAQCXYGLLKTHCPLRAAVT 420
QY 421 PAAGVCAREKPGQSVAAPEEEDTPRRLVOLLRQSSPWQVYGFVRACLRRLVPPGLWGS 480
Db 421 PAAGVCAREKPGQSVAAPEEEDTPRRLVOLLRQSSPWQVYGFVRACLRRLVPPGLWGS 480
QY 481 RINERFLRNTKFTSLGKHAKLSLOELTWKMSVRDCAWLRES PGVGVCPAAEHLRREI 540
Db 481 RINERFLRNTKFTSLGKHAKLSLOELTWKMSVRDCAWLRES PGVGVCPAAEHLRREI 540
QY 541 LAKFLHMLSVVVELLSFFVYTTTFOKNLFFYRKSVMKLSQSIGIRQHLKRVQRE 600
Db 541 LAKFLHMLSVVVELLSFFVYTTTFOKNLFFYRKSVMKLSQSIGIRQHLKRVQRE 600
QY 601 LSEAEVRQHREARPAALLTSRLRPIPKDGLRPIVNDYVVGARTFRREKRAERLT SRVKA 660
Db 601 LSEAEVRQHREARPAALLTSRLRPIPKDGLRPIVNDYVVGARTFRREKRAERLT SRVKA 660
QY 661 LFSVLNTERARRPGLLGASVLGLDDIHRAWRTFVLVRVRAQDPPPELYFKVDVTGAYDTI 720
Db 661 LFSVLNTERARRPGLLGASVLGLDDIHRAWRTFVLVRVRAQDPPPELYFKV----- 710
QY 721 PODRLTEVIASIIKQNTYCVRRYAVQKAAHGHVRKAFKSHVSTLTDLQPYMRQFVAHL 780
Db 711 --DLTEVIASIIKQNTYCVRRYAVQKAAHGHVRKAFKSHVSTLTDLQPYMRQFVAHL 768
QY 781 QTSPLRDVAVTEQSSSLEASGLFDVFLRPMCHHAVIRKSVYVCGQIPQGSILSTL 840
Db 769 QTSPLRDVAVTEQSSSLEASGLFDVFLRPMCHHAVIRKSVYVCGQIPQGSILSTL 828
QY 841 LCSLCYGMENKLFAGIRDDGLLRVDDFLAVTHTLTHAKTFLRTLRGVPEYGVNVL 900
Db 829 LCSLCYGMENKLFAGIRDDGLLRVDDFLAVTHTLTHAKTFLRTLRGVPEYGVNVL 888
QY 901 RKTVVNFPVEDEALGCTAFVQMPAHGLFPWCGLLLDTRTLEVSQSDYS 947
Db 889 RKTVVNFPVEDEALGCTAFVQMPAHGLFPWCGLLLDTRTLEVSQSDYS 935

RESULT 48

AAW61349
ID AAW61349 standard; protein; 949 AA.
XX
XX AAW61349;
AC

25-MAR-2003 (revised)
DT 12-OCT-1998 (first entry)
XX

DE Human telomerase protein 2 (TP2) partial polypeptide.

XX TP2; human; telomerase protein 2; cancer; AIDS; ageing; therapy.

OS Homo sapiens.

XX Key Location/Qualifiers

XX 1..640

FT Protein /note= "Claim 24"

FT Protein 1..563
FT Region /note= "Claim 24"
FT Protein 582..587
FT Protein 640..940
FT /note= "Claim 22"
FT Region 644..648
FT Protein 696..953
FT /note= "Claim 24"
FT Protein 696..940
FT /note= "Claim 24"
FT Region 852..857
FT Region 884..8894

PN WO9821343-A1.

XX 22-MAY-1998.

XX 13-NOV-1997; 97WO-US021248.

XX 15-NOV-1996; 96US-00751189.

PR 11-JUN-1997; 97US-00873039.

PR 16-OCT-1997; 97US-00951733.

XX (AMGE-) AMGEN INC.

PA (AMGE-) AMGEN CANADA INC.

XX Harrington LA, Robinson MO;

XX WPI; 1998-297946/26.

DR N-PSDB; AAV27872.

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PS Claim ld; Fig 6; 150pp; English.
CC This polypeptide comprises a large portion of human telomerase protein 2 (TP2), a novel protein of the telomerase complex. Its amino acid sequence was deduced from partial cDNA clone 32 (see AAV27872), obtained from a human colon tumour cell line LIM1863 CDNA. A full-length polypeptide sequence (see AAW61350) is also disclosed. Expressing TP2 in a cell is used to increase telomerase activity and thus proliferation for treatment of e.g. HIV infection, AIDS and ageing disorders, while expressing an inactive mutant of TP2 (or molecule antisense to the gene) is used to decrease telomerase activity, e.g. for treatment of cancer. TR2 polypeptides can also be used to screen for agents that inhibit TP2 activity or its binding to TRIP1 (see AAW61347) or telomerase RNA, potentially useful therapeutically, also to raise specific antibodies useful in immunoassays and therapeutically as inhibitors. Also contemplated are transgenic animals in which the TP2 gene has been inactivated or is overexpressed. TP2 polypeptides are administered i.v., s.c. or orally, or they are delivered from engineered cells or gene therapy vectors. (Updated on 25-MAR-2003 to correct PR field.)

Sequence 949 AA;

Query Match 82.2%; Score 4900; DB 2; Length 949;
Best Local Similarity 100.0%; Pred. No. 0;

Matches 927; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPRAPRCRAVRSLRLSHRYEVLPLATFVRRLGPGQWRVLVQRGDPAAFRALVAQCILVCVPW 60

Db 23 MPRAPRCRAVRSLRLSHRYEVLPLATFVRRLGPGQWRVLVQRGDPAAFRALVAQCILVCVPW 82

QY 61 DARPPPAAPSPQVSCSLKELVARVLQRLCERGAKNVLAFGFPALLDARGGPEAPTTSVR 120

Db 83 DARPPPAAPSPQVSCSLKELVARVLQRLCERGAKNVLAFGFPALLDARGGPEAPTTSVR 142

QY 121 SYLNTVTTDALRGSGAWGLLLRRVGDVLLVHLLARCALFVLVAPSCAVQVCGPPLYQLGA 180

Db 143 SYLNTVTTDALRGSGAWGLLLRRVGDVLLVHLLARCALFVLVAPSCAVQVCGPPLYQLGA 202

QY 181 ATOARPPPHASGRRRLGECERAWNHSVREAGVPLGLPAPGARRRGGSSASRSILPLPKRPRR 240
Db |||||
QY 203 ATOARPPPHASGRRRLGECERAWNHSVREAGVPLGLPAPGARRRGGSSASRSILPLPKRPRR 262
Db |||||
QY 241 GAAPEPERTVQGGSWAHPGTRGSDRGFCVWSPARPAERATSLLEGALSGTRSHSPSVG 300
Db |||||
QY 263 GAAPEPERTVQGGSWAHPGTRGSDRGFCVWSPARPAERATSLLEGALSGTRSHSPSVG 322
Db |||||
QY 301 FOHAGPSTSRPRPMDTPCPVVAETKHFLYSSGDKQELRPSFLSSLRPSLTGARRL 360
Db |||||
QY 323 ROHAGPSTSRPRPMDTPCPVVAETKHFLYSSGDKQELRPSFLSSLRPSLTGARRL 382
Db |||||
QY 361 VETIFLGSPPMPGTPRRLPRLPQRYWQMRPLFLELLGNHQAQCPYGVLLKTHCPILRAAVT 420
Db |||||
QY 383 VETIFLGSPPMPGTPRRLPRLPQRYWQMRPLFLELLGNHQAQCPYGVLLKTHCPILRAAVT 442
Db |||||
QY 421 PAAGVCAREKPGQGSVAAPPEEDTPRRLVQLLRHSSPWQVYGFVRACLRRLVPPGLWGS 480
Db |||||
QY 443 PAAGVCAREKPGQGSVAAPPEEDTPRRLVQLLRHSSPWQVYGFVRACLRRLVPPGLWGS 502
Db |||||
QY 481 RHNERRFLRNTKFKFISLGKHAQLSLQELTWKMSVRDCAWLRSPGVGCVPAAEHRLREEI 540
Db |||||
QY 503 RHNERRFLRNTKFKFISLGKHAQLSLQELTWKMSVRDCAWLRSPGVGCVPAAEHRLREEI 562
Db |||||
QY 541 LAKFLHLMVSVVVELLSRFFYVTTTQKRLFPYKSVWSKLQSGIQRHQLKRVQLRE 600
Db |||||
QY 563 LAKFLHLMVSVVVELLSRFFYVTTTQKRLFPYKSVWSKLQSGIQRHQLKRVQLRE 622
Db |||||
QY 601 LSEAEVROHREARPALTSRLRFLPKPDGLRPIVNMVYVVGARTFRREKRAERLTSRVKA 660
Db |||||
QY 623 LSEAEVROHREARPALTSRLRFLPKPDGLRPIVNMVYVVGARTFRREKRAERLTSRVKA 682
Db |||||
QY 661 LFSVLNVERARRPGLLGASVLGLDDIHRARWTFVLRVRAQDPPPELYFVKVDVTGAYDTI 720
Db |||||
QY 683 LFSVLNVERARRPGLLGASVLGLDDIHRARWTFVLRVRAQDPPPELYFVKVDVTGAYDTI 742
Db |||||
QY 721 PODRLTEVIASIIIPQNTYCVRRYAVQKAAGHVHRKAFKSHVSTLTDLPYMQFVAHL 780
Db |||||
QY 743 PODRLTEVIASIIIPQNTYCVRRYAVQKAAGHVHRKAFKSHVSTLTDLPYMQFVAHL 802
Db |||||
QY 781 QETSLRDAVVEQSSSLEASSGLFDVFLRFMCHHVRIRKSVVOCQIPQGSILSTL 840
Db |||||
QY 803 QETSLRDAVVEQSSSLEASSGLFDVFLRFMCHHVRIRKSVVOCQIPQGSILSTL 862
Db |||||
QY 841 LCSLCYGMENKLFAGIRRDGLLLRLVDDFLVTPHLLTHAKTFLRLTVRGVPEYGCVVNL 900
Db |||||
QY 863 LCSLCYGMENKLFAGIRRDGLLLRLVDDFLVTPHLLTHAKTFLRLTVRGVPEYGCVVNL 922
Db |||||
QY 901 RKTVVNFFVEALGGTAFVQMPAHL 927
Db |||||
QY 923 RKTVVNFFVEALGGTAFVQMPAHL 949
Db |||||

RESULT 49
ADG90609
ID ADG90609 standard; protein; 1152 AA.
XX
AC ADG90609;
XX
DT 25-MAR-2004 (first entry)
XX
DE TERT consensus sequence SEQ ID NO:12.
XX
KW immune response; telomerase reverse transcriptase; TERT; cytostatic;
KW immunostimulant; cancer; cytotoxic T cell response.
XX
OS Unidentified.
XX
FN WO2004002408-A2.
XX
PD 08-JAN-2004.
XX
PF 24-JUN-2003; 2003WO-US019844.

XX 27-JUN-2002; 2002US-0393295P.
PR (GERO-) GERON CORP.
XX
XX Majumdar A, Ferber IA, Frolkis M, Wang Z;
XX WPI; 2004-071946/07.
XX
XX Eliciting an immune response in a mammal specific for its own telomerase
PT reverse transcriptase (TERT), useful for treating or preventing cancer,
PT comprises administering a composition containing TERT of another
PT mammalian species.
XX
PS Claim 10; SEQ ID NO 12; 44pp; English.
XX
XX The invention relates to a novel method for eliciting an immune response
CC in a mammalian subject that is specific for its own telomerase reverse
CC transcriptase (TERT), comprising administering an immunogenic composition
CC containing a protein with at least 20 consecutive amino acids of TERT of
CC another mammalian species, or a nucleic acid encoding the protein. A
CC composition of the invention has cytostatic, and immunostimulant
CC activity. The protein or the nucleic acid encoding the protein is useful
CC in the manufacture of a medicament for the treatment of cancer in a human
CC or for eliciting a cytotoxic T cell response in a human.
XX
SQ Sequence 1152 AA;
Query Match 75.7%; Score 4515; DB 8; Length 1152;
Best Local Similarity 76.4%; Pred. No. 0;
Matches 880; Conservative 87; Mismatches 165; Indels 20; Gaps 6;
QY 1 MPRAPRCRAVRLSHRYREVLPLATFVRLGPGQWRLVQRGDPAAFRALVAQCLVCVPW 60
Db |||||
QY 1 MPRAPRCRAVRLSHRYREVLPLATFVRLGPGQWRLVQRGDPAAFRALVAQCLVCVPW 60
Db |||||
QY 61 DARPPPAAPSFQVSCUKELVARVLQRLCERGANVLAFFALLDARGGPEPFAFTTSVR 120
Db |||||
QY 61 GARPPPAAPSFHQVSSYLKELVARVQRLCERGERNVLAFFALLDARGGPEPFAFTTSVR 120
Db |||||
QY 121 SYLPTVTTDALRGSGAWGLLRLRVGDDVLVHLLARCALFVLVAPSCAVQVCGPPLYQLGA 180
Db |||||
QY 121 SYLPTVTTDALRGSGAWGLLRLRVGDDVLVHLLARCALFVLVAPSCAVQVCGPPLYQLGA 180
Db |||||
QY 181 ATQARPPPHASG-PRRRLG-----CERAWNHSVREAGVPLGLPAPGARRRGGSSASRS 231
Db |||||
QY 181 TTQARPPPHASGPRRPVGRNFTNLGFCERAWNHSVREAGVPLGLPSPGAKRRGGSSASRS 240
Db |||||
QY 232 LPLPKRPRRGAAPERTPTVQGGSWAHPGTRGSDRGFCVWSPARPAERATSLLEGALSG 291
Db |||||
QY 241 LPLPKARRGAAPERTPTVQGGSWAHPGTRGSDRGFCVWSPARPAERATSLLEGALSG 300
Db |||||
QY 292 TRHSHPSVGRQHHAGPSTSRPRPMDTPCPVVAETKHFLYSSGDKQELRPSFLSSLR 351
Db |||||
QY 301 LSLSGSVCCCHKPSSPSSLPSPRPNAFQRLPVTAETKHFLYSSGGRRLRPSFLSSLIQ 360
Db |||||
QY 352 PSLTGARRLVETIFLGSRRPMPGTPRRLPRLPQRYWQMRPLFLELLGNHQAQCPYGVLLKT 411
Db |||||
QY 361 PSLTGARRLVETIFLGSRRPMTSGPLCTRRLSRYWQMRPLFQELLGNHARCPVYRLRS 420
Db |||||
QY 412 HCPILRAAVTPAAGVCAREKPGQGSVAAPPE-----EDTDPRRLVQLLRHSSPWQVYGFVR 466
Db |||||
QY 421 HCPILRAAVTPAAGVCAREKPGQGSVAAPPEEQEQTDLSTLMLQLLRHSSPWQVYGFVR 480
Db |||||
QY 467 ACLRLVPPGLWGSRRHNRRLRNTKFKFISLGKHAQLSLQELTWKMSVRDCAWLRSPGV 526
Db |||||
QY 481 ACLRLVPPGLWGSRRHNRRLRNTKFKFISLGKHAQLSLQELTWKMSVRDCAWLRSPGV 540
Db |||||
QY 527 GCVPAAEHRLREEILAK---FHLWMSVYVVELLSRFFYVTTTQKRLFPYKSVWSKLQSGI 583
Db |||||
QY 541 ESVPAAEHRLREEILAKFHLWMSVYVVELLSRFFYVTTTQKRLFPYKSVWSKLQSGI 600
Db |||||
QY 584 LQSIGIRQLKRVOLRELSEAEVROHREARPALTSRLRFLPKPDGLRPIVNMVYVVGAR 643
Db |||||

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Db 601 LQSIGVQHLEVRRLRELSQEVROHQEAWPAMPICRLRFIPKPNGLRPIVNMVSMGTR 660
Qy 644 TFRREKRAELTSRVKALFSLVNLVYERRRPGILGASVLGLDDIHRARWTEFVLVRAQPPP 703
Db 661 AFRGRKQAHFTQRTUKTLFSLVNLVYERTKHPHLGLGASVLGMDIYRTWRTFVLVRVALOPT 720
Qy 704 PELYFKVDVTGAYDTIPQDRLETVIASIILK-PONTYCVRRYAVVQKAAHGHVRKAFKSH 762
Db 721 PRMYFVKADVTGAYDAIPQDKLVLEVIANNIRHSESTYCIQYAVVORDAQOGVHKSFRQ 780
Qy 763 VSTLTDLPQYMKQFVAHLOET--SPIRDVAVIEQSSSLNEASSGLFDVFLPMCHAVRI 820
Db 781 VSTLSDLPQYMGQFLKHLQDSASALRNSVVEIQSISLNEASSSLFDFFLRLHRSVVKI 840
Qy 821 RGKSVVQCGIPIQGSILSTLCLSCVGMENKLPAGIRRDGILLRLVDDFLLVTHLTHA 880
Db 841 GRCRTVQCGIPIQGSLSLTLCLSCVGMENKLPFAEVORDGILLRLVDDFLLVTHLTHA 900
Qy 881 KTFELTLVRGVPYECVGNLRTKTVNFPVVEDEALGCTAFVQMPAHGLFPWCGLLIDTRTL 940
Db 901 KTFELTLVRGVPYECVGNLRTKTVNFPVVEDEALGCTAFVQMPAHGLFPWCGLLIDTRTL 960
Qy 941 EVQDSYSYARTSIRASITFNKRGKAGNMRKLFGLVRLKCHSLFGLDQVNSLQTVCTN 1000
Db 961 EVFCDYSYARTSIRASITFNKRGKAGNMRKLFGLVRLKCHSLFGLDQVNSLQTVCTN 1020
Qy 1001 IYKILLQAYRFHACVLOLPHQOQVKNPTFPLRVISDTASLCYSILKAKNAGMSLGAG 1060
Db 1021 IYKIFLLQAYRFHACVLOLPHQOQVKNPTFPLRVISDTASLCYSILKAKNAGMSLGAG 1080
Qy 1061 AAGPLPSEBAVOWLCHQAFLLKILTRHRVTYVPLLSLRTAQTSRLKPLGTTILALEAAN 1120
Db 1081 AAGSPPEAHLWCQAFLLKILTRHRVTYVPLLSLRTAQTSRLKPLGTTILALEAAN 1140
Qy 1121 PALPSDFKTIILD 1132
Db 1141 PALSTDFQTIILD 1152

RESULT 50
AAW46997
ID AAW46997 standard; protein; 807 AA.
XX AC AAW46997;
XX DT 13-AUG-1998 (first entry)
XX DE Human telomerase reverse transcriptase Delta182 variant.
XX KW Human; telomerase reverse transcriptase; hTERT; TRT; diagnosis; prognosis;
XX KW cell proliferation; cancer; ageing; ribonucleoprotein.
XX OS Synthetic.
XX OS Homo sapiens.
XX PN GB2317891-A.
XX PD 08-APR-1998.
XX PF 01-OCT-1997; 97GB-00020890.
XX PR 01-OCT-1996; 96US-00724643.
XX PR 18-APR-1997; 97US-00844419.
XX PR 25-APR-1997; 97US-00846017.
XX PR 06-MAY-1997; 97US-00851843.
XX PR 09-MAY-1997; 97US-00854050.
XX PR 14-AUG-1997; 97US-00911312.
XX PR 14-AUG-1997; 97US-00912951.
XX PR 14-AUG-1997; 97US-00915503.
XX PA (GERO-) GERON CORP.
XX PA (UYTE-) UNIV TECHNOLOGY CORP.
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XX Cech TR, Lingner J, Nakamura T, Chapman KB, Morin GB, Harley CB;
PI Andrews WH;
DR WPI; 1998-171633/16.
XX N-PSDB; AAW22382.
PT Pure and recombinant human Telomerase Reverse Transcriptase and its
PT variants - are useful in the diagnosis, prognosis and treatment of cell
PT proliferation conditions especially cancer and ageing.
XX Disclosure; Fig 20; 387pp; English.
XX The present sequence represents a human telomerase reverse transcriptase
CC (hTERT) variant from the present invention. The present invention also
CC describes the following methods: (A) determining whether a test compound
CC is a modulator of hTERT, by detecting the change in hTERT recombinant
CC protein or polynucleotide, on administration of the compound; (B)
CC preparation of a telomerase RNA component; (C) detection of the hTERT RNA or
CC of hTERT with a telomerase RNA component; (D) detection of the hTERT RNA or
CC protein in a sample by binding a relevant probe to the sample and
CC detecting the complex formed or in the case of RNA detection, amplifying
CC the product and correlating the presence of complex or amplification
CC product with presence of hTERT in the sample; and (D) increasing the
CC proliferation of a vertebrate cell by increasing hTERT expression; and (E)
CC the use of an agent that causes an increase in cell vertebrate cell
CC proliferation to create a medicament that inhibits ageing. A protein
CC preparation of hTERT and the polynucleotide encoding hTERT can be used in
CC the manufacture of medicaments for inhibiting the effect of ageing or
CC cancer. Inhibitors of telomerase activity can be used to treat conditions
CC that are associated with high telomerase activity. A protein preparation
CC of hTERT can also be used in the new methods
XX
SQ Sequence 807 AA;
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Query Match 68.0%; Score 4052; DB 2; Length 807;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 763; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MPAPRCRAVRSILRSHYREVLPATFVRRIGPQGRWLVQGRDPAAPFALVAQCIVCPW 60
Db 1 MPAPRCRAVRSILRSHYREVLPATFVRRIGPQGRWLVQGRDPAAPFALVAQCIVCPW 60
Qy 61 DARPPAPAPSPQVSCIKELVARVQLRCERAGKLVAFGLDLDGARGGPEAFTTSVR 120
Db 61 DARPPAPAPSPQVSCIKELVARVQLRCERAGKLVAFGLDLDGARGGPEAFTTSVR 120
Qy 121 SYLPTNTVTDALRGSGAWGLLRLRVGDDVLLVHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180
Db 121 SYLPTNTVTDALRGSGAWGLLRLRVGDDVLLVHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180
Qy 181 ATQARPPPHASGPRRRRGCEAWNHSVREAGVPLGAPAGARRGGASRSILPLKPRRR 240
Db 181 ATQARPPPHASGPRRRRGCEAWNHSVREAGVPLGAPAGARRGGASRSILPLKPRRR 240
Qy 241 GAAPERTPVQGSWAHPGRTGRGFCVSPARPAEATSLGALSSTRHSHPSVG 300
Db 241 GAAPERTPVQGSWAHPGRTGRGFCVSPARPAEATSLGALSSTRHSHPSVG 300
Qy 301 RQHAGPSTSRPRPMDTTPCPVYAEKHFYSSGDKQLRPSFLLSSRLPSLTGARRL 360
Db 301 RQHAGPSTSRPRPMDTTPCPVYAEKHFYSSGDKQLRPSFLLSSRLPSLTGARRL 360
Qy 361 VETIFLGSRPMPGTPRRLLPRLPORYQWMPRLFLLELGNHACQPYGVLLKTHCPRAAVT 420
Db 361 VETIFLGSRPMPGTPRRLLPRLPORYQWMPRLFLLELGNHACQPYGVLLKTHCPRAAVT 420
Qy 421 PAAGVCAREKPGQSVAAPEEEDTPRLVQLLRHSSPWQYGVFVACLRRLVPPGLWGS 480
Db 421 PAAGVCAREKPGQSVAAPEEEDTPRLVQLLRHSSPWQYGVFVACLRRLVPPGLWGS 480
Qy 481 RHNERRFLRNTKFTISLGHAKLSLQELTWKMSVRDCAWLRRSPGVCPVAAEHLRBEI 540
Db 481 RHNERRFLRNTKFTISLGHAKLSLQELTWKMSVRDCAWLRRSPGVCPVAAEHLRBEI 540
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Db	481	RHERRFLRNTKKFISLGHAKLSIQELTWKMSVRDCAWLRRSPGVCVPAEHLREEI	540
Qy	541	LAKFLHMLMSYVVVELLSRPFYVTTETTFQKNRLFFYRKSWSKLQSIGIROHLKRVOLRE	600
Db	541	LAKFLHMLMSYVVVELLSRPFYVTTETTFQKNRLFFYRKSWSKLQSIGIROHLKRVOLRE	600
Qy	601	LSEAEVROHREARPALLTSLRPFIPKPDGLRPIVNMDYVVGARTFRREKRAERLTSRVKA	660
Db	601	LSEAEVROHREARPALLTSLRPFIPKPDGLRPIVNMDYVVGARTFRREKRAERLTSRVKA	660
Qy	661	LFSVLNTERARRPGLGASVLGLDDIHRAWTFVLVRQAQDPPPELYFVKVDVTGAYDTI	720
Db	661	LFSVLNTERARRPGLGASVLGLDDIHRAWTFVLVRQAQDPPPELYFVKVDVTGAYDTI	720
Qy	721	PODLTEVIASIIKPONTYCVRRYAVVQKAAHGHVRKAFKSHV	763
Db	721	PODLTEVIASIIKPONTYCVRRYAVVQKAAHGHVRKAFKSHV	763

Search completed: August 5, 2005, 14:07:57
Job time : 197 secs

GenCore version 5.1.1.6
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OM protein - protein search, using sw model

Run on: August 5, 2005, 14:04:33 ; Search time 50 Seconds
(without alignments)
2178.348 Million cell updates/sec

Title: US-10-053-758-225
Perfect score: 5961
Sequence: 1 MPRAPRCRAVRSLLRSHYRE.....TALEAAANPALPSPDKTILD 1132
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_79:.*
1: pir1:.*
2: pir2:.*
3: pir3:.*
4: pir4:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	5961	100.0	1132	2 T03844	telomerase catalyt
2	724.5	12.2	1123	2 T51517	telomerase reverse
3	594.5	10.0	989	2 T03838	telomerase catalyt
4	395	6.6	1132	2 T31107	telomerase reverse
5	363	6.1	1117	2 T14891	telomerase (EC 2.7
6	356.5	6.0	884	2 S53396	telomerase catalyt
7	176.5	3.0	3530	2 A59266	unconventional myo
8	172.5	2.9	560	1 Q0BE3	BHLF1 protein - hu
9	144	2.4	3511	2 A52955	unconventional myo
10	142.5	2.4	1560	2 T00080	hypothetical prote
11	140.5	2.4	1892	2 T18314	hypothetical prote
12	140	2.3	1460	1 EDBE1F	immediate-early pr
13	139.5	2.3	552	2 F75311	ABC transporter, A
14	138.5	2.3	924	2 S27923	gene LF3 protein -
15	135	2.3	1356	1 C45219	N-methyl-D-asparta
16	134.5	2.3	946	2 JC7810	inositol 1,4,5-tri
17	134	2.2	606	2 G75302	orotidine 5'-phosp
18	133	2.2	1106	2 JQ0405	hypothetical 119.5
19	132	2.2	860	2 S55543	RNA-directed DNA p
20	131.5	2.2	1184	2 G01763	atrophin-1 - human
21	131	2.2	1446	1 A45344	immediate-early pr
22	130.5	2.2	1184	2 S50832	atrophin-1 - human
23	130.5	2.2	2715	2 T13049	eyelid - fruit fly
24	129.5	2.2	383	2 S32975	gene BCRF2 protein
25	129	2.2	403	2 S52796	prpl2 protein - hu
26	129	2.2	1776	2 G86280	protein TSE2.13 [
27	128.5	2.2	628	2 S01955	hypothetical prote
28	128	2.1	376	2 C75580	adenine deaminase-
29	127.5	2.1	1048	2 T31425	C-terminal domain-

ALIGNMENTS

RESULT 1

T03844
telomerase catalytic chain - human
N:Alternate names: telomerase reverse transcriptase
C:Species: Homo sapiens (man)
C>Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004
C:Accession: T03844
R:Nakamura, T.M.; Morin, G.B.; Chapman, K.B.; Weinrich, S.L.; Andrews, W.H.; Lingner, J.
Science 277, 955-959, 1997
A:Title: Telomerase catalytic subunit homologs from fission yeast and human.
A:Reference number: Z15111; MUID:97400623; PMID:9255227
A:Accession: T03844
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-1132 <NAK>
A:Cross-references: UNIPROT:O14746; EMBL:AF015950; NID:g2330016; PIDN:AAC51672.1; PID:g-
A:Experimental source: kidney
C:Genetics:
A:Gene: TRT
A:Map position: 5p

Query Match	100.0%	Score 5961	DB 2	Length 1132
Best Local Similarity	100.0%	Pred. No. 0		
Matches 1132	Conservative 0	Mismatches 0	Indels 0	Gaps 0
QY	1	MPRAPRCRAVRSLLRSHYREVLPATFVRRLGPGQWRVLVQRCDDPAAFRALVAQCLVCPW	60	
DB	1	MPRAPRCRAVRSLLRSHYREVLPATFVRRLGPGQWRVLVQRCDDPAAFRALVAQCLVCPW	60	
QY	61	DARPPAAPSPROVSKELVARVLQRLCERGAKNVLAFGFALLDGGAGGPPPEFTTSVR	120	
DB	61	DARPPAAPSPROVSKELVARVLQRLCERGAKNVLAFGFALLDGGAGGPPPEFTTSVR	120	
QY	121	SYLPTNTVDALRGSGAWGLLRVGGDDVLVHLLARCALFVLVAPSCAYQVCGPPPLYQLGA	180	
DB	121	SYLPTNTVDALRGSGAWGLLRVGGDDVLVHLLARCALFVLVAPSCAYQVCGPPPLYQLGA	180	
QY	181	ATQARPPHAGSPRRRLRCERANWHSREAGVPLGLPAGARRRGGSASRSLPLPKRPRR	240	
DB	181	ATQARPPHAGSPRRRLRCERANWHSREAGVPLGLPAGARRRGGSASRSLPLPKRPRR	240	
QY	241	GAAPPEPTPVQGSWAHPGTRGSDRGFCVSVSPARPAEEATSLEGALSGRTHSHPSVG	300	
DB	241	GAAPPEPTPVQGSWAHPGTRGSDRGFCVSVSPARPAEEATSLEGALSGRTHSHPSVG	300	
QY	301	RQHAGPSTSRPRPMDTPCPVVAETKHFLYSSGDKQLRPSFLLSSLRPSLTGARRL	360	
DB	301	RQHAGPSTSRPRPMDTPCPVVAETKHFLYSSGDKQLRPSFLLSSLRPSLTGARRL	360	
QY	361	VETIFLGSRPWMPGTPRRLPRLPQRYQWMRPLFLELLGNHQAQCPYGVLLKTHCPRAAVT	420	
DB	361	VETIFLGSRPWMPGTPRRLPRLPQRYQWMRPLFLELLGNHQAQCPYGVLLKTHCPRAAVT	420	

proline-rich prote
actin-depolymerizi
probable mucin DKF
mixed-lineage prot
hypothetical prote
hypothetical prote
probable nucleic a
transposase, uncha
pol protein - silk
Wiskott-Aldrich sy
wiskott-aldrich sy
viral proteinase -
tenascin Y precurs
immediate-early pr
N-methyl-D-asparta
hypothetical prote

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Qy 421 PAAGVCAREKPGQGSVAAPAEEDTDPRRLVQLLRQHSSPMQVYGFVRACLRLVPPGLWGS 480
Db 421 PAAGVCAREKPGQGSVAAPAEEDTDPRRLVQLLRQHSSPMQVYGFVRACLRLVPPGLWGS 480
Qy 481 RHNEERFLRNTKFTSLGKHAKLSLOELTWKMSVRDCAWLRRSPGVCVPAAEHRLREEI 540
Db 481 RHNEERFLRNTKFTSLGKHAKLSLOELTWKMSVRDCAWLRRSPGVCVPAAEHRLREEI 540
Qy 541 LAKFLHLWMSVYVVELLSFFVYTTTQKRLFFYRKSVMKLSQSGIRQHLKRVQVLR 600
Db 541 LAKFLHLWMSVYVVELLSFFVYTTTQKRLFFYRKSVMKLSQSGIRQHLKRVQVLR 600
Qy 601 LSEAEVRQHRREARPAALLSRFLPKPDGLRPIVNMDDYVGARTFRREKRAERLTSRVKA 660
Db 601 LSEAEVRQHRREARPAALLSRFLPKPDGLRPIVNMDDYVGARTFRREKRAERLTSRVKA 660
Qy 661 LFSVLNYERARRPGLLGASVLGLDDIHRARWTFVLRAQDPPPELYFVKVDVTGAYDTI 720
Db 661 LFSVLNYERARRPGLLGASVLGLDDIHRARWTFVLRAQDPPPELYFVKVDVTGAYDTI 720
Qy 721 PQDRLETVIASIIKPNQTYCVRRYAVVQAAHGHVKAFKSHVSTLTLDQPYMRQFVAHL 780
Db 721 PQDRLETVIASIIKPNQTYCVRRYAVVQAAHGHVKAFKSHVSTLTLDQPYMRQFVAHL 780
Qy 781 QETSLRDAVIEQSSSLNEASSGLFDVFLRPMCHAVIRGKSYVQCGIPQGSILSTL 840
Db 781 QETSLRDAVIEQSSSLNEASSGLFDVFLRPMCHAVIRGKSYVQCGIPQGSILSTL 840
Qy 841 LCSLCYGMENKLFAGIRBDGLLRLVDDELLVTPHLTHAKTFLRTLVRGPEYGCVVNL 900
Db 841 LCSLCYGMENKLFAGIRBDGLLRLVDDELLVTPHLTHAKTFLRTLVRGPEYGCVVNL 900
Qy 901 RKTVMNFFVEALGGTAFVQMPAHGLFPWCGLLDDTRTLEVOSSYSSYARTSIRASLTF 960
Db 901 RKTVMNFFVEALGGTAFVQMPAHGLFPWCGLLDDTRTLEVOSSYSSYARTSIRASLTF 960
Qy 961 NRGKAGNRMRKLFGLVRLKCHSLFLDLQVNSLTQVCTNIVKILLQAYRFHACVLQLP 1020
Db 961 NRGKAGNRMRKLFGLVRLKCHSLFLDLQVNSLTQVCTNIVKILLQAYRFHACVLQLP 1020
Qy 1021 FHQVWKNTPLRLVISTASICYSILKAKNAGSLGAKGAGLPSEAVOMLCHOAELL 1080
Db 1021 FHQVWKNTPLRLVISTASICYSILKAKNAGSLGAKGAGLPSEAVOMLCHOAELL 1080
Qy 1081 KLTHRVTVYVPLGLSLRTAQTLSRLPGTTLTALAAANPALPSDFKTILD 1132
Db 1081 KLTHRVTVYVPLGLSLRTAQTLSRLPGTTLTALAAANPALPSDFKTILD 1132

RESULT 2
TS1517
telomerase reverse transcriptase - Arabidopsis thaliana
N:Alternate names: protein F5E19_190
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 18-Aug-2000 #sequence_revision 18-Aug-2000 #text_change 09-Jul-2004
R:Sato, S.; Nakamura, Y.; Kaneko, T.; Kato, T.; Asamizu, E.; Kotani, H.; Tabata, S.; Mew
submitted to the Protein Sequence Database, August 2000
A:Accession: TS1517
A:Reference number: Z25394
A:Accession: TS1517
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1123 <SAT>
A:Cross-references: UNIPROT:Q9SPU7; EMBL:AL391147
A:Experimental source: cultivar Columbia; BAC clone F5E19
C:Genetics:
A:Map position: 5
A:Introns: 100/3; 125/3; 147/3; 185/1; 300/3; 325/1; 369/2; 414/3; 765/3; 942/2; 1033/2
A>Note: F5E19_190

Query Match 12.2%; Score 724.5; DB 2; Length 1123;
Best Local Similarity 23.8%; Pred. No. 3.2e-41;
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Matches 294; Conservative 199; Mismatches 511; Indels 233; Gaps 39;
Qy 1 MPRAPRCRAVRSLLRSHYREVLPLATFV-----RRLGPGQGR-----L 38
Db 1 MPRKPRHRVPEILLWRLFGNRAARNLDAI VDLI PNRTIQPEQCRGCGCLGSSDKKPAFL 60
Qy 39 VQRGDPAAFRALVAQCLVCPWDARPPPAAPSFRQVSLKELVARVLQRL---CERGAKN 95
Db 61 LRSDDPITHYRKLHRCFV-VLHEQTPPLDDSPTSWMSQREIIVERIIEEMOSGCD--CON 117
Qy 96 VLAFGFALLGARGGPEAFTTSVRSVLPNTVTDALRGSGAGWLLLRVGGDDVLVHLIAR 155
Db 118 VICARYDKYDOS-----SPILSILT-SSWFEELKRVGHVDMVYLLOQ 159
Qy 156 CALFVLVAPSCAYQVCGPPPLYQLGAAT-----QARPPPHASGPRRLRGCEAANHSVRE 209
Db 160 TSIFLPLLGKKHQVSGPPLCIKHKRTLSVHENKRRDDNVQPTTKRQLWSSAVDDCPKD 219
Qy 210 AGVPLGLPAG-----ARRRGSASRSLPLPKRPRGA-----APEPTPVGQGSWA 257
Db 220 DSATI-TPIVGEDVDHREKTKTKRSRIYLRKRRKQKRVNPKVDNACAPITP----- 271
Qy 258 HPGRTGPSDRGFCVSPARPABEATSLEGALSGTRHSHPSVGRQHHAGPSTSRPPRP 317
Db 272 ---STNGKVTG-----NDEMNLHIGINGSLTDFVKQAKQ----- 303
Qy 318 DTPCPVYAEATKFLYS-SGDKEQLRPSFLSLSLRPSLTGARRLIVETIFLGSRRPMPGTP 376
Db 304 -----VKRNKPKFGLSETYSVIPNHILKTLRPNCSDSLMLMNHIFGSEVNMSTTPS 356
Qy 377 RRLPRLPQ-----RYWQMRPLFLELLGHAQCPYVLLKTHCP-----LRAAVTPAAG 424
Db 357 HGKNCPSGSGICLYHSLKSLKLNIGTKSHLKMLLDKHCPVLLQLODALKSGTTSQSS 416
Qy 425 VCAREK-----PQGSVAA-----PEEEDTDRELVLQLLRQHSSPMQVYGFVRACLRLVPPG 476
Db 417 --RQKADKPLHGSSSQTKPKCPSVEERKL-----ICTNDQVVSFIWICRIYVDES 468
Qy 477 LMGSRHNRERPLRNTKFPISLGKHAQLSLOBLTWKMSVRDCAWLRRSPGVCVPAAEHRL 536
Db 469 LLGTHQMRVLKRNIAFVSRNRNEKCTVQFLHKVXPSDFPPFARKE--LCCMVNGHEL 526
Qy 537 REE-----ILAKFLHLWMSVYVVELLSFFVYTTTQKRLFFYRKSVMKLSQSIG 588
Db 527 QSESIRSTQOMLCTKWISLWFLFVVKLVHFNFTATESQGGRLNIYYTRKSWERLISKE 586
Qy 589 IROHLKRVQLRELSEAEVROHREARPAALLTSRLRFPKPDGLRPIVNMDDYVVGARTFRRE 648
Db 587 ISKALDGYLVDDAEASSRK-----LSKFRFLPKANGVRMVD-----FSSS 630
Qy 649 KRAERLTSRVKALFSVLNYERARRPGLLGASVLGLDDIHRARWTFVLRAQDPP-PELY 707
Db 631 SRSQSL---RDTHAVLKDIQLKEPFDVLGSSVFDHDDFYRNLCVPLIHLRSQSGLPPLY 686
Qy 708 FVKVDVTGAYDTIPQDRLTEVIAIIKPNQTYCVRRYAVVQAAHGH-----YRKAPKS 761
Db 687 FVADVFKAFDSDVDQGLLHVLIQSLFKDE--YILNCRCLVCCGRKSNMWNKILVSSDKNS 744
Qy 762 HVSTLTDLQPYMRQFVAHLQBSTPLRDAVIEQSSSLNEASSGLFDVFLRPMCHAVIR 821
Db 745 NFSRTSTVPYNA-----LQ-----SIVVDKGENHRVKKDLMWITGNMLKNNMLQID 792
Qy 822 GKSYVQCGIPQGSILSTLCSLCYGMENKLPAGI-----RRDGL----- 862
Db 793 KSFVYQIAGIPQGHRLSSLLCCFYVYGHLERTLIVPFLBEASKDVSSKECSREEELIPTS 852
Qy 863 --LLRLVDDPELLVTPHLTHAKTFLRTLVRGPEYGCVVNLKRTVNVNPPVEDE----- 912
Db 853 YKLLRFIDDDYLFVSTSRDQASSFHYRLKHGPKDYNCFMNETKFCINCFDKBEHRCSNRM 912
Qy 913 --ALGGTAFVOMPAHGLFPWCGLLDDTRTLEVOSSYSSYARTSIRASLTFNRGKAGNRM 970
Db 913 FVGDNVGFVFR-----WTGILLINSRTFEVQVDYTYLSGHLSSTSVAWQNKPVN 964
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Qy      971 RRKLFGLRLKCHSLFDLDQVNSLQTCTNYIKILLQAVRFHACVLQLPFFHQOVWK-NP 1029
Db      965 ROKLCYFLVPCKPHILFDSNINSGEIVRLNIYOIFLLAAMKFHCYYVEV---SRFWKLHP 1021
Qy     1030 TTFRLRVIDSTASLCYSTLKAKNAAGMSLGAK-GAAGPLPSEAVOMLCHOAFLLKLTTRHYT 1088
Db     1022 QTLFKFTISVRWFRLINRRVRINTGSSFRPVLYKEEVIWLGDIDAYIOVLKKONS 1081
Qy     1089 YVPLLGSRLRTAOQT--LSRKLPGTTLTALEAAANPAL 1123
Db     1082 YMLLIYLKSALSCHSLSQSLSSELRYATDRSNSSL 1118

RESULT 3
T03838
telomerase catalytic chain - fission yeast (Schizosaccharomyces pombe)
N;Alternate names: telomerase reverse transcriptase 1
C;Species: Schizosaccharomyces pombe
C;Date: 23-Apr-1999 #sequence revision 23-Apr-1999 #text_change 09-Jul-2004
C;Accession: T03838; T03839; T40085
R;Nakamura, T.M.; Morin, G.B.; Chapman, K.B.; Weinrich, S.L.; Andrews, W.H.; Lingner, J. Science 277, 955-959, 1997
A;Title: Telomerase catalytic subunit homologs from fission yeast and human.
A;Reference number: Z15111; MUID:97400623; PMID:9252327
A;Accession: T03838
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-989 <NAK>
A;Cross-references: UNIPROT:O13339; EMBL:AF015783; NID:g2340167; PIDN:AAC49803.1; PID:g2420168
A;Experimental source: strain 972h(-)
A;Accession: T03839
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-524, 526-989 <NA2>
A;Cross-references: EMBL:AF015783; NID:g2340167; PIDN:AAC49802.1; PID:g2340168
R;Lyne, M.; Rajandream, M.A.; Barrell, B.G.; Voickaert, G. submitted to the EMBL Data Library, March 1998
A;Reference number: Z21904
A;Accession: T40085
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-524, 526-989 <LYN>
A;Cross-references: EMBL:AL022299; PIDN:CAA18391.1; GSPDB:GN00067; SPDB:SPBC29A3.14c
C;Genetics:
A;Gene: trt1; SPBC29A3.14c
A;Map position: 2
A;Introns: 86/3; 113/3; 153/2; 241/1; 372/1; 395/3; 485/3; 524/3; 582/2; 644/1; 653/3; 7
C;Keywords: alternative splicing

Query Match          10.0%; Score 594.5; DB 2; Length 989;
Best Local Similarity 22.3%; Pred.No. 2e-32;
Matches 238; Conservative 202; Mismatches 380; Indels 247; Gaps 42;

Qy      5   PCRVAWSLRSHRYEVLPPLATEFVRRLPGOGMWELVGDPGAFAFRALVAACL----- 55
Db      7   PKSKRLR-FLENQVYLCTLNDVV-----QLVLRGSPASSYSNICERLSDVTSPFS 57
Qy      56   -----VCVPWDARPPPAAPSFRQVSCLK-ELVARVLQRLCERG----AKNVLAFGPAL-ID 105
Db      58   IFLHSTVVGFDSPDEGV-QFSSPKCSQSSELIANVVKOMPDESFERRRLLMKGFSGMHNE 116
Qy     106   GARGGPPEATTTSVRSVLPNTVDALRGSAWGALLRRVGGDDLVHLARCALFVLVAPS 165
Db    117   DFRAMHVNGQNDLVSTFPNYLISILE-SKNQQULLIEIGSDAHMYLLKSGSFEPALPD 175
Qy     166   CATQCVCPPPLYQLGAATAQRPPPHASGRPRRLGCERAWNHVSREAGVPLGLPAPGARRRG 225
Db    176   NYLQISGIPLPK-----NNVFEEIV-----SKKKX 200
Qy     226   GSASRSIPLPKRPRRGAAPPERTPVQGGSWAHPGTRGPSDRGFCVWSPARPAEATS 285

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Db 201 RTTETSIQNKSARK-----EVSW----- 211
 Qy 286 EGALSGTRHS--HPSVGRQHAGHPSTSRPRPMDTPCPPVYAETKHF-LYSSGDGKEQLR 342
 Db 220 -NGISISRFSIFYRSSYKK-----FKQDLVFNLSICIDRNTVH 256
 Qy 343 PSFLLSSLSLGTG-----ARRLVETIFLGSRRPMPGTPRRL-----PRLPORYWQMPRL 392
 Db 257 --MWLOWIFRQGLINAFQVQLHKVIFLVSOSTV--VPKRLLKVVPLIEQTAKRLHRI 312
 Qy 393 FLELLGNHAGCPYGVLLTKHCPLRAAAVTPAAGVUCAREKPGSGVAAPBEEDTPRRLVOLL 452
 Db 313 SLSKVYNH-YCPY---IDTH-----DDE-----KIL 334
 Qy 453 RQHSPPQVGVFVRACLRRLLVPGLWGRSRRNERPRLNTKFPISLGKHAUKLSOELTWOM 512
 Db 335 SYSCLKNQVAFRLSILVRVFPKLWGNORIFEIILKDLFTFLKLSRYESFSLHYLSMNI 394
 Qy 513 SVRDCAWL---RSPGVGCVPAAEHRLREBEILAKFLHMLSVVYVVELLRSFFYTETTFQ 569
 Db 395 KISEIEWLVGKKSNAKML--SDFEKRRQIFAEFIYWLNSFIPIQLQSFFYITESDL 452
 Qy 570 KNLRLFFYRKSVKSLQSIGIRQHLKRVQLRELSAEARVQHREARPALLTSLRIFPKPDG 629
 Db 453 RNRVTYFRKIW-KLLCRPFIITSMKEAFSEKINENNVMDTQ-KTTLPPAVIRLLPKKNT 510
 Qy 630 LRPIVMNDYVGARTFRPREKARELTSRVKALFSVLNYERARRP-----GLGASVLGL 683
 Db 511 FRLLITNL-----RKRFLLIKQMGSKKMLVST---NOTLRPVASILKHLINBESSGI 558
 Qy 684 D--DIHRAWRTF---VLRVRAODPPPELYFVKVDVTGAYDTIPQDRLTEVIASLIKPN 737
 Db 559 PFNLEVMYKLLTKKOLLKRMFG--RKKTFRVIDIKSCVDRIKQDLMFRIKVKKKLDKPE 616
 Qy 738 TYCVRRYAVVQKAAGHVRKAFKSHSVTLTDLQPYMRQFVAHLQETSPLRDAVAVIEQSS 797
 Db 617 -FVIRKYATIH-ATSDRATKNFVSEAFSYEDMPFEKVVOLLSMKTS---DTLFVDFVDY 671
 Qy 798 LNEASSGLPDVFLRPMCHAVRIGKSYVQCGIPOGSIILTLCSLCYCGDMENKLPAGI 857
 Db 672 WTKSSSEIFKMLKEHLSGHVTKVIGNSQYLOKVGIPQGSILSSFFCHTFYMEDLIDEYLSFT 731
 Qy 858 RRDG-LLLRLVDDFLVTPHLTHAKTFLRTLVRGVPEYGCVVNLRKTVNPNPVDDEALGG 916
 Db 732 KKGSVLLRVVDDFLFTVYNKDAKKFLNLSRGFEKHNFPSTSEKTVINPENSNGIINN 791
 Qy 917 TAFVQMPAHGLFPWCGLLDRTLLEV-----QSDYSSYARTSTIRASITFNRGFKAGRNMR 971
 Db 792 TPFNESKR--MPFFGFSVNMRLDTLLACPKIDEALFNSTSVBELTKHMGKSF-----842
 Qy 972 RKLFGVLRLLKCHS---LFLDLQVNSLTQVCTNIYKI-----LLLOAY 1010
 Db 843 --FYKILRSLASFAQVFIDITHNSKFNSCCNIRYLGYSCMCAQAY 887

RESULT 4
 T31107
 telomerase reverse transcriptase - Oxytricha trifallax
 C/Species: Oxytricha trifallax
 C/Date: 02-Sep-2000 #sequence_revision 02-Sep-2000 #text_change 09-Jul-2004
 C/Accession: T31107
 R:Bryan, T.M.; Sperger, J.M.; Chapman, K.B.; Cech, T.R.
 Proc. Natl. Acad. Sci. U.S.A. 95, 8479-8484, 1998
 A/Title: Telomerase reverse transcriptase genes in Tetrahymena thermophila and
 A/Reference number: Z20985; MUID:98337940; PMID:9671703
 A/Accession: T31107
 A/Status: preliminary; translated from GE/EMBL/DBJ
 A/Molecule type: DNA
 A/Residues: 1-1132 <BRY>
 A/Cross-references: UNIPROT:O76332; EMBL:AF060230; NID:g33342795; PID:g33342796;
 C/Genetics:
 A/Genes: TERT

R;Du, Z.
submitted to the EMBL Data Library, February 1995
A:Description: The sequence of *S. cerevisiae* cosmid 8543.
A:Reference number: S53390
A:Accession: S53396
A:Molecule type: DNA
A:Residues: 1-884 <DUZ>
A:Cross-references: UNIPROT:Q06163; EMBL:U20618; NID:g2258165; PID:g662136; GSPDB:GN0001
A:Experimental source: strain S288C (AB972)
C:Genetics:
A:Gene: SGD:EST2; MIPS:YLR318W
A:Cross-references: SGD:S0004310; MIPS:YLR318W
A:Map position: 12R

Query Match 6.0%; Score 356.5; DB 2; Length 884;
Best Local Similarity 22.1%; Pred. No. 3.1e-16;
Matches 167; Conservative 127; Mismatches 309; Indels 151; Gaps 28;
QY 329 KHLVSSGDKQLRPS--FLLSLRPSLTGARRLV---ETIFLGSRPWPGTPRRLPLRP 383
DB 185 KQFLH---KLNINSSFFPYSKILPSSSIKGLTDLREAIF-----PTNLVKIP 230
QY 384 QRYWQMRPLFLE-LLGNHAQCPGVLLKTHCPRAAVTPAAGVCAREKPGGVAAPDEED 442
DB 231 QRLKVRINLTQQLKLRKRLNYSILNSICP-----PLEGTVL----- 269
QY 443 TDPRLVLQRLHSSPWQVYVFRACRLRLVPPGLWGRHNRFRRLNTKKFISLGKIAK 502
DB 270 ----DLSHLSRO-SPKRVLKIIVILQKLLQEMFGSKNKGKIKNLLLSLPLNGY 324
QY 503 LSLQELTWKMSVRDCAWLRSPGVGCVPAAEHLRL--EELAKFLHWSVYVVELLSRF 560
DB 325 LPEFDSLLKRLKDFRML---FISDIWTKNFENLNQLAICFISWLPQLIPKIIQTF 380
QY 561 FYVTETTPQKNRLFVRKSVWSKLSQIGIRQHLKRVQLRELSEAEV-ROHREARPAALT- 618
DB 381 FYCTEIS-STVTIVYFRHDTWKNLITPFIYVEFKTY-----LVNNVCRNHSYTLNFNH 435
QY 619 SRLRFPKPDGLRPIVNMDDYV-----GARTFRREKRAERLTSRVKALFSLVNYERAR 672
DB 436 SKNRIIPKKS-----NNEFRIIAPCRGADSEEFYIKENHNKAIQPTOKILEYLRNCR 489
QY 673 PGLGASVLGLDDIHRAMRTFVLRV--RAQDPPPELYFKVDVGTAYDITPQDRLTEVIA 730
DB 490 PTFST-TKIYSPQIADRIKEFKORLLKFNVLPELYFKFVKDVKSCYDSI PRMECWRLK 548
QY 731 SIIKPONTVCVRYAVVQAAHGHVRKAFKSHVSTLTDLOPYMRQFVAHLQETSPURDAV 790
DB 549 DALKNENGPFVRSQYFFN--TWTGVLKLF-NVYNASRVKPY-----EL 589
QY 791 VIEQSSSLNEASSGLPDLFRMCHHAVIRKGSYVQCQIGIPQGSITLSTLLCSLCYGDN- 849
DB 590 YIDNVRTVHLSQDVINVVEMEIFKTALWVEDKCYIREDLGFGQSSLSAPIVDLVYDDL 649
QY 850 --ENKLFAGIRRGILLRLVDVDFLLVTHLTHAKTFLRTLVRGVYPYGVCMRLKTV-VN 906
DB 650 EYSEFKASPSQDTLLKLADELIIISTDQOQVINIKKLMGGFPQYNKAKNEDKILAVS 709
QY 907 FPVEDBALGGTAFVQMPAHGLFPWCGLLDLTRLEVOSSYSSYARTSIRASLITFNKGPKA 966
DB 710 SQSDDDT-----VIOFCAMHIFVKELEVKHSSTNNPHIRS-----KS 748
QY 967 GRNMRKLFGLVRLKCHSLFLDLQVNSLOTVCNTI-----YK-----ILLQA 1009
DB 749 SGIGFSLIALFNTRISYKTIIDTNLSNTVLMQIDHVVKNISSECYKSAFKOLSINVTQN 808
QY 1010 YRFHACVLQLPFHQVQWKNPTFLRVISDTASLC 1043
DB 809 MQFH-----SFLQRIENTVSC 826

RESULT 7
A59266

unconventional myosin-15 - human
C:Species: Homo sapiens (man)
C:Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 09-Jul-2004
C:Accession: A59266
R:Liang, Y.; Wang, A.; Belyantseva, I.A.; Anderson, D.W.; Probst, F.J.; Barber, T.D.; M.
an, T.B.; Fridell, R.A.
Genomics 61, 243-258, 1999
A:Title: Characterization of the human and mouse unconventional myosin XV genes respons
A:Reference number: A59266; MUID:20021762; PMID:10552926
A:Accession: A59266
A>Status: preliminary; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-3530 <LIA>
A:Cross-references: UNIPROT:Q9UKN7; GB:AF144094; NID:g6224682; PID:AAF05903.1; PID:g62
F:1225-1887/Domain: myosin motor domain homology <MMO>
Query Match 3.0%; Score 176.5; DB 2; Length 3530;
Best Local Similarity 20.6%; Pred. No. 0.0041;
Matches 263; Conservative 144; Mismatches 392; Indels 475; Gaps 68;
QY 107 ARGGPPEAFRTTS-----VRSYLP-----NTVTDALRGGGAWG 138
DB 2313 SRGGKVVFGNSWDSDEDMSTRPQOEHPKVLDSGYSYSHNQDGTNGTEAQRGT-ATH 2371
QY 139 LLLRRVGDVLLHLLARCALFVLVAP-----SCAYQVCGPPLYQLGAA----- 181
DB 2372 QESDSLGEPAVPHKGLDCLYDLSLFDVLSYGDADLEKPTAIAYRMKGQGPQGGSSSGTE 2431
QY 182 -TQARPP---PHASGPRRLGCERAWNHSVRAGV---PLGLPAPCARRRGGSSAS-RSLP 233
DB 2432 DTPRPPEPKPTIGLDASTLALQQAIFH--KQAVLLARGMTTQATLQAOPLSAALRSLP 2489
QY 234 LPKRRRGAAAPERTPVGGGSAHPGRTRGPRSDRGFCVVSPARPAEATELEGALSGTR 293
DB 2490 ASKPP-----APAAQPTSVGTGPPAPVLR-----ATPKPLAPA----- 2524
QY 294 HSHPSVGRQHHAGPSTSRPPMPDTPCPVYA-----ETKHFLYSSGDKQLRSPFLL 347
DB 2525 -----PLAKAPRLPIKPAAPVLAQQAQSPET-----TSPSELVRYSTLN 2565
QY 348 SSLRPSLTGARLLETIFLGSRPWPGTPRRLPLRPQRYWQMRP-----LFLELLGNH 400
DB 2566 SEHFPT--QQIKNIVRQYQQPFRGRPEALRKDGKGVKMRKPPDPHEALMILKQOMTH 2623
QY 401 AQCPYG-----VLLK--THCPLRAAVTPAAGVCAREKPGGSAVAPEE-EDTDPRRLV 449
DB 2624 LAAAGTQVSRRAVALVKVTSAP-RPSMAPTSAL-----PSSLEPPELTQTLRHLRI 2677
QY 450 --QLLRQSHSSPMQVYGFVR-----ACLR-----RL 472
DB 2678 NENFYGYQDAPWKI--FLRKEVFPKDSYHPVQLDLLFRQILHDLTSEACLRISDERL 2735
QY 473 VPPGLWGRSHNRERRFLNRYKFIISLG-KHAKLSLOELTWKMSVRDCAWLRSPSGVCVPA 531
DB 2736 RMKALFAQOQ-----LDTQKPLVTSVKRAVVSTARDTWEV-----YFSRIFPATGSVGT 2785
QY 532 ASHRLREELTAKFLHWSVYVVELLR-----SFFVYVTEFTT-OKNR 572
DB 2786 G-----VQLLA-----VSHVGIKLLRMVMVKGQAGGQLRVLRAYSFADILFTVMPSONM 2834
QY 573 LFFYRKSVMWSKLSQIGIRQHLKRVQLRELSEAEVQRHREARPAALTSLRLRFPKPDGLRP 632
DB 2835 LEFNLAS--EKVILSARAH---QVKTLDVDFILELKK----- 2867
QY 633 IVNMDYVVGARTFRREKRAERLTSRVKALFSLVNYERA-----RRPGLLGAS----- 679
DB 2868 --DSDYVAVARNFLPEDPA-----LLAFHKGDIIHLQPLEPRVGVSGACVVR 2913
QY 680 --VLGLDDIHR-----AWRTFVLVRQAQDPPPELTFVKVDVTGAYD-----TIP-QDRLT 726
DB 2914 RKVYVLEELRRRGPDPFGWRFGTIGHRGVGRFPSEL-----VOPAAAPDFLOLPTPEGRGAA 2969
QY 727 EVIASIIRKPNQTCYVRRY-----AVVQKAAHGHVRKAFKSHVSTLTDLOPYMRQFVAHLQ 781

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Db 2970 AVAAVAGAAAEVRRREGPPVARSADHGEDALALPPY-TMLEFAQKFRDQRRPQ 3028
QY 782 E-----TSPRLDAVVIEQSSLINEASSGLFDFVFLRFMCHAVR 819
Db 3029 DGLRLKKEPRESRTLEDMLCTKTPLQESLIELSDSLSKWATDMFLAVRMFGDAPLK 3088
QY 820 IRGKSYVOQGIPOGSIILSLCSICYGD---MENKLPAGI-----RRDG 861
Db 3089 GQSDLDVLN-----LLKLC-GDHEVMRDECYQVVKQITDNTSSKQDSCQGW 3136
QY 862 LLRLVDDF---LLVTPHLTHAKTFLTLVR--GVPEYG---CVNLRKTVNFFVED 911
Db 3137 RLLYIVTAYHSCSEVHHLTR---FLQVSRTPGLPFGGIKACQEQNLQKTL----- 3186
QY 912 EALGCTAFVQMPAHGLFPWCGLLLDTRTEVQSDYSYARTSIRASLTFRNGFKAGNNR 971
Db 3187 -RFGG-----RLPSS-----TELRAWL-----AGRSSK 3210
QY 972 RKLK---GV---LRLKCHSLFLDQVNSLQTVCT-----NIYKILLQLQYRPHA 1014
Db 3211 RQLFLPGLGLERHLKIKTKTVALDV---VEEICAEMALTRPEAFNEYVIFVVTNRGQHV 3266
QY 1015 CVL-----QLPEHQVWKNPTEF-----LRVSDTASLCY 1044
Db 3267 CPLSRRAVLIDVASEMEQVGGYMLWFRKVLMDQLKFENELYVTMHNQVLPDYLKGLF 3326
QY 1045 SILKARNAGMSIGAKGAAPLFPSEAVQWMLCHQAFLLKLTTRHVT---YVPLLGLSLRTAQ- 1100
Db 3327 SSVPASR-----PSEQ---LLQVSKLASLQHRKADHFYLP---SVREYQE 3366
QY 1101 ---TQLSRKLPGTT 1111
Db 3367 YIPAQLYRTTAGST 3380

RESULT 8
QBEE3
BHLF1 protein - human herpesvirus 4 (strain B95-8)
C:Species: human herpesvirus 4, Epstein-Barr virus
C>Date: 25-Feb-1985 #sequence_revision 25-Feb-1985 #text_change 09-Jul-2004
C:Accession: A03742
R:Bankier, A.T.; Deininger, P.L.; Farrell, P.J.; Barrell, B.G.
Mol. Biol. Med. 1, 21-45, 1983
A:Title: Sequence analysis of the 17,166 bp EcoRI fragment C of B95-8 Epstein-Barr virus
A:Reference number: A93065; MUID:85035713; PMID:6092825
A:Accession: A03742
A:Molecule type: DNA
A:Residues: 1-660 <BAN>
A:Cross-references: UNIPROT:P03181
R:Baer, R.; Bankier, A.T.; Biggin, M.D.; Deininger, P.L.; Farrell, P.J.; Gibson, T.J.; H
Nature 310, 207-211, 1984
A:Title: DNA sequence and expression of the B95-8 Epstein-Barr virus genome.
A:Reference number: A03794; MUID:84270667; PMID:6087149
A:Contents: annotation; protein coding region
C:Comment: The sequence contains four perfect repeats (residues 149-273, 274-398, 399-52
C:Superfamily: human herpesvirus 4 BHLF1 protein

Query Match 2.9%; Score 172.5; DB 1; Length 660;
Best Local Similarity 26.1%; Pred. No. 0.00078;
Matches 94; Conservative 16; Mismatches 159; Indels 91; Gaps 16;
QY 167 AVQVC--GPPLYQLGAATQA--RPPPHASGPRRLGCRANMHSVREAGVPLGLPAGAR 222
Db 244 AAQRCFAGPPPTRSGAAQAQTHRRPPGCPRSARNPCPRTWR---RRSGAQRGHPPGAG 300
QY 223 RGGSGASRLP-LPKRPRGAPEP-ERTPVQGSMAHPGTRGSDRGFCV-VSPAR-- 277
Db 301 QRPSPGTGGRPAAGPAGTPAAGPGGGAAPVSGATPHRPGSGPADPAAARLPPEQOE 360
QY 278 -----PAAEATSLEGAL-----SGTRHSH 297
Db 361 PRLPDALAAQRCFAGPPPTRSGAAQAQTHRRPPGCPRSARNPCPRTWRRRSGAQRGHP 420
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QY 298 SVGRQHAGPSTSRPRPW--DTPCPR-----VVAETKHFLYSSGDKE-----QLR 342
Db 421 PPGAGQPSGTGCTGPAAPAGAPGTAAAPGPGGAAVPSGATPHRPGSGPADPAAARLP 480
QY 343 PSFLLSSLRSLTCARLIVETIFLGSRPWMPG-----TPRELRLPQ-----RYQM 389
Db 481 PEREPRLPDALAAQRCP-----AGPPPTRSGAAQAQTHRRPPGCPRSARNPCPRTWR 536
QY 390 RPLFLELLGNHAQCPYGVLLKTHCPL--RAAVTPAAGVCAREKPKQGSVAAPEEEDTPRR 447
Db 537 RS-----CAQRGHPPGAGQRPSCGTGCRPAAPGAGCTPAAPGCGGAAVPSGATPHPER 591

RESULT 9
A59295
unconventional myosin-15 - mouse
C:Species: Mus musculus (house mouse)
C>Date: 09-Jun-2000 #sequence_revision 09-Jun-2000 #text_change 09-Jul-2004
C:Accession: A59295
R:Liang, Y.; Wang, A.; Belyantseva, I.A.; Anderson, D.W.; Probst, F.J.; Barber, T.D.; Mi
an, T.B.; Fridell, R.A.
Genomics 61, 243-258, 1999
A:Title: Characterization of the human and mouse unconventional myosin XV genes responsi
A:Reference number: A59266; MUID:20021762; PMID:10552926
A:Accession: A59295
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-3511 <LIA>
A:Cross-references: UNIPROT:Q9QZ4; GB:AF144095; NID:G6224684; PIDN:AAF05904.1; PID:G622
C:Genetics:
A:Gene: MGI:Myo15
A:Cross-references: MGI:1261811
A:Map position: 11:33.9
F:1209-1871/Domain: myosin motor domain homology <MMO>
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Query Match 2.4%; Score 144; DB 2; Length 3511;
Best Local Similarity 17.6%; Pred. No. 0.68;
Matches 189; Conservative 117; Mismatches 385; Indels 380; Gaps 44;
QY 3 RAPRCRAVRSLLRSHYREVLPATFVRRLGPGQWRLVQRGDPAAAFRALVAQCLVCP-- 59
Db 677 RPRLASPYSLRQH-----PPW-----AAAHVFPFPQA 707
QY 60 --WDARPPAA-----PSFQVSCCLKELVARVLQRLCERGAKNVLAFGFA 102
Db 708 NMGWFAEPGTSPEVAPDLLAFPPVPSPFR-----ASRSRRAAYGFP 751
QY 103 LLDGARGGPEAFVTSVRSYLPNTVTD--ALRSGANGLLLRVGDVVLHLLARCALFV 160
Db 752 -----SPSLIGSRRRPHLPSPQPSLRSLPQGQ----- 778
QY 161 LVAPSCAYQVCGPLYQLGAATQAQAPPPPHASGPRRLGCRANMHSVREAGVPLG----- 215
Db 779 -----YHSLGCLPUSQLSLRGFPQFPFPFPPRRPQSLREAF--SLRASRGLGPPRSP 830
QY 216 ----LPAGARRRGSGASRLPLPKR-----PRGAAPERT---PVGGS 255
Db 831 VLGSFRRPSPPLLLKHGPRHRSNLNLPGLRPLRTRRLSEPPTRAVKFWHRAYPSPPSAGP 890
QY 256 WAHPCRTRGSDRGFCVVSAPARPAEATSLLEGALSGTRHSHPSVGRQHAGPPSTRPDR 315
Db 891 W---GASTGALE-----QENQREADESETPTWTFPLAPSVDVMPPTQRPSPS 935
QY 316 PWDTPC-----PPVVAETKHFLYSS-----GDKEQLRPSFLIS 348
Db 936 PWPISGLSLRGFSRPPVPENPPLLEHTSPSCPOSEDRVSNLTGIFLQHHDPGPGQLTK 995
QY 349 SLRPSLTGARRLVTETIFLGSRPWMPGTFRRL-PRLPQRYWQMRPLFLELLGNH----- 400
Db 996 SADPSL---EKPEEVTILGD-PQPAPBEALNPTPNKNVSVSRKVLRSASVPLVTCQK 1051
QY 401 --AQCP---YGVLLKTHCPLRAAVTPAAGVCAREKPKQS----- 434
```

Db 1052 ABATPQWHRWKTSTRTAPLAPGAPLLKAGEQRAEPGRFAVMPQVRGVSSFRPK 1111
QY 435 ----VAAPDEEDTDPR-----LVOLLROHSSPMOVYGFVRAC 468
Db 1112 GAPVQPPHPDDEQAPQACSLRWCLWPPPTDAHCLWSRITYSSQSHLRHGDC 1171
QY 469 LRLR---VPPGLWGRHNRFLRNTKFKISGKHAQLSLQBLTWKMSVRDCAWLRSPG 525
Db 1172 HKSLWKTRPSW---QNKWHSIRNLPMSRSEQRHEDGVEDMTQLEDIQTTLAN--- 1225
QY 526 VCVPAAEHLREELAKEL-----HMLMSVYVVELLSF-----FYTT 564
Db 1226 ----LKTRFRNLITYIGSILSVNPFYRFAIYGPQVOQYSGRALGENPHLFAITA 1279
QY 565 ETTFOK-----NRLFFYR-----KSVMSKL-----OSIGIRQHLKRVQLRELSE 603
Db 1280 NLAFKMLDAKQNCQVIIISGSGSKTEATKILRLCLAMNQRRDVMQIKILEATPLE 1339
QY 604 A-----EVQHREARPALTSRLRFPKPDGLRPIVNMVYVVGARTFRREKRAER----- 653
Db 1340 AFGNAKTVRNDSNR---FGKVEIFEGGVICGAITSQYLLKSKRIVFOAKNERNYHF 1396
QY 654 ----LTSRVKALSVLNYE-----RARRPGLIGASVLGLDDIHRAWRTFVLVRAQD 701
Db 1397 YELLAGLPAQLRQAFSLQEAETYYLNOGNCNCEIAGKS--DADDFR----- 1441
QY 702 PPELYFVKVDVTGYADTTPQRLTEVIASIIKPNQTYCVRRYAVVQKAAHGHRKAFKS 761
Db 1442 ----LLAMEVLG-FTSDDQSIFRILASILHLGNVYFEKHETDAQEA----- 1485
QY 762 HVTSLTLDQPMYRQFVAHLQETSP--LRDAVIEQSSLSNEASSGLFDVFLRMCCHAVR 819
Db 1486 SVVSAREIOA-----VAELQVSPGLQKAITFKVTETIRE-----KIFTPLTVESAVD 1534
QY 820 IRGKSYVQCGIPQSSILSTLCSLCYGMENKLPAGI--RRDGLLLRLVD 868
Db 1535 AR-----DATAKVLVALLFGWLITRVNALVSPKQDTLSIALD 1572

RESULT 10
T00080
hypothetical protein KIAA0522 - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 22-Jan-1999 #sequence_revision 22-Jan-1999 #text_change 09-Jul-2004
C:Accession: T00080
R:Nagase, T.; Ishikawa, K.; Miyajima, N.; Tanaka, A.; Kotani, H.; Nomura, N.; Ohara, O.
DNA Res. 5, 31-39, 1998
A:Title: Prediction of the coding sequences of unidentified human genes. IX. The complete
A:Reference number: Z14086, MUID:98290545; PMID:9628581
A:Accession: T00080
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-1560 <NAG>
A:Cross-references: UNIPROT:060275; EMBL:AB011094; NID:G3043567; PIDN:BAA25448.1; PID:G3
A:Experimental source: brain; clone HG1393
C:Genetics:
A>Note: KIAA0522

Query Match 2.4%; Score 142.5; DB 2; Length 1560;
Best Local Similarity 29.5%; Pred. No. 0.28;
Matches 65; Conservative 15; Mismatches 89; Indels 51; Gaps 12;

QY 173 PPLYOLGAATQARPAPHASGRRRLGCEBAAWNSHREAGVP-----LGLPAGARRGG 226
Db 1365 PPLPOLGST-----PPPPASAP--PVGPHR---HFHAHGVPVPGQHYTLGRPCRAPRRGAG 1415
QY 227 SASRSLPLPKRP-RKGAAPEPRTPVGQGSWAHPGRTGSPDRGFCVSWSPAPAEATSL 285
Db 1416 GHPQAPGHRHLHQRTSLPLYSAPQPPAH---KQPKKFISSHHPMPMPAAGAAGG 1472
QY 286 EGAL-SGTRHSPSVGRGHAGGPSTSR---PPRFMDTFCPPVYAEKHF----- 331

Db 1473 PGSRPFGSGYSHP-----HHQSPISPHSPPIPHPSYPLPPSPHTSPHTSPPLPTSPHGP 1527
QY 332 LYSSGDKEQLRPSFLLSLRPSLTGARRLVETIFLGRPW 371
Db 1528 LHASFPAPQPTPP--VQTPRPSQA-----GSAFW 1554

RESULT 11
T18314
hypothetical protein L7610.4 - Leishmania major
C:Species: Leishmania major
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T18314
R:Oliver, K.; Murphy, L.; Quail, M.; Lawson, D.; Harris, D.; Rajandream, M.; Ivens, A.;
submitted to the EMBL Data Library, May 1999
A:Reference number: Z18876
A:Accession: T18314
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-1892 <OLI>
A:Cross-references: UNIPROT:O97007; EMBL:AL034356; NID:G1371878; PID:G1371559; PIDN:CAA
C:Genetics:
A>Note: L7610.4

Query Match 2.4%; Score 140.5; DB 2; Length 1892;
Best Local Similarity 23.4%; Pred. No. 0.51;
Matches 111; Conservative 47; Mismatches 195; Indels 121; Gaps 25;

QY 44 PAAPFALVAQCLVCVWDARPPAPSPROVSCLELVARVLQRCERGAKNVLAGFAL 103
Db 366 PSSLHPQOPVILVLP---QPRAPPQOERPLRYSSTTRPAGGSPRGAVQNNIYAGMAA 422
QY 104 LDGARGGPEAFTTSVRS-----YLPNTVTDALRGSGAWGLLRVVDVLLHARCAL 158
Db 423 EDTSGASEVTSRSTRQVRRAPVATSDIPTGS-PYGAM-----PT 465
QY 159 FVLVAPSCAYQVCGPPLYQLGAATQARPPPHASG-----PRRRLG-----ERAWN 204
Db 466 YAVVMPQ--RSLPAPPKTGASAASAGLPPSPAEEAQAQPHNSRCPSPSSRSPSPQESRD 523
QY 205 HSVREAGVPLGLPAPGAR-----RRGSGASRLP-----LPKRP--RRGAAPPERT 249
Db 524 HAAREQ--PLPQPPQKRPALPQRHQPORAETAKSQLPPRMFLPADFPFYSEELIPEQR- 580
QY 250 PVGQGSWAHPGRTGSPDR-GFCVVSAPPA-----EBAATSELEGALSGTRHSHP-SVGRQ 302
Db 581 ---EGAWGNASTQSGHGRGHSVRVPSQQQLSLSHEEDLSAMLSATVAAPISTKTD 637
QY 303 HHAGPPSTRPPRPMDTFCPPVYAEKHFLYSSGDKQLRPSFLLSLRPSLTGARRL-V 361
Db 638 PVAGHTAPDGEPRPLHVPMPPIIQRP---YAATEE-----GAPRFVS 678
QY 362 ETIFLGRPMWGTTPRPLRPLRQVWQMRPLELLELGNHQAQCPYG--VLLKTHCPLRAA- 418
Db 679 RKVTAPORESAPSPSRSP-----PAEHTLLHSRGAADAGEAAAKETREQLSAAK 728
QY 419 ---VTPAAGVCAREKPO-----GSVAAPEEDTDPRILVQ---LLRQHSSP 458
Db 729 EAVTAMTTAGVQSSKKPQLOLQHEPDGS---PNGDVD---ELLEADDLIMQPSRP 777

RESULT 12
EBE1F
immediate-early protein IE180 - suid herpesvirus 1 (strain Indiana-Funkhauser)
C:Species: suid herpesvirus 1
C:Date: 30-Jun-1990 #sequence_revision 30-Jun-1990 #text_change 09-Jul-2004
C:Accession: S04713
R:Cheung, A.K.
Nucleic Acids Res. 17, 4637-4646, 1989
A:Title: DNA nucleotide sequence analysis of the immediate-early gene of pseudorabies v
A:Reference number: S04713; MUID:89315207; PMID:2546124
A:Accession: S04713
A:Molecule type: DNA

of calcium homeostasis. This enzyme is particularly sensitive to Ca²⁺ in the presence of

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Query Match      2.3%; Score 134.5; DB 2; Length 946;
Best Local Similarity 19.5%; Pred. No. 0.5;
Matches 125; Conservative 78; Mismatches 256; Indels 183; Gaps 25;
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	QY	178	LGAATQARPPPHASGRP-----RRLCERAWNHVSREAGVPLGLPAPGARRRG-----	225
Db	:	:	: :	:
350	LGSETS--FAPERGGPRDGPPEGKMG-	-KYLPCGMPSGSGPEVGKRPEET	397	
QY	226	----GSAGRSILPKRRPRRGAAPER----	TPVGQSWAHPPGRTGRGSDRGFCVVSPA	276
Db	:	:	:	:
398	VSVQSARESSDSLSWSRLPALASVGEARS	GPNVGGRWQLS	DRVEGGS-	447
QY	277	RPAEATSLEGALSGTRHSHSPVGRHHAGPSTSRPPRP-WDT-----	PCPPVVAET	328
Db	448	-----PTLGLGGSPSAQPGTGNVEAGIPSGRMLEPLPCWDAAKDLKEPOCPP-----	495	
QY	329	KHFLYSGDKQELRPSELSSLRPSLTGARLLVEITFLGSRPWMFGT	PRLRLPORYWQ	388
Db	496	-----GDRVGVQPG-----NSRVMQGTMEKAGLAWTRGTGVQ-----	SEGTWE	533
QY	389	MR-----PLFELLGNHAQCYPGVLLKTHCPURAAVTPA--	AGVCAREKPQGSVAA	437
Db	534	SQRQSDALPSP---ELLQDQDKPF-----	LRKACSPNIPAVIIIDMGTOEDGA	581
QY	438	PEEEDTPRLVOLGRQHSSPMQVGF-----	VRACLRLVPGLMSRHNRFP	487
Db	582	LEETQSGPRNLPLRLKLSSASSASTGFSSSYEDSBEDISSDPERTLDPN	SFAHLTLDDOOK	641
QY	488	LRNTKKFISLGHAKSLSLQELTWKMSVRDCWLRLSPGVGCVPAA-----	EHR	535
Db	642	PRVKSWRKIKNWHWSPTFVNSFK---KKYPWQLAGHAGSPKAANGRI	LKHCHESOR	698
QY	536	LREEILAKFLHLMYSVY-----	VVELLRSF-----FYVTTFQ	569
Db	699	CLDRLMVDVLRFVPAYTHGDVVKGDBRYNQMDLLADFDSPCMCDCKMGIRTYLEBELTK	758	
QY	570	KURLFFYRKSVWSKLOSIGIRQHLKVQL-RELSEAEVQHRE--	ARPALLTSRLRFIPK	626
Db	759	ARKKPSLRXDMYQKMIEVDPEAPTBEKAAQRAUTPRYNQMRETISSTATLOFR	IEGIKK	818
QY	627	PDGLRPIVMNDYVVGARTFRREKRBRLTSRVKALFSVLNYERRARRPGI-----	675	
Db	819	EDG---TVNRDF---KKTITRQQTVEAFREFTKGNHILLIAYDRDLKARTILEVSP	FPFK	872
QY	676	----LGASVLGLDDIHRAWRTFLVLRQAODPPPPLYFVKVDV	713	
Db	873	CHEVIGSSLFIHDHKKEAQKVMWDIFGKTTPLPEGGOTLQHDV	914	

RESULT 17
G75302
orotidine 5'-phosphate decarboxylase - Deinococcus radiodurans (strain R1)
C:Species: Deinococcus radiodurans

C;Accession: G75302
R;White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;
M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; Ma
S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
Science 286, 1571-1577, 1999
A;Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
A;Reference number: A75250; MUID:20036896; PMID:10567266
A;Accession: G75302
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-606 <WHI>
A;Cross-references: GB:AE002053; GB:AE000513; NID:G6459999; PIDN:AAF11749.1; PID:G64600C
A;Experimental source: strain R1
C;Genetics:
A;Gene: DR2200
A;Map position: 1

```
Query Match          2.2%; Score 134; DB 2; Length 606;
Best Local Similarity 22.4%; Pred. No. 0.3;
Matches 100; Conservative 45; Mismatches 137; Indels 164; Gaps 21;

QY 132 KGSAGWGLLRRVGDVLLHLLARCALFVLVAPSCAYVCGPPLVQLGAATQARPPPHAS 191
DB 21 RRSERFGVALLQIGERRVHLTARHPAFLOV-----LGAVER----- 57
QY 192 GPRRLGCERAWNHSVREAGVPLGLPAPFCARRGGSASRSPLPKRRPRGAPEP----- 246
DB 58 -PSRRFG-----VGVEVGQRRG-----VVLDPQR-----POPFQVFE 91
QY 247 -ERTVPQGSWAHPGTRGSDRGFCVVSPPARPAEATSLEGALSCTHSHSPSVGRQHA 305
DB 92 RQRT-----GVLRAAKQO-----VVKVEOPRQFAAGV-GVVVGAQ-VHPVVGQAAYA 136
QY 306 GPPSTSRPPRPMDTPCPPVYAEHFKFLYSYSGDKEQLRPSFLSLRPSLTGARRLVETIF 365
DB 137 A-----PRP-----RAQRRLPAPVAARLVP---GPQRQOT--- 167
QY 366 LGSRPMPGTPRRLPRLPORYWQMRPLFLELGNHAQCPYGVLLKTHCPLRAAVTPAAGV 425
DB 168 AGERQLVFG-----LPCRHV-----QARPCEDVALNRHVPREAARP--GV 209
QY 426 CAR-----EKPGSVAAPBEEDTPRLVQLLRQHSPPHVVGFVYACLR 471
DB 210 AARAGEGALPVRADQPELPLLDVGVLTKAGDGLRVEPLREBPQOTFRTRIGVDIALRR 269
QY 472 LVPPGLGWSRHNERRFLNRTKFKISLGHAKHLKSLQELTWKMSVRDCAMLRSPGVG---- 527
DB 270 YRPHAAHEGQ-----RPHRELAHRDAEVA-----GPGVAPHDR 306
QY 528 -----CVPAEHRLEILAKFLHW 547
DB 307 KGHAQCCTGPAQHPPFPVQLRPLHW 332

RESULT 18
JQ0405
hypothetical 119.5K protein (uvrA region) - Micrococcus luteus
N:Alternate names: ORF 1 protein
C:Species: Micrococcus luteus, Micrococcus lysodeikticus
C>Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 04-Feb-2000
C:Accession: JQ0405
R:Shiota, S.; Nakayama, H.
Mol. Gen. Genet. 217, 332-340, 1989
A>Title: Micrococcus luteus homolog of the Escherichia coli uvrA gene: identification of
A:Reference number: S04781; MUID:89364717; PMID:2549377
A:Accession: JQ0405
A:Molecule type: DNA
A:Residues: 1-1106 <SHI>
A:CROSS-references: EMBL:X15867
A>Note: this reading frame extends between two stop codons and does not begin with a sta
A:Note: the gene encoding this protein overlaps uvrA gene
C:Superfamily: collagen alpha 1(I) chain; fibrillar collagen carboxyl-terminal homology;
```

```
Query Match          2.2%; Score 133; DB 2; Length 1106;
Best Local Similarity 23.9%; Pred. No. 0.79;
Matches 129; Conservative 33; Mismatches 198; Indels 180; Gaps 25;

QY 185 RPPHASGPRRLGCE-----RAWNHSVREAGVPLGLPA--PGARRGGSGAS-----RSLP 233
DB 516 RGPFOHGPGERARGRVRHGRHPPAHARGHGVLLGAAADGPGAADRGFGAOGDPGAPGVP 575
QY 234 LPKRPRGAAPERTPVQGSWAHPGTRGSDRGFCVVSPPARPAEATSLEGALSCTR 293
DB 576 AGERPR---VPQ-----RAGRHPLRRG-----PAHPGHTDLR---AGRR 613
QY 294 HSHPSVGROHAGPSTSRPPRPMDTPCPVVAETHKFLYSYSGDKEQLRPSFLSLRPS 353
DB 614 PLRP---RAVHRPAPAGPPHPPPPAPAGPQHPHRRRRARRGHD--RRGLDGRHPS 668
QY 354 LTGARRLVETIFL--GSRPMPGTPRRLPRLPORYWQMRPLFLELGNHAQCPYGVLLKT 411
```

```
DB 669 RGRVRRGRALGLPGSGQGEHAVRRLPLRP-----PL----- 702
QY 412 HCPLRAAAVTTPAAGVCA-----REKPGQSVVA-----APEEED-----TD 444
DB 703 HRGAGASRPEGARADGPRPGQPEGRLGPGPARGPHGDRVLRVLRQVHADQDPLQG 762
QY 445 PRLVQLLRQHSPPWQYVGFVACLRRLRVLPPGLMGSRHNRFLRNTKFKISLGHAKLS 504
DB 763 PGQPAORQARAPAPVRGGTRA-----PGQGGPRGPEPH-----RAHATLQ 804
QY 505 LQELTWKMSVRDCAWLRSP---GVGCVPAEHRLEILAKFLHLWLSVVVVELLRSPFF 561
DB 805 PRHLHVR--RDPQALRGDPRGEGF--LPAGPVL----- 837
QY 562 YVTETTFQKRLFFYRKSVMSKLSIGIRQHLKRVQLRELSEAEVQRHREARPALLTSRL 621
DB 838 -----OH-----QGRALGVRGRHAEDEDELPAGR 864
QY 622 RPI-PKPDG-LRPIVNDYVVGARTFRREKAER-----LTSRVKALFSLVYERARRPGL 675
DB 865 RAVRGVPRGPVQGDARGHLQGEHRRGPRHADRGRLQVRHPLAVPGHARRRRSGL 924

RESULT 19
S55543
RNA-directed DNA polymerase (EC 2.7.7.49) - fruit fly (Drosophila melanogaster) transpos
N:Alternate names: reverse transcriptase
C:Species: Drosophila melanogaster
C>Date: 27-Oct-1995 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C:Accession: S55543; S55544
R:Judomkit, A.; Forbes, S.; Dalgleish, G.; Finnegan, D.J.
Nucleic Acids Res. 23, 1354-1358, 1995
A>Title: BS a novel LINE-like element in Drosophila melanogaster.
A:Reference number: S55543; MUID:95273172; PMID:7753626
A:Accession: S55543
A>Status: preliminary; nucleic acid sequence not shown
A:Molecule type: DNA
A:Residues: 1-860 <UDO>
A:CROSS-references: UNIPROT:Q95SX7; EMBL:X77571
A:Experimental source: strain Y Hw
A>Note: the nucleotide sequence was submitted to the EMBL Data Library, February 1994
A>Note: the complete translation is not shown
A:Accession: S55544
A>Status: preliminary; translation not shown
A:Molecule type: DNA
A:Residues: 57-860 <UD2>
A:CROSS-references: EMBL:X77571
A:Experimental source: strain Y Hw
C:Genetics:
A:Gene: FlyBase:BS
A:CROSS-references: FlyBase:FBgn0000224
A:Mobile element: transposable element BS
C:Keywords: nucleotidyltransferase

Query Match          2.2%; Score 132; DB 2; Length 860;
Best Local Similarity 19.1%; Pred. No. 0.65;
Matches 140; Conservative 100; Mismatches 250; Indels 244; Gaps 37;

QY 358 RRLVETIFL--GSRPMPGTPRRLPRLPORYWQMRPLFLELGNHAQCPYGV----- 407
DB 110 RELALSVTGAKILATGSPTRYPVFHS-----TPSCIDPAVYH-----GIPDHATITQ 160
QY 408 ---LLKTHCPRLAAVTPAAGVCAREKPGQSVAAPEEEDTPRLVQLLRQHSPPWQYVGF 464
DB 161 SWLDSDDLPLIISI-----ETDSTHV-----NPSP----- 186
QY 465 VRACLRRLVPLGWSRHNERRFLNRTKFKISL-----GKHAKLSLQELTWKMSVRDC 517
DB 187 -----RLV-----TKHTDLLAFSRQLESLSLNTLNSGEIEMAVDNLT--ESIHA 232
QY 518 AWRRSRPGVGCVP-----AAEHLREEL-----L 541
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Db 233 AAVTSP-----VPIRTTGVIVLTREARELLTKRRLRRRAIRNSODPWDRLLWNRAKQL 288
QY 542 AKFLHLMVYVVELLSFFYVTTTFQKNRLFYFKRSVMSKLOSGIGRHLKRVOLR-- 599
Db 289 RNVLRRLSNFFEQKLASWDYTDAGY-----SLWKCTKSLK-RQPFQVPIRCP 337
QY 600 --ELSE-----AEVROHREARPAALLTSRURFIPKPDGLRPIYN 635
Db 338 GGELAKNEBEQANCFANHLETRFTHQFATTEQYQETLDSLETPLQMSLP-----IKPI-R 392
QY 636 MDVVCARTFRREKRAERLTSRVKALFSLVNYERARRPGLGASVLGLDDIHRWR-TFV 694
Db 393 VSEIVEAISKLPKSGPDINVCNATLKALPVRTILYLALITYNAILURVQFFQKQMAAI 452
QY 695 LRVRAODPP---PELY---FVKVDVTGAYDTIPQDRLTEVIAS-IIPQNTYCVRRYAVV 747
Db 453 LMIHKPKPEESPESYRPISSLSSLSKLWERLIANRLNDIMTERRILPDHQFGFRQ---- 508
QY 748 QXAAHGHVKAFAK--SHVSTLTDLPYMQFVAHLOET--SPURDAVTEQSSLSNEASS 803
Db 509 --GHSTVQVHRLTKHILQAFDDKEYCNAVFTDMQOAFDRVWHQGLISKVKKLPAPYY 565
QY 804 GLFDVFL---RMCHHAVIRKSY---VQCGIPIQSGSTLSCSLCYGDM--ENKLF 854
Db 566 GVLKSYLEDRREM----VVRV-NSYSIPRMVRAGVPGSGVLGPLYSVFTADLPCCNAYH 620
QY 855 AGIRRDGLLLRLVDDLLVTPHLTHAKTEFLTLVRGVPEY-----GCVNLRKT 903
Db 621 MADPRKALLATYADDIALL-----YSSNCCNEARGLOEYLTTLAACKRWNLKYNPQKT 675
QY 904 V-----VNFVDEALGGTAFVQMPAHGLFPWCGLLDLTLTLVQSDYSYART 952
Db 676 INPCFTLTKLSPVTABIELE-----GVILD-----QPSQAKYLG 710
QY 953 SIRASLTNNGFKA 966
Db 711 TLDKRLTFGPHLKA 724

RESULT 20
G01763
atrophin-1 - human
C:Species: Homo sapiens (man)
C>Date: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change 09-Jul-2004
C:Accession: G01763
R:Margolis, R.L.
submitted to the EMBL Data Library, March 1995
A:Reference number: G08343
A:Accession: G01763
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-1184 <MAP>
A:Cross-references: UNIPROT:P54259; EMBL:U23851; NID:g915325; PID:g915326
C:Genetics:
A:Gene: GDB:DRPLA; B37
A:Cross-references: GDB:270336; OMIM:125370
A:Map position: 12p-12p

Query Match 2.2%; Score 131.5; DB 2; Length 1184;
Best Local Similarity 22.8%; Pred. No. 1.1;
Matches 89; Conservative 23; Mismatches 153; Indels 125; Gaps 17;
QY 162 VAPSCAYQVCGPLYOLGAATQARPPH-----ASGPRRLGGERAWNSVREA 210
Db 188 VFTGTGHAMEPPTSRMFQAPGAPPPHPOLYVGGTGGVLSG----- 230
QY 211 GVPLGLPAPCARRR--GGASRSRLPLKRP-----RRGAAP-EPERTVQGGSWAHPG 260
Db 231 --PMGPKGGAASSVCGPNRGKHPPPTTPIVSSSSGASGAPPTKPTTPVGGN----- 283
QY 261 RTRGSDRGFCVVSVPARAEATSLGALSGTRHSHPSVGRQ-----HHAG----- 306
Db 284 LPSAPPANFPHVTPLNLPPLPALR---PLNNASAPPLGLAQPLPGLHPSHAMGGIGG 340

RESULT 21

A45344

immediate-early protein - suid herpesvirus 1 (strain Kaplan)

C:Species: suid herpesvirus 1

C>Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004

C:Accession: A45344

R:Vicek, C.; Kozmik, Z.; Paces, V.; Schirm, S.; Schwyzler, M.

Virology 179, 365-377, 1990

A:Title: Pseudorabies virus immediate-early gene overlaps with an oppositely oriented o

A:Reference number: A45344; MUID:91021039; PMID:2171211

A:Accession: A45344

A>Status: translation not shown

A:Residues: 1-1446 <VLC>

A:Molecule type: DNA

C:Cross-references: UNIPROT:P33479; GB:M34651; NID:g334070; PID:AAA47470.1; PID:g33407

C:Superfamily: herpesvirus immediate-early protein IBL75

C:Keywords: DNA binding; early protein; transcription regulation

Query Match 2.2%; Score 131; DB 1; Length 1446;
Best Local Similarity 21.4%; Pred. No. 1.6;
Matches 105; Conservative 37; Mismatches 156; Indels 192; Gaps 25;

QY 46 AFRLVAQCLVCVPWDARPPPAAPSRQVSCUKELVARVLQRCERGAKNVLAFGALLD 105
Db 693 ACRGVLELLPC-PLRLPAPAPAAALGPAACLEEVTAALL-----ALRD 735
QY 106 GARG-GPPEAFTTSVRSYLPNTVTDALRGSGAWGLLRVGGDVLVHLARCALFVLVAP 164
Db 736 AIPGAGPAER-----RONADSA--LVAR-----TVAP 761
QY 165 SCAYQVCGPLYQLG-----AATQARPPPHASGPRRLGGERAWNH- 205
Db 762 LVRYSDGARAREAAWTYAAALFAPANVAARLAEEAARPGPAEPAP---GLPPLWPEQ 817
QY 206 -----SVREAGVPLGLPAG-----ARRRGGSASRSLLPLK-----RPRGA 242
Db 818 PGLVVVPAPAAAAGAPSGLPGSGSPASTKSSSTKSSSTKSGLSGSGVYASSPAAGP 877
QY 243 APEPERTVQGGSWAHPGRTGPGSDRGFCVVSVPAR--AEEATSLG-ALSTGRSHPSV 299
Db 878 DPAPER-----RKRRRAPGAR-----RPGGEDEGLSGAALRGDGHGRD- 919
QY 300 CRQHAGAGPSTSRP-----PRPMDTPCPVYAETKHFLYSSGDKQLRPSFLSSLRPSLT 355
Db 920 -DEEDRGPRRKERSLGLGPAP--DPAPALLSSSS-----SSSEDDLRL-----RP--- 961
QY 356 GARRLVETIFGSRPMPGTPRRLPRLPQRYVQWMPRLFLELIGNHAQCPYGVLLKTHCPL 415
Db 962 -----LCPMPHEHPADCGFRVPAG-----ETHTPRPSAALAAAYCP- 998
QY 416 RAAVTPAAGVCAREKPGQSVAAPEEE-----DTPRELVLQRLRHSSSPWQVYGV 465
Db 999 -----PEVARALVDOEVFPELWRPALTFDPAALAHIAARRGAPLRRRA--- 1041
QY 466 RACLRLRVPP 475

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Db      1042 -AMNRQTADP 1050

RESULT 22
S50832
atrophin-1 - human
C:Species: Homo sapiens (man)
C:Date: 14-Jul-1995 #sequence_revision 21-Jul-1995 #text_change 07-May-1999
C:Accession: S50832
R:Nagafuchi, S.; Fangsgisawa, H.; Ohsaki, E.; Shirayama, T.; Tadokoro, K.; Inoue, T.; Yam
Nature Genet. 8, 177-181, 1994
A:Title: Structure and expression of the gene responsible for the triplet repeat disorder
A:Reference number: S50832; MUID:95144175; PMID:7842016
A:Accession: S50832
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-1184 <NAG>
A:Cross-references: EMBL:D31840
C:Genetics:
A:Gene: GDB:DRPLA; B37
A:Cross-references: GDB:270336; OMIM:125370
A:Map position: 12p13.31-12p13.3112p-12p

```

Query Match	2.2%;	Score 130.5;	DB 2;	Length 1184;
Best Local Similarity	22.6%;	Pred. No. 1.3;		
Matches	88;	Conservative 23;	Mismatches 154;	Indels 125; Gaps 161
Qy	162	VAPSCAYVCQPPPLYOLGAATQARPPH-----ASGPRRLGCRAWNHSVREA	210	
Db	189	VTPTGYHAPMEPTTSMFQAPPGAPPPHPQLYPGGTGGVLGSP-----	231	
Qy	211	GVPLGLPAPGARR--GGASRSKLPLPKRP-----RRGAAP-EPERTPVQGSWAHPG	260	
Db	232	--PMGPKGGGAASSVGGNGKGQHPPTTPTTSVSSSGASGASGAPPTKPTTTPVGGCN-----	284	
Qy	261	RTRGSDRGFCVVSPPARPAEATSLEGALSCTRSHSPVGRQHAG-----	306	
Db	285	LPSAPPPANFPHVPTNLNPPPPALR---PLNNASAPPGGLGAQPLPGHLPSPYAMQGQMGG	341	
Qy	307	-----PPSTSRPPRPMDTPCPVVAETKHFLYSGDKEQLRPSFLLSLRPSL	354	
Db	342	LPPGPEKGPTLAPSPHSLPPASSSAPAPPM-----RFPYSSSSSSSAAAS-----SSSSSSS	393	
Qy	355	TCARRLVETIFLGSRPMMGTPTREL-----PRLP-QRYQMPRLFLELLGNHAQ	402	
Db	394	SSASPPFASQALPSYPHSPFPPTTSLSVSNQPPKYTQPSLPSQAVMSQGP-----PPP	445	
Qy	403	CPYGVLLKTHCPLRAAVTPAAGVCAREKPGQSVAAPPEEDTPRLVLORH-----SSPW	459	
Db	446	PPYGELLANSNAHPGPPFPSTGASTAHPVSTHHHHHQOQOQOQOQHGNSSGP-504		
Qy	460	QVYGFVRACLRRLVPPGLW-----GSRHN	483	
Db	505	-----PPPGAFPHPLEGSSGSHH	521	

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RESULT 23
Tl3049
eyelid - fruit fly (Drosophila melanogaster)
C:Species: Drosophila melanogaster
C:Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 09-Jul-2004
C:Accession: Tl3049
R:Treisman, J.E.; Luk, A.; Rubin, G.M.; Heberlein, U.
submitted to the EMBL Data Library, March 1998
A:Reference number: Z17592
A:Accession: Tl3049
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-2715 <TRE>
A:Cross-references: UNIPROT.Q81N94; EMBL.AF053091; NID:g2981220; PID:g2981221; PIDN:AACCG
C:Genetics:
A:Gene: eld

```

A;Cross-references: FlyBase:FBgn003013
C;Function:
A;Description: could act as a transcription factor antagonistic to the wg pathway
C;Keywords: DNA binding

Query Match 2.2%; Score 130.5; DB 2; Length 2715;
Best Local Similarity 22.5%; Pred. No. 4;
Matches 80; Conservative 29; Mismatches 140; Indels 107; Gaps 18;

Qy 173 PPLVOLGAATCARPPHASGP---RRRLGCERA-----WNHSVREAGVPL-----GLPAPG 220
Db | | | | | | | | | | : | | | | | | | | | | | | | | | | | | | | | |
Qy 1293 PPQQGGGGGGGGPPSVCGPPPAPQGHGPGGVPPSPQOHVRPAAGAAPPYPPGSGYTTPV 1352
Db | | | | | | | | | | : | | | | | | | | | | | | | | | | | | | | | |
Qy 221 ARRGGSASRSLPLPKPRRGA-----APEPERTVGQGSWAHGTRTGRPSDRG 269
Db | | | | | | | | | | : | | | | | | | | | | | | | | | | | | | | | |
Qy 1353 SRTFGS-----PYPSQP--GAYGOYGSSDQYNATGPPGPFQGGPQGYPPQNRN----- 1399
Db | | | | | | | | | | : | | | | | | | | | | | | | | | | | | | | | |
Qy 270 FCVVSPARPABEA-----TSLEGALSGTRHSHPSVG-----ROHHAGPPSTSRPPRPWDT 319
Db | | | | | | | | | | : | | | | | | | | | | | | | | | | | | | | | |
Qy 1400 --MYPPYGEAGEAPTGANQCYGYSRYPQSGPPGFPQTQTVAAGPPAGGAPGAPSS 1457
Db | | | | | | | | | | : | | | | | | | | | | | | | | | | | | | | | |
Qy 320 PCPPVYAETHFLFYSSGDKE---QLRPSFLLS-----LRPSLTGARLLETIFLGSR 369
Db | | | | | | | | | | : | | | | | | | | | | | | | | | | | | | | | |
Qy 1458 AYTGRPSQDYOPPPDPQSPQRPHDFIKDSQPYGYNARPOIYGA----- 1505
Db | | | | | | | | | | : | | | | | | | | | | | | | | | | | | | | | |
Qy 370 PWMFPTRRLLRLPQO---RYWQMPELFLELLGNHAQCPLYGVLLKTHCLPRAAAVTAPAGV 425
Db | | | | | | | | | | : | | | | | | | | | | | | | | | | | | | | | |
Qy 1506 -WQSGTQOYRPOYSSPAPNWGGAP-----PRGAAPPCAPHGPPIQQPAGV 1552
Db | | | | | | | | | | : | | | | | | | | | | | | | | | | | | | | | |
Qy 426 CA----REKPGSVAAPBEEEDTPRRLVOLLRHQSPW-QVYGFVRACLRRLVPPG 476
Db | | | | | | | | | | : | | | | | | | | | | | | | | | | | | | | | |
Qy 1553 AQMDQHRYPPQGPPPPQOOQOPOQ-----QQOQPPYQQVAG-----PPG 1593
Db | | | | | | | | | | : | | | | | | | | | | | | | | | | | | | | | |

RESULT 24
S32975
gene BCRF2 protein - human herpesvirus 4
N;Alternate names: Gene BWRf1 protein
C;Species: human herpesvirus 4, Epstein-Barr virus
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
C;Accession: S32975; S02383; S32976; S32977; S32978; S32979; S32980; S32981; S32982; S32983; submitted to the EMBL Data Library, March 1988
A;Reference number: S32973
A;Accession: S32975
A;Molecule type: DNA
A;Residues: 1-383 <FAR>
A;Cross-references: UNIPROT:Q04397; UNIPROT:Q8AZK8; UNIPROT:Q8AZK6; UNIPROT:Q8AZK5; UNIPROT:Q8AZK4; PID:g1334836; PID:g1334837; PID:g1334838; PID:g1334839; PID:g1334840; PID:g1334841; PID:g1334842; PID:g1334843; PID:g1334844; PID:g1334845; PID:g1334846; PID:g1334847; PID:g1334848; PID:g1334849; PID:g1334850; PID:g1334851; PID:g1334852; PID:g1334853; PID:g1334854; PID:g1334855; PID:g1334856; PID:g1334857; PID:g1334858; PID:g1334859; PID:g1334860; PID:g1334861; PID:g1334862; PID:g1334863; PID:g1334864; PID:g1334865; PID:g1334866; PID:g1334867; PID:g1334868; PID:g1334869; PID:g1334870; PID:g1334871; PID:g1334872; PID:g1334873; PID:g1334874; PID:g1334875; PID:g1334876; PID:g1334877; PID:g1334878; PID:g1334879; PID:g1334880; PID:g1334881; PID:g1334882; PID:g1334883; PID:g1334884; PID:g1334885; PID:g1334886; PID:g1334887; PID:g1334888; PID:g1334889; PID:g1334890; PID:g1334891; PID:g1334892; PID:g1334893; PID:g1334894; PID:g1334895; PID:g1334896; PID:g1334897; PID:g1334898; PID:g1334899; PID:g1334900; PID:g1334901; PID:g1334902; PID:g1334903; PID:g1334904; PID:g1334905; PID:g1334906; PID:g1334907; PID:g1334908; PID:g1334909; PID:g1334910; PID:g1334911; PID:g1334912; PID:g1334913; PID:g1334914; PID:g1334915; PID:g1334916; PID:g1334917; PID:g1334918; PID:g1334919; PID:g1334920; PID:g1334921; PID:g1334922; PID:g1334923; PID:g1334924; PID:g1334925; PID:g1334926; PID:g1334927; PID:g1334928; PID:g1334929; PID:g1334930; PID:g1334931; PID:g1334932; PID:g1334933; PID:g1334934; PID:g1334935; PID:g1334936; PID:g1334937; PID:g1334938; PID:g1334939; PID:g1334940; PID:g1334941; PID:g1334942; PID:g1334943; PID:g1334944; PID:g1334945; PID:g1334946; PID:g1334947; PID:g1334948; PID:g1334949; PID:g1334950; PID:g1334951; PID:g1334952; PID:g1334953; PID:g1334954; PID:g1334955; PID:g1334956; PID:g1334957; PID:g1334958; PID:g1334959; PID:g1334960; PID:g1334961; PID:g1334962; PID:g1334963; PID:g1334964; PID:g1334965; PID:g1334966; PID:g1334967; PID:g1334968; PID:g1334969; PID:g1334970; PID:g1334971; PID:g1334972; PID:g1334973; PID:g1334974; PID:g1334975; PID:g1334976; PID:g1334977; PID:g1334978; PID:g1334979; PID:g1334980; PID:g1334981; PID:g1334982; PID:g1334983; PID:g1334984; PID:g1334985; PID:g1334986; PID:g1334987; PID:g1334988; PID:g1334989; PID:g1334990; PID:g1334991; PID:g1334992; PID:g1334993; PID:g1334994; PID:g1334995; PID:g1334996; PID:g1334997; PID:g1334998; PID:g1334999; PID:g1335000; PID:g1335001; PID:g1335002; PID:g1335003; PID:g1335004; PID:g1335005; PID:g1335006; PID:g1335007; PID:g1335008; PID:g1335009; PID:g1335010; PID:g1335011; PID:g1335012; PID:g1335013; PID:g1335014; PID:g1335015; PID:g1335016; PID:g1335017; PID:g1335018; PID:g1335019; PID:g1335020; PID:g1335021; PID:g1335022; PID:g1335023; PID:g1335024; PID:g1335025; PID:g1335026; PID:g1335027; PID:g1335028; PID:g1335029; PID:g1335030; PID:g1335031; PID:g1335032; PID:g1335033; PID:g1335034; PID:g1335035; PID:g1335036; PID:g1335037; PID:g1335038; PID:g1335039; PID:g1335040; PID:g1335041; PID:g1335042; PID:g1335043; PID:g1335044; PID:g1335045; PID:g1335046; PID:g1335047; PID:g1335048; PID:g1335049; PID:g1335050; PID:g1335051; PID:g1335052; PID:g1335053; PID:g1335054; PID:g1335055; PID:g1335056; PID:g1335057; PID:g1335058; PID:g1335059; PID:g1335060; PID:g1335061; PID:g1335062; PID:g1335063; PID:g1335064; PID:g1335065; PID:g1335066; PID:g1335067; PID:g1335068; PID:g1335069; PID:g1335070; PID:g1335071; PID:g1335072; PID:g1335073; PID:g1335074; PID:g1335075; PID:g1335076; PID:g1335077; PID:g1335078; PID:g1335079; PID:g1335080; PID:g1335081; PID:g1335082; PID:g1335083; PID:g1335084; PID:g1335085; PID:g1335086; PID:g1335087; PID:g1335088; PID:g1335089; PID:g1335090; PID:g1335091; PID:g1335092; PID:g1335093; PID:g1335094; PID:g1335095; PID:g1335096; PID:g1335097; PID:g1335098; PID:g1335099; PID:g1335100; PID:g1335101; PID:g1335102; PID:g1335103; PID:g1335104; PID:g1335105; PID:g1335106; PID:g133

Db 96 CPSEEGTGT-EPGLPASR-RPGLRSLPSVKECLR-----GATLGAQAP 144
QY 221 AARRGGSASRLPLKPRRGAAPERTPVGGSWAHPGRTRGSDRGF-----C-- 271
Db 145 SRQGG-----HLRVP--PRVPGQEPGR-----QGRQRQPVPRFPGLQSGCGPP 188
QY 272 -----VVSPPARPAEATSLEGALSGTRHSHPSVGRQHAGPSTSPRPPWPTPCPVYA 326
Db 189 EGTGLGVSPPLQARASPSRRGASLG-----PQV--QPHRDPSGDPPTGP--SLCFF-- 236
QY 327 ETKHFLYSSGDKLEQLRPSFLLSRLPSLTGARRLVETIFLGRPMWPGTPRRLPLRQY 386
Db 237 -----APLQSLHPRQLL-----ASPFGPGPEG-PRQPGRV 268
QY 387 -----WQMRPLFLELLGNHAQCPYGVLLKTHCPRAAATPAAGVCAREKPGQSVAP 438
Db 269 APFLPWLPLP-----ASHPSPLSLPHRVHQA-----GRRDPGPGFVSV 307

RESULT 25

S52796

prip2 protein - human (fragment)

C:Species: Homo sapiens (man)

C:Date: 19-May-1995 #sequence_revision 10-Nov-1995 #text_change 10-Sep-1997

C:Accession: S52796

R:Ruhlmann, A.; Kreideweis, S.; Nordheim, A.

submitted to the EMBL Data Library, March 1995

A:Reference number: S52796

A:Accession: S52796

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-403 <RUH>

A:Cross-references: EMBL:X86019; NID:g762950; PID:g762951

Query Match 2.2%; Score 129; DB 2; Length 403;
Best Local Similarity 25.8%; Pred. No. 0.37;
Matches 64; Conservative 11; Mismatches 91; Indels 82; Gaps 10;

QY 173 PPLYOLGAATQARPPPHASGRRRLGCRANWHSVREACVPLGLPAGARR----- 224
Db 80 PRPDVGSKDPSIPPPVSTP-----RPIQSSLNHRGSP---PVPGGPRPSGPTPP 129
QY 225 -----GGSASRS-----LPLKPRRGA--APEERTPVGGSWAHPG 260
Db 130 PFGNGRTALGGGSIQSPSSSPSNRPLPTPSRALDKPPPPPVGNRPSIHRE 189
QY 261 RTRGSDRGFCVVSPPARPAEATSLEGALSGTRHSHPSVGRQHAGPSTSPRPPWPTP 320
Db 190 AVPPPPPPQNNKPPVSTP-----RPSAPHRPLRPPPPSRPGPP--P 229
QY 321 CPVVVAETHKFLYSSGDKQLR---PSFLLSLRPSLTGARRLVETIFLGRPMWPGTPR 377
Db 230 LPP-----SSGNDTPLRQNLSSLSTPLPSGR-----SGPLPPPVPS 272
QY 378 RLRLPQR 385
Db 273 ERPPPPVR 280

RESULT 26

G86280

protein T5E21.13 [imported] - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)

C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004

C:Accession: G86280

R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,

Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Creasy, T.H.; Dewar, K.;

ansen, N.P.; Hughes, B.; Huizar, L.

Nature 408, 816-820, 2000

A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.

C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Matzali,

Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A:Reference number: A86141; MUID:21016719; PMID:11130712
A:Accession: G86280
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1776 <STO>
A:Cross-references: UNIPROT:Q9MA20; GB:AE005172; NID:g7527720; PIDN:AAF63169.1; GSPDB:G
C:Genetics:
A:Gene: T5E21.13
A:Map position: 1

Query Match 2.2%; Score 129; DB 2; Length 1776;
Best Local Similarity 21.8%; Pred. No. 2.8;
Matches 131; Conservative 63; Mismatches 204; Indels 204; Gaps 33;

QY 252 GGSWAHPGRTRGSDRGFCVVSPPARPAEATSLEGALSGTRHSHPSVGRQHHA-----G 306
Db 664 GGVGYGDPNSFPGA-----APFPPRP-----GVPTVRPLPPQNLAALNLRP 706
QY 307 PESTSRP--PRWDTP--CPVVAETHKFLYSSGDKLEQLRPSFLLSRLPSLTGARRLVET 363
Db 707 PPSVQYGPAPRLGVPMMQPMYQQ--HQLSMSGPHG--HPSMMGR--PPMQPVVRKV--- 758
QY 364 IFLGRSPWMPGTPRRLPLRPLRQYMWQRPFLFLELLGNHAQCPYGVLLKTHCPRAAATPAA 423
Db 759 -----PPPGSQFSHQVQPYGQLPPLSMGMW-----QPPPAEMP-- 796
QY 424 GVCAREKPGQSVAAPEEDTDP--LV-----QLLRHSSPWQVYGFVACLRVLV 473
Db 797 -----PPPGGEAPPPLPEPEPKQKLDDESALVPEDQFLAQHPG--ATIRVSK 843
QY 474 PPLWGRSHRNERFLRNTKFTS--LG-----KHAKLSLOELTWKMSV 514
Db 844 P-----NENDGQVMEITVQSLSENVGSLKEKIAGEMQIPANKQRNPYVFERTW--- 893
QY 515 RDCAWLRSPGVCVGAHRLREI--LAKFLHLSVYV---VBL 556
Db 894 ---WEKEIETGGPREMPFNLLIQIRCSLIDVFWWPKLYVPYEDALLVFCGIIIVSG 949
QY 557 L-----RSFVVTETTFQKNRLFY-----RKSVMKLSQIGIR----- 590
Db 950 ILSLSQYSQWRLNGRSFFKRLITSREINRWYFLKQTHRLKMFSSMQLPLEAPPTDCK 1009
QY 591 -----QHL--KRVQLRELSEAEVQHREAPALITSRLFT-----PKPDGLRPIVNM-- 637
Db 1010 LGPLPSQLTQOEVEEREL--QAEQNNSLAPPAVATHTTIGITHPPPD--IRTIVEKTA 1067
QY 638 YVVGARTFRREKRAERLTSRVKALPSVLYNERARRPGLIGASVLGLDDIHRARWTFVLRV 697
Db 1068 QFVSKNGLEFEKRI-----IVSNEKNAKENFLKSS---DPVHAFYQHKLTVEY 1111
QY 698 RAQD-----PPPELYFVKVDTGAYDTIP-----QDRLEVIASIKKQNTVC 740
Db 1112 RAQNKDGAQGTDDSDGTTDPQDTCADSEAGDTPDLQAQFRIPSKPLEAPEK-YT 1170
QY 741 VR 742
Db 1171 VR 1172

RESULT 27

S01955

Hypothetical protein, 69K - turnip yellow mosaic virus

C:Species: turnip yellow mosaic virus, TYMV

C:Date: 21-Nov-1993 #sequence_revision 26-May-1995 #text_change 09-Jul-2004

C:Accession: S01955

R:Morich, M.D.; Boyer, J.C.; Haenni, A.L.

Nucleic Acids Res. 16, 6157-6173, 1988

A:Title: Overlapping open reading frames revealed by complete nucleotide sequencing of t

A:Reference number: S01955; MUID:86289359; PMID:3399388

A:Accession: S01955

A>Status: preliminary
A:Molecule type: genomic RNA
A:Residues: 1-628 <MOR>
A:Cross-references: UNIPROT:P10357; EMBL:X07441; NID:G62222; PIDN:CAA30321.1; PID:G62223
A>Note: the authors translated the codon ACG for residue 459 as U
C:Superfamily: hydroxyproline-rich glycoprotein

Query Match 2.2%; Score 128.5; DB 2; Length 628;
Best Local Similarity 27.6%; Pred. No. 0.74;
Matches 89; Conservative 21; Mismatches 130; Indels 83; Gaps 18;

QY 172 GPLYQLGAATQARPPPHAS-GPRRLGCRANWHSVREAGVPLGL-----PAPGARRG 225
Db 157 GVLVETETPTSVQPRGATRG-----SFRPILLKVVVHDDPPHSSLSRPR 204
QY 226 GSASRSL-----PL-----PKRP-----RRGAAPERTPTVQCGSWAHPG 260
Db 205 GSRSLQLQPTVRRLAPNQFHSPPQPLSDDDGILGPRPLAHSRDP-----PP 256
QY 261 R--TRGPSD-----RGFCVVSPPARAEATSLGALSCTRHHSPSVGRQHHAGPPSTSRPP 314
Db 257 REITPGSNTHDLRLSLVLRTPSR-----RGLLENPRRHTSTG---HIPPTTTSRPT 307
QY 315 RPDWTFPCPVVAETKHYLYSSGDKQLRPSFL-----LSSLRPSLTGARRLVETIFLGRSP 370
Db 308 GP-----FSRLQRPVHLVQSSPHTFNFRSSIRKDALQTGRLGHLRLGQPANLRTSE 362
QY 371 WMPGTFRRLPLRPQRYWQMRPLFLELLG---NHAQCPYGVLLKTHCPRLA-AVTPAAGVC 426
Db 363 RSPPTKRRLPRSSSEPNRLKPLPEATLAPSYEHRR-PYPLFPNPAALPSIATYSSRGI 421
QY 427 AREKPGQSVAAPEE-EDTDPRRL 448
Db 422 HHSLPKG--ALPKGAPPPPRRL 442

RESULT 28
C75580
adenine deaminase-related protein - Deinococcus radiodurans (strain R1)
C:Species: Deinococcus radiodurans
C>Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C:Accession: C75580
R.White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;
S.; Smith, H.O.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; Ma
Science 286, 1571-1577, 1999
A>Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
A:Reference number: A75250; MUID:20036896; PMID:10567266
A:Accession: C75580
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-376 <WHI>
A:Cross-references: UNIPROT:Q9RYP2; GB:AE001863; GB:AE001825; NID:G6460670; PIDN:AAF1237
A:Experimental source: strain R1
C:Genetics:
A:Gene: DRA0268
A:Map position: 2

Query Match 2.1%; Score 128; DB 2; Length 376;
Best Local Similarity 25.1%; Pred. No. 0.39;
Matches 99; Conservative 23; Mismatches 123; Indels 150; Gaps 20;

QY 3 RAPRCRVRSLRSHYREVLPLATFVRRLGPGWBLVORGDDPAAPRALVAQCLVCPWDA 62
Db 93 RADRAGRAGSAAGARYREI-----LGPAR-----PRGDR-----PWVS 125
QY 63 PPPAPSPFRQVSCLELVARVLQRLCERGAGNVLAFGALLDARG-----GPPPEAF 115
Db 126 RLRLAARLAL-----RGAGN-----LRGRGSAARRRDAPPARW 161
QY 116 TTSVRSYLPNTVTDALRGSGAWGLLLRRVGGDVLVHLLARCALFVLVAPSCAYQVCGPPL 175
Db 162 RRRPRARL-----GRG-----HLRSARAL-----AHAPDVSRRPDR 191

QY 176 YQLGAATQARPPPHASGPRRLGCR-----AMNHSVREAGVPLGLPAP 219
Db 192 HRACGAGQRRRP---AGRRRLRARRVVVELLDVQORPARRRHPGHQSARRAS---GGPAR 245
QY 220 GARR---RGGSASRSLPLPKPRPGAAPEPERTVQCGSWAHP---GRTR---GPSDRGFC 271
Db 246 RQRGPARGGSGARTARRRHRPGRGRGPRAVAPALRGSDDRPASGRGRRRCFGPGDGG--- 303
QY 272 VVSPARPAEATSLGALSCTRHHSPSVGRQHHAGPPSTSRPPRWDTPCPVVAETKHF 331
Db 304 -----GALAGL---HLALSRH-----PEFSRPERDSGAQADAARPARDG 341
QY 332 LYSGDKKEQRPS-----FLSSLRPSL--TGAR 358
Db 342 VAIAGPGRVRRPSAHASFALHLTIARPEVRHTGAQ 376

RESULT 29
T31425
C-terminal domain-binding protein ra4, splice form 2 - rat (fragment)
C:Species: Rattus norvegicus (Norway rat)
C>Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
C:Accession: T31425
R.Yuryev, A.; Paturajan, M.; Litingtung, Y.; Joshi, R.V.; Gentile, C.; Gebara, M.; Cord
Proc. Natl. Acad. Sci. U.S.A. 93, 6975-6980, 1996
A>Title: The C-terminal domain of the largest subunit of RNA polymerase II interacts wit
A:Reference number: 221024; MUID:96293459; PMID:8692929
A:Accession: T31425
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-1048 <YUR>
A:Cross-references: UNIPROT:Q63627; EMBL:U49058; NID:G1438535; PID:G1438537; PIDN:AAAC526
A:Experimental source: hippocampus

Query Match 2.1%; Score 127.5; DB 2; Length 1048;
Best Local Similarity 22.4%; Pred. No. 1.7;
Matches 109; Conservative 38; Mismatches 169; Indels 171; Gaps 25;

QY 8 RAVSLRLSHYR---EVLPLATFVRRLGPGQWRLVQRGDPAAFRAL--VAQCLVCPWDA 62
Db 472 RALQKLSRGNYKVNQSIKIA-----WAL-NKGIKADFKQYWDVGLGVTVIPWD- 519
QY 63 RPPAPSPFRQVSCLELVARVLQRLCERGAGNVLAFGALLDG----- 106
Db 520 -----KVKAEELESFCEGG-----MLDSDTLNPDKWGIKKPEN 553
QY 107 --ARGGPEAFTTSVRSYLPNTVTDALRGSGAWGLLLRRVGGDVLVHLLARCALFVLVAP 164
Db 554 EVAQNGAGAEASHTEPVSPIPKPV-----PVPVPALPVPAPITVPPPP 594
QY 165 SCAYQVCGPPLYQLGAATQARPPPHASGPRRLGCRANWHSVREAGVPLGLPAPGARRR 224
Db 595 QVPHQPGPPV--VGA---LQPP--AFTP-----PLGIPPPGF--- 625
QY 225 GGSASRSLPLPKPRRGAAPERTPTVQCGSWAHPGRTRGSDRGFCVVSPPARPAEATS 284
Db 626 -GPGVPPPPPPPPPPFGFNPMLPPG---FLPPG-PPPIITPPVSIPTTPTTPISTPN 680
QY 285 LEGALSGTRHSHPSVGRQHHAGPPSTSRPPRWDTPCPVVAETKHYLYSSGDKQLRPS 344
Db 681 LVSGARGNAESADSAKMYGSAGPFAA-----FTSLTPFPV-TQPVSLGTQG-----VAPG 730
QY 345 FLSSLRPSLTGARRLVETIFLGRSPWM-----PGTP-----RRLPLRPQRYWQMRPLFL 394
Db 731 PVIGLQAPS-----TGLLGGRPGLIPLQRPFGMPPHLQRFPPWMPPR--PMPPHMM 779
QY 395 ELLGNHAQCPYGVLLKTHCPRLA-AVTPAAGVCAEKPOGSAAP-----BE 440
Db 780 ---HRGPPPG---PGFAMPPPHGMKGFPPHPGFVRPGMPLGPGPGPGGS 827
QY 441 EDTDPRR 447

C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C/Accession: A53800; 158395
R/Gallo, K.A.; Mark, M.R.; Scadden, D.T.; Wang, Z.; Gu, Q.; Godowski, P.J.
J. Biol. Chem. 269, 15092-15100, 1994
A/Title: Identification and characterization of SPRK, a novel src-homology 3 domain-cont
A/Reference number: A53800; MUID:94253068; PMID:8195146
A/Accession: A53800
A/Status: Preliminary
A/Molecule type: mRNA
A/Residues: 1-847 <GAL>
A/Cross-references: UNIPROT:Q16584; GB:U07747; NID:G464027; PIDN:AAA19647.1; PID:G464028
R/ing, Y.L.; Leung, I.W.; Heng, H.H.; Tsui, L.C.; Lassar, N.J.
Oncogene 9, 1745-1750, 1994
A/Title: MLK-3: identification of a widely-expressed protein kinase bearing an SH3 domain
A/Reference number: 158395; MUID:94239754; PMID:8183572
A/Accession: 158395
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-847 <RES>
A/Cross-references: GB:L32976; NID:G488295; PIDN:AAA59859.1; PID:G488296
C/Genetics:
A/Gene: GDB:MLK3; PTKJ; SPRK
A/Cross-references: GDB:134755; OMIM:600050
A/Map position: 11q13.1-11q13.3
C/Superfamily: mixed-lineage protein kinase 3; protein kinase homology; SH3 homology
C/Keywords: ATP; leucine zipper; phosphotransferase; serine/threonine-specific protein k
F:48-100/Domain: SH3 homology <SH32>
F:115-383/Domain: protein kinase homology <KIN>
F:123-131/Region: protein kinase ATP-binding motif
F:403-424/Region: leucine zipper motif
F:438-459/Region: leucine zipper motif
F:468-482/Region: basic

Query Match 2.1%; Score 127; DB 1; Length 847;
Best Local Similarity 23.1%; Pred. No. 1.4;
Matches 122; Conservative 49; Mismatches 179; Indels 178; Gaps 34;
QY 44 PAAFRALVAQCLVCPWDARPPAPSPQV-SCLKELVARVLQRL-----CERGAKN 95
Db 348 PEPFALMADC-----W-AQDPHRRPDPFASLIQQLALEAQVLEMRDPSFHSMQEGWKR 401
QY 96 VLAFGFALLDARG-----GPPEAFTTSVRSYLVNTVTDALRGS-----GAW----- 137
Db 402 ETQ-----GLFDELRAKEKELLSEBELTRAAR-ORSAEQLRREHLLAQWELVFERE 456
QY 138 -GLLRRV-----GDDVLVHLLARCAFLVLAQVAPSC-----A 167
Db 457 LTLQLQVDRERPHVRRRGTFRKSLRARDGGERISMPLOFKHRTTVOASPLDRRRNV 516
QY 168 YQVCGP---PLYQLAANTQARP---PPHAG---PRR-----RLGCERAWNHSVREAG 211
Db 517 FEV-FGFGDSPTFRFRATOLEPAEPGQAWGRSPRLRDSNGERRAC-WAWGFS----- 569
QY 212 VPLGLPAPGARRRGGSAGR-----SLPL-----PKPRRGAAPERT 249
Db 570 ----SPKFGAQNRRSRSMDEATWYLDSDSSPLGSPSTPALNGNPPRSLSEEPFR 625
QY 250 PVGQSWAHGTRGSPDRGFCVSP---ARPAEATSLGALSCTRHSHPVSGRQHAG 306
Db 626 PV-----PAERGSSTGPKLTQALLRGTTALLASGLGLRDLQPPGGPRERG 672
QY 307 PPSTSRPPRPWDTPCP--PVYAEATHFLYSSGDKQLRPSFLSSJ-----RPSLTGARR 359
Db 673 ESPTT-PTTETPACPTTEPPPSPLICFSLKTPDSPP-TPAPLLDLGIPVQGRSAKSPRR 730
QY 360 LVE-----TIFLSRRWMPGTPLRPLRQYQWMPRLFLELLGNHAQCPYGVLLKTH-CP 414
Db 731 EEEPRGGTV---SPP--PGTSASAGTP-----GTPRSPLGLISRPSP 771
QY 415 LRAAVTPAAGVCAREKPGQSVNAPEEDTPRLVOLLRQHSPQVY 462
Db 772 LRSRIDPWSFVSAGPRP-SPLSPQPA---PRR-----APWTLF 806

RESULT 34

T46289
hypothetical protein DKFZp434A1010.1 - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 09-Jul-2004
C/Accession: T46289
R/Duesterhoeft, A.; Lauber, J.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.
submitted to the Protein Sequence Database, January 2000
A/Reference number: Z23035
A/Accession: T46289
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-862 <AAA>
A/Cross-references: UNIPROT:Q9NT23; EMBL:AL137579
A/Experimental source: adult testis; clone DKFZp434A1010
C/Genetics:
A/Note: DKFZp434A1010.1

Query Match 2.1%; Score 127; DB 2; Length 862;
Best Local Similarity 21.8%; Pred. No. 1.4;
Matches 102; Conservative 28; Mismatches 147; Indels 130; Gaps 23;
QY 43 DPAAFRALVAQCLVCPWDARPP-----PAAPSFQV 74
Db 316 DPLTFR-----CSSPTPGDPAPPASPAPPASAPPRVTPQAISPRGPTSPASPAALDI 370
QY 75 SCLKELVARVLQRLCERGAKNVLAFGFALLDARGGPPPEAFTTSV---RSYLVNTVTD 130
Db 371 S--EPLAVSVPPAVLE-----LLGAGAPASATPTPALSFGRSIRPHILPLL 415
QY 131 LRSGAWGLLLRRVGGDVLVHLLARCAFLVLAQVAPSCYQVCG----- 172
Db 416 LRGAEA-----PLTDACQOEMCSKLGAQGLPGDMESPLP 451
QY 173 -PPLYQL--GAATOARPPPHASGPRRLG---CERAWNHSVREA-----GVPLGLPAPGA 221
Db 452 PPPUSLRPGA-----PPPPKNPARLMALAAQAAQVAAEQSQOQECGGTTPASQSPFH 507
QY 222 RRRGGSASRSLPLPKRP--RRGAAPERTPVGQGSWAHPG----- 260
Db 508 R-----SLSLVGVGELGTSGSGPPP-----NSLAHPGAWVGPVPPPLPQQSDGSL 554
QY 261 ----RTGPSDRGFCVSPAPPAEATSLGALSCTRHSHPVSGRQHAGPSTSRPP-- 314
Db 555 LRSQRPMTGTSRRGL-----RGPAQVSAQLRA--GGGGRDAPEAAQAQSPCVSPQVPTGPF 607
QY 315 -RPWDTPC-PPVYAEATHFLYSSGDKQLRPSFLSSLRPSLTGARRLVETIFLGSRRPM 372
Db 608 FSPAPRCLPFLGVPRGLYPLGP-----PSFQSPSPAP-----VWR 645
QY 373 P--GTPRRLRPLRQYQWMPRLFLELLGNHAQCPYGVLLKTHCPURA 417
Db 646 SSLGPPAPLDRGENLYE-----ICASEGSPYSGLTRSWSPFRS 684

RESULT 35

T35878
hypothetical protein SC9B10.09 - Streptomyces coelicolor
C/Species: Streptomyces coelicolor
C/Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C/Accession: T35878
R/Oliver, K.; Harris, D.; Parkhill, J.; Barrrell, B.G.; Rajandream, M.A.
submitted to the EMBL Data Library, November 1997
A/Reference number: Z21592
A/Accession: T35878
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-1039 <OLI>
A/Cross-references: UNIPROT:O50516; EMBL:AL009204; PIDN:CAA15799.1; GSPDB:GN00070; SCOE
A/Experimental source: strain A3(2)
C/Genetics:
A/Gene: SCOEDB:SC9B10.09

234	Db	ARVPDGLLLTPGLEPQVILGLRDQFE---ARRDQASQGEASQ---REOQORDER- 287
271	QY	CWSPARPAAEATSELEGALSGTRHSHPSVGRQHAGPSTSRPRPMDTPCPVVAETKH 330
288	Db	-QRNEDPRONA---EGRAPADREDPRRSEQRVSRRSEDRPREDR---FRDRR 339
331	QY	FLYSSGKEQLRPSFLLSSLRPSLTGARRLVETITFLGSRPWPMTGTPRRLPL- ---PORY 386
340	Db	---REGRRDRFRPS- -PGPDPTTGTGR-----RDDAPARPAELERFTFEAPQQA 384
387	QY	---WQMRPLFLELLGNHACQCYVLLKTHC-----PL----- 415
385	Db	PAPSEDLWPEPEIVF---SDHA---PQNVP- -THTVSSGPDAPPLPTPTPLADTLSEADA 437
416	QY	---RAAVTPAAGVCARE-----KPGGSVAAPEEEEETDPR 446
438	Db	GDAAAQVTPAELFVAEHAAPVSSSAQTFEPO--VEAPEPEAAEQ 480

RESULT 37
E98119
transposase, uncharacterized, truncation [imported] - Streptococcus pneumoniae
C:Species: Streptococcus pneumoniae
C:Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 09-Jul-2004
C:Accession: E98119
E: Hoskins, J.A.; Alborn Jr., W.; Arnold, J.; Blaszcak, L.; Burgett, S.; DeHoff
e, R.; LeBlanc, D.J.; Lee, L.N.; Lefkowitz, E.J.; Lu, J.; Matsushima, P.; McAhr
y, P.; Sun, P.M.; Winkler, M.E.
J. Bacteriol. 183, 5709-5717, 2001
A: Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskun
A: Title: Genome of the Bacterium Streptococcus pneumoniae Strain R6.
A: Reference number: A97872; MUID: 21429245; PMID: 11544234

[illegible]

Db 29 WILWALRSNSSAGKRSFSAIW-LLEKMAAAGCETGQGRGAPARRGRAPAYHSGPRR 87
QY 196 RLGCERAMNHSVREAGVPLGLPAPGARRRGSGASRSLP-LPKRRPRGAPEPERTPVGO- 253
Db 88 R-----APRRPGRGQGRGQPGARCAPSSPCTPGSGARSRRAFFARS 132
QY 254-----GSAH-PGRTRGSDRGFCVVSAPAEATSLGAL-----SGTRHSH-- 296
Db 133 AFSQADAPGPRHSPG---GRAGALRPSAAGCATQANSGRSALPRLRGTTTAAHWR 189
QY 297-----PSVGR-----QHAGPPSTS---RPPRPDTPCPVVAETKFLY 333
Db 190 LFIANSFWPAPRGGAALSAARSQHPGRPELSPRPDPAQASPAQDLAEET----- 244
QY 334 SSGDKQLRPSFLLSRLSLTGARRLVETIFLGRPMMPGTPRR-LP---RLPOR-YWQ 388
Db 245-----SGPWISGSPRTPLPLGGKLRASGH 270
QY 389 MRPL-FLELLGNHAQCPYGLVLTHTCPLR-AAVTAAAGVCAREKPGQGVAA 437
Db 271 SRTLGFIRILE-----PARLVOPAPAAAARGRAKAFGASAA 306
RESULT 46
A30411
synapsin Ia - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 23-Oct-1990 #sequence_revision 23-Oct-1990 #text_change 09-Jul-2004
C:Accession: A30411; B30411
R:Suedhof, T.C.; Czernik, A.J.; Kao, H.T.; Takei, K.; Johnston, P.A.; Horiuchi, A.; Kana
Science 245, 1474-1480, 1989
A:Title: Synapsins: mosaics of shared and individual domains in a family of synaptic ves
A:Reference number: A30411; MUID:89388265; PMID:2506642
A:Accession: A30411
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-704 <SUB>
A:Cross-references: UNIPROT:P09951; GB:M27812; NID:G206920; PIDN:AAA42145.1; PID:G206921
A:Accession: B30411
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-659, 'KA', 662, 'PAQAP' <SU2>
A:Cross-references: GB:M27924; NID:G206932; PIDN:AAA42148.1; PID:G206933
C:Keywords: actin binding; alternative splicing; phosphoprotein
Query Match 2.1%; Score 123.5; DB 2; Length 704;
Best Local Similarity 25.8%; Pred. No. 1.9;
Matches 69; Conservative 18; Mismatches 67; Indels 113; Gaps 15;
QY 172 GPPLYQLGAATQARPPP-----HASGPRRLRGGERAWNHSVREAGVPL--GLPAPGARRRG 225
Db 476 GPPL-----QORPPQOQHLSG---LG-----PPAGSPLPQLRPSPTAAPQ- 514
QY 226 GSASRLSLP-----PKRPRGAPEPER----- 248
Db 515 QSASQATPMTQOGRSQRSRPVAGGCPGAPPAARPPASPSPORQAGPQATQASISGPAPPK 574
QY 249 ----TPVCGSWAHPCRTGPDGFCVVSAPAEATSLGALSGTGHSHPSVGRQH 304
Db 575 VSGASPGGQGRGPPKPPGPA-----GPTRQASQAG-----PGPRTGPTTQQPRP 621
QY 305 AGPPSTSRPPR-----WDTFCPPVVAETKFLYSSGDKQLRPSFLLSRLPSLTGA 357
Db 622 SCGFAGRTKQLQAKSQSDVP-PPITAAAGPPHPQLNKSQ-----SLTVA 668
QY 358 RELVETIFLGRPMMPGTPRRPLRLPQ 384
Db 669 FNLP-----PAPPR--PSLSQ 683

RESULT 47
T42214
otogelin - mouse

N:Alternate names: mucin-like extracellular matrix protein
C:Species: Mus musculus (house mouse)
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 16-Aug-2004
C:Accession: T42214
R:Cohen-Salmon, M.; El-Anraoui, A.; Leibovici, M.; Petit, C.
Proc. Natl. Acad. Sci. U.S.A. 94, 14450-14455, 1997
A:Title: Otogelin: A glycoprotein specific to the acellular membranes of the inner ear.
A:Reference number: 222079; MUID:98070772; PMID:9405633
A:Accession: T42214
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-2910 <COH>
A:Cross-references: UNIPROT:O55225; EMBL:U96411; NID:G2760883; PID:G2760884; PIDN:AAB965
A:Experimental source: strain BALB/c
A:Note: Component of all the acellular membranes of the inner ear
C:Superfamily: von Willebrand factor type A repeat homology; von Willebrand factor type

Query Match 2.1%; Score 123.5; DB 2; Length 2910;
Best Local Similarity 18.8%; Pred. No. 13;
Matches 236; Conservative 115; Mismatches 393; Indels 513; Gaps 60;
QY 111 PPEAFTTSVRSYLPNTVTDALRGSGAWGLLLRRVGGDDVLVHLLARCALFVLVAPSCAVQV 170
Db 1473 PP---TTSABOQLP-----QGLPGASAYS-----PAPVPVAPPTS--A 1505
QY 171 CGPLYQLGAATOAR-PPPHASGP--RRRLGCERA-----WNHSVREAG----- 211
Db 1506 PNPPM---AATEGAPSPGSGTQPLTPIGLTNNPFPAGTTEATAREGAASLLTTSHP 1561
QY 212 -----VPLGLPAPGARRRG-----ASRSLPLPKRP---RRGAAP 244
Db 1562 PGFSSLSPLSQMPTSGIVSGATETTKVTITFTGSPNTTVASRSPPIPRFFLMTRAVTVP 1621
QY 245 EPERTPVG---QGSWAHPGRTGRGFCVVSAPR- 278
Db 1622 SHDSFPVKTTPLOQSWLMSLSRPMWLSGATSWPTSPGSHLSTAVTKVANKTWSLSVL 1681
QY 279 ABEATSLGALSG--TRHSHP-----SVGRQHAG-----PPSTSRPPRPW 317
Db 1682 AOSTSSSQPLAAVTAHRAFPASPLVTKGLVSVATEKEAGHSQLTLPVSPPPSPAPI 1741
QY 318 DTPCPPVVAETKFLYSSGDKQLRPSFLLSRLSLTGARRLVETIFLGRPMMPGTPR 377
Db 1742 DLHPACHTTT-----APGPSALSPG-ILAGSPS-TGAHRPGATALASLEPTRP--PH 1791
QY 378 RLPLPQRYWQMRPLFLELLGNHAQ-----CPYGVLL 409
Db 1792 LLSGLPLD-----TSLPLAKVGTSPVATPGSKGYIPTPPPOHQAATTLATMTVSLTOSL 1847
QY 410 KTHCPRLAAVTPAAGVCAREKPGQSVAAPEBEDTDPRRLVQLLRQHSSFWOVYGFVRACL 469
Db 1848 SLTVPLMSAVEQAHSPSPKPPQGTGMAPDQ-----MLGATLPSFGASSVIAG----- 1895
QY 470 RRLVPPGLWGRHNRRLNKKFISLGKHAULS-----LOELTWKMS--VR 515
Db 1896 ---VPPTVSAAPRKS-----TTQRAAILSK-KVSPPTLISDSVQGGTELTPIVSHVT 1945
QY 516 DCAMLRSPGVGCVPAAEHRLREELAKFLHLMWSVYVVELLSRFFYVTEFTFQKRLFF 575
Db 1946 PLATEAEGRAGTVP-----LVPTTYS----- 1967
QY 576 YKSWMSKLSIGIRQHLKRVQLRELSEAEVRQREARPAALLTSRLRIPKPDGLRPIVN 635
Db 1968 -----LSRVASARTAS-----REGPLVLLPOLAEAYGTPAGLQP--Q 2001
QY 636 MDYVVGARTFRKRAEELTSRVKALFSLVNY----- 667
Db 2002 EDLMQATTEQSGRSAPQAQSAEESMEAEVNTSATCPVIAEODCVHHICLEGQLIRVNOT 2061
QY 668 -----ERARRP--GLLGASV-LGLDDIHRW-----RTFVLVRQAQPPPELVKVDVTGA 716
Db 2062 QHCPQGAVRPRCGVLGLAVRVGGDRCCPQWECACRCSIF-----PDLSFVTFD--GS 2111


```
QY 656 SRVKALFSLVNTERRARRPGLGASVLGLDDIIRAWRTFVLVRADQPPPELYFV----- 709
Db 591 -----FDRVWHPGGL-----YKAKELF-----PQLLVVVKSFLE 620
QY 710 -----KVDVTGAYDTI-----PQDLTEVIASILKPNQYCVRRYAVVQKAHGHVRKA 758
Db 621 ERTFHVVDGYKSSIKPIAGVQ-----GSVLGP-----TLYSV----- 655
QY 759 FKSHVSTLTDLQYMRQFVAHLQETSPL-----RDAVVIEQSSSLNEASSGL---FDVPL 810
Db 656 FASDMPTHTP-----VTEVDEEDVLATYADDTAVLTKSILAAATSGIQEYLDARQ 707
QY 811 RFWCHAVRIRKSVQVOCIGIFQGSILSTLLSLCVGMENKLP-----GIRDDGLL 863
Db 708 OWAENWNRINAEL-----CA-----NVTFAVRTGSCFVSLNGRL 743
QY 864 LR-----LVDDFLAVTPLTHAKTFLTLV-----RGVPEYGCVVNLRTKV 904
Db 744 IRHQAKYKLGITLDRKLTFSRHITNIOAFRTKVARMSWLIAPRNKLSLGCCKVNIYKSI 803
QY 905 VNFVPEDEALGGTAFVQMPAHGLFPWGL-----LLDTRTLEVSQSYSSYART 952
Db 804 -----LAPCLFVLQVGYIAAKSHLNKIRILQAKTLRISGAPWYMT 846

RESULT 50
PHUSD
salivary proline-rich glycoprotein precursor PRB4 (large allele) (validated) - human
N:Contains: basic proline-rich protein IB-5; proline-rich peptide P-D
C:Species: Homo sapiens (man)
C:Date: 19-Feb-1984 #sequence revision 12-Apr-1996 #text change 09-Jul-2004
C:Accession: S03176; S03175; S10890; D25372; E38355; A03295; A61294; S62891
R:Lyons, K.M.; Stein, J.H.; Smithies, O.
Genetics 120, 267-278, 1988
A:Title: Length polymorphisms in human proline-rich protein genes generated by intrageni
A:Reference number: S02127; MUID:89121440; PMID:2851479
A:Accession: S03176
A>Status: translation not shown
A:Molecule type: DNA
A:Residues: 35-310 <LY1>
A:Cross-references: UNIPROT:P10163; UNIPROT:P10162; EMBL:X07715
A>Note: large allele
A:Accession: S03175
A>Status: translation not shown
A:Molecule type: DNA
A:Residues: 35-36 'E' 38-112 155-310 <LY2>
A:Cross-references: EMBL:X07704
A>Note: medium allele
A:Accession: S10890
A>Status: preliminary; translation not shown
A:Molecule type: DNA
A:Residues: 1-38, 60-112, 'T', 114-115, 'P', 117-121, 185-271, 'A', 273-310 <LY3>
A:Cross-references: EMBL:X07882; NID:G35647; PID:CA30729.1; PID:G296670
R:Maeda, N.; Kim, H.S.; Azen, E.A.; Smithies, O.
J. Biol. Chem. 260, 11123-11130, 1985
A:Title: Differential RNA splicing and post-translational cleavages in the human salivar
A:Reference number: A92492; MUID:85289325; PMID:2993301
A:Accession: D25372
A:Molecule type: mRNA
A:Residues: 1-36, 'E', 38-112, 'T', 114-115, 'P', 117-121, 185-271, 'A', 273-310 <MAE>
R:Kaufman, D.L.; Bennick, A.; Blum, M.; Keller, P.J.
Biochemistry 30, 3351-3356, 1991
A:Title: Basic proline-rich proteins from human parotid saliva: relationships of the cov
A:Reference number: A38355; MUID:91190884; PMID:1849422
A:Accession: E38355
A:Molecule type: protein
A:Residues: 241-254, 'KN', 257-310 <KAU>
R:Saitoh, E.; Iemura, S.; Sanada, K.
J. Biochem. 93, 495-502, 1983
A:Title: Complete amino acid sequence of a basic proline-rich peptide, P-D, from human P
A:Reference number: A03295; MUID:83186122; PMID:6841349
A:Accession: A03295
A:Molecule type: protein
```

```
A:Residues: 241-310 <SAI>
R:Shimomura, H.; Kanai, Y.; Sanada, K.
J. Biochem. 93, 857-863, 1983
A:Title: Amino acid sequences of glycopeptides obtained from basic proline-rich glycopro
A:Reference number: A61294; MUID:83265671; PMID:6874667
A:Accession: A61294
A:Molecule type: protein
A:Residues: 54-57, 'E', 59-73, 'R', 82-101 <SHI>
R:Charlton, A.J.; Baxter, N.J.; Lilley, T.H.; Haslam, E.; McDonald, C.J.; Williamson, M.
FBS Lett. 382, 289-292, 1996
A:Title: Tannin interactions with a full-length human salivary proline-rich protein dis
A:Reference number: S62891; MUID:96184506; PMID:8605987
A:Accession: S62891
A:Molecule type: protein
A:Residues: 241-252 <CHA>
A>Note: amino end of peptide designated basic proline-rich protein IB-5
A>Note: it is unclear from the peptide sequence whether this is a product of the PRB2 (1
C:Genetics:
A:Gene: GDB:PRB4
A:Cross-references: GDB:119514; OMIM:180990
A:Map position: 12p13.2-12p13.2
A:Introns: 22/1; 34/1
A>Note: the list of introns may be incomplete
C:Superfamily: proline-rich protein
C:Keywords: glycoprotein; saliva; tandem repeat
F:1-16/Domain: signal sequence #status predicted <SIG>
F:241-310/Product: proline-rich peptide P-D #status experimental <MAT>
F:66-87, 171/Binding site: carbohydrate (Asn) (covalent) #status experimental
F:108, 150, 192, 213, 234/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 2.1%; Score 122.5; DB 1; Length 310;
Best Local Similarity 23.7%; Pred. No. 0.72;
Matches 72; Conservative 13; Mismatches 86; Indels 133; Gaps 17;

QY 172 GPLYOLCAATQARPPHASPGRRLGCRANHNSVRAGVPLGLPAPCARRRGGSARS 231
Db 59 GPP-PQGNQSQGPPPP-----PGKPEGRPPQGNQSQGPP--- 93
QY 232 LPLKPRRR-----GAAPEP-----ERTPVG-----QGSWAHPGRTGRPSDRG--- 269
Db 94 -PHGKPERPPPPQGNQSQGPPPHGKPERPPQGHQSQQPPTFGKEGPPPPQGNQS 152
QY 270 -FCVVSPARPABEATSLGALSGTNRHSHPSVGRQHAGPPSTSRPRPMDTCPVPYAT 328
Db 153 QGTPPPPGKP-----EG-----RPPQGNQSQGPPPHGKPERP-----PP----- 188
QY 329 KHFLYSSGDKQLRPSFLLSLRPSLTGARRLVETIFLGSRPWMFGTPRRLPRLPORYWQ 388
Db 189 -----QGNQSHRP-----PPPGKPERPP-----PQG----- 211
QY 389 MRPLFLELGNHAOCFYGVLLKTHCFLRAAVTPAAGVCARE-----KPGSVAAPPEED 442
Db 212 -----GNQSQGP-----PPHKGKEGPPPPQGNKRSARSPPGKPGQ-----PQOQG 254
QY 443 TDPK 446
Db 255 NKQ 258

Search completed: August 5, 2005, 14:20:11
Job time : 62 secs
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 5, 2005, 14:04:33 ; Search time 189 Seconds
(without alignments)
3067.056 Million cell updates/sec

Title: US-10-053-758-225
Perfect score: 5961
Sequence: 1 MPRAPRCRAVRSLLRSHYRE.....TALEAAANPALPSPDFKTLTD 1132

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt_03.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	5961	100.0	1132	1 TERT HUMAN	O14746 homo sapien
2	5583.5	93.7	1069	2 Q8NG46	Q8NG46 homo sapien
3	4089.5	68.6	1123	1 TERT CANFA	G6A548 canis faml
4	4052	68.0	807	2 Q8NGC3	Q8A6C3 homo sapien
5	3973	66.6	795	2 Q8NG38	Q8NG38 homo sapien
6	3628	60.9	1128	2 Q9QXZ4	Q9QXZ4 mesocricetu
7	3529.5	59.2	1125	2 Q673L6	Q673L6 rattus norv
8	3514.5	59.0	1119	2 Q673L5	Q673L5 rattus norv
9	3505	58.8	1122	1 TERT MOUSE	O70372 mus musculu
10	2825	47.4	524	2 Q9UBR6	Q9UBR6 homo sapien
11	2590	43.4	1346	2 Q6RD80	Q6RD80 gallus gall
12	2316.5	38.9	1191	2 Q9DE32	Q9DE32 xenopus lae
13	2207.5	37.0	523	2 Q9A407	Q9A407 homo sapien
14	2016	33.8	575	2 Q9UK99	Q9UK99 rattus norv
15	1408	23.6	615	2 Q673L3	Q673L3 rattus norv
16	1373	23.0	514	2 Q9R266	Q9R266 mus musculu
17	724.5	12.2	1123	2 Q9SE99	Q9SE99 arabidopsis
18	724.5	12.2	1123	2 Q9SPU7	Q9SPU7 arabidopsis
19	688	11.5	1259	2 Q9AU13	Q9AU13 oryza sativ
20	654.5	11.0	1261	2 Q8LKW0	Q8LKW0 oryza sativ
21	594	10.0	988	1 TERT SCHPO	O13339 schizosacch
22	478	8.0	1032	2 Q7Z1L1	Q7Z1L1 eplotes cr
23	474	8.0	1032	2 Q8WUB3	Q8WUB3 eplotes cr
24	469.5	7.9	939	2 Q7SD71	Q7SD71 neurospora
25	450	7.5	85	2 Q9UN56	Q9UN56 homo sapien
26	450	7.5	940	2 Q6C9D0	Q6C9D0 varrowia li
27	449	7.5	116	2 Q8OSU5	Q8OSU5 rattus norv
28	448.5	7.5	1031	1 TERT EUPAE	Q00939 eplotes ae
29	441	7.4	1032	2 Q7Z1L0	Q7Z1L0 eplotes cr
30	408	6.8	823	2 Q8SQQ0	Q8SQQ0 encephalito
31	397	6.7	104	2 Q9J1M1	Q9J1M1 mus musculu

32	395.5	6.6	1135	2 Q818Z7	Q818Z7 sterkiella
33	395	6.6	1132	1 TERT OXYTR	O76332 oxytricha t
34	394	6.6	73	2 Q9UNR4	Q9UNR4 homo sapien
35	392	6.6	1108	2 Q818Z6	Q818Z6 sterkiella
36	389.5	6.5	861	2 Q8CSS0	Q8CSS0 kluyveromyc
37	365	6.1	867	2 Q9P8T3	Q9P8T3 candida alb
38	364	6.1	895	2 Q9GRCS	Q9GRCS paramecium
39	363	6.1	1117	1 TERT TETTH	O77448 tetrahymena
40	361	6.1	867	2 Q9P8T2	Q9P8T2 candida alb
41	356.5	6.0	884	1 TERT YEAST	Q06163 saccharomyc
42	355.5	6.0	894	2 Q6BU66	Q6BU66 debaromyce
43	342	5.7	896	2 Q8MUQ8	Q8MUQ8 paramecium
44	339	5.7	79	2 Q7YR69	Q7YR69 felis silve
45	338	5.7	79	2 Q76K45	Q76K45 canis faml

ALIGNMENTS

RESULT 1	ID	TERT HUMAN	STANDARD	PRT	1132 AA
AC	O14746	O14746			
DT	30-MAY-2000	(Rel. 39, Created)			
DT	30-MAY-2000	(Rel. 39, Last sequence update)			
DT	25-OCT-2004	(Rel. 45, Last annotation update)			
DE	Telomerase reverse transcriptase (EC 2.7.7.-) (Telomerase catalytic subunit) (HES2) (Telomerase-associated protein 2) (TP2).				
DE	Name=TERT; Synonyms=EST2, TCS1, TET;				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
OX	NCBI_TaxID=9606;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	TISSUE=Kidney;				
RX	MEDLINE=97400623; PubMed=9252327; DOI=10.1126/science.277.5328.955;				
RA	Nakamura T.M., Morin G.B., Chapin K.B., Weinrich S.L., Andrews W.H.,				
RA	Lingner J., Harley C.B., Cech T.R.;				
RT	"Telomerase catalytic subunit homologs from fission yeast and human.";				
RL	Science 277:955-959(1997).				
RN	[2]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=97433088; PubMed=9288757; DOI=10.1016/S0092-8674(00)80538-3;				
RA	Meyerson M., Counter C.M., Eaton E.N., Ellisen L.W., Steiner P.,				
RA	Caddle S.D., Ziaugra L., Beijersbergen R.L., Davidoff M.J., Liu Q.,				
RA	Bacchetti S., Haber D.A., Weinberg R.A.;				
RT	"hEST2, the putative human telomerase catalytic subunit gene, is up-regulated in tumor cells and during immortalization.";				
RL	Cell 90:785-795(1997).				
RN	[3]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=9267414; PubMed=10333526; DOI=10.1016/S0378-1119(99)00108-0;				
RA	Wick M., Zubov D., Hagen G.,				
RT	"Genomic organization and promoter characterization of the gene encoding the human telomerase reverse transcriptase (hTERT).";				
RL	Gene 232:97-106(1999).				
RN	[4]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=9267414; PubMed=10333526; DOI=10.1016/S0378-1119(99)00108-0;				
RA	Wick M., Zubov D., Hagen G.,				
RT	"Sequence of a BAC carrying the entire hTERT gene.";				
RL	Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.				
RN	[5]				
RP	FUNCTION IN TELOMERASE ACTIVITY, TISSUE SPECIFICITY, ASSOCIATION WITH				
RP	TEPI, AND MUTAGENESIS OF ASP-868; ASP-869 AND ASP-712.				
RX	PubMed=9389643;				
RA	Harrington L., Zhou W., McPhail J., Oulton R., Yeung D.S., Mar V.,				
RA	Bass M.B., Robinson M.O.;				
RT	"Human telomerase contains evolutionarily conserved catalytic and structural subunits.";				
RL	Genes Dev. 11:3109-3115(1997).				
RN	[6]				
RP	ASSOCIATION WITH TEPI.				

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RX PubMed-11029039;
RA Beattie T.B.; Zhou W., Robinson M.O., Harrington L.;
RT "Polymerization defects within human telomerase are distinct from
RL Mol. Biol. Cell 11:3329-3340(2000).
CC -!- FUNCTION: Telomerase is a ribonucleoprotein enzyme essential for
CC the replication of chromosome termini in most eukaryotes. It
CC elongates telomeres. It is a reverse transcriptase that adds
CC simple sequence repeats to chromosome ends by copying a template
CC sequence within the RNA component of the enzyme.
CC -!- SUBUNIT: Component of the telomerase ribonucleoprotein complex at
CC least composed of TEP1, EST1A, POT1 and a telomerase RNA template
CC component (TER). Interacts with PINK1.
CC -!- SUBCELLULAR LOCATION: Nuclear.
CC -!- DISEASE: Activation of telomerase has been implicated in cell
CC immortalization and cancer cell pathogenesis.
CC -!- SIMILARITY: Belongs to the reverse transcriptase family.
CC Telomerase subfamily.
CC -!- SIMILARITY: Contains 1 reverse transcriptase domain.
CC
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC
CC EMBL; AF015950; AAC51672.1; -.
CC EMBL; AF018167; AAC51724.1; -.
CC EMBL; AF128894; AAD30037.1; -.
CC EMBL; AF128893; AAD30037.1; JOINED.
CC EMBL; AY007685; AAG23289.1; -.
CC PIR; T03844; T03844.
CC Genew; HGNC:11730; TERT.
CC MIM; 187270; -.
CC GO; GO:0000781; C:chromosome, telomeric region; TAS.
CC GO; GO:0042162; F:telomeric DNA binding; TAS.
CC GO; GO:0003721; F:telomeric template RNA reverse transcriptase. . .; TAS.
CC InterPro; IPR000477; RVTse.
CC InterPro; IPR003545; Telomerase_RT.
CC Pfam; PF000078; RVT; 1.
CC PRINTS; PR01365; TELOMERASERT.
CC PROSITE; PS50878; RT_POL; 1.
KW DNA-binding; Nuclear protein; Ribonucleoprotein;
KW RNA-directed DNA polymerase; Telomere; Reverse transcriptase.
FT DOMAIN 605 935
FT MUTAGEN 868 868 D->A: Loss of telomerase activity.
FT MUTAGEN 868 869 DD->AA: Loss of telomerase activity.
FT MUTAGEN 869 869 D->A: Loss of telomerase activity.
FT MUTAGEN 712 712 D->A: Loss of telomerase activity.
FT CONFLICT 516 516 D -> G (in Ref. 2).
SQ SEQUENCE 1132 AA; 126996 MW; 94E35469C4CA33A0 CRC64;

Query Match 100.0%; Score 5961; DB 1; Length 1132;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPRAPRCRAVRSLLSHRYEVLPATFVRRLPQGRVLRVQGRDPAAFRALVAQCILVCVPW 60
DB 1 MPRAPRCRAVRSLLSHRYEVLPATFVRRLPQGRVLRVQGRDPAAFRALVAQCILVCVPW 60

QY 61 DARPPPAAPSPQVSCLEKELVARVLQRLCERGAKNVLAFGFALLDGAAGGPPPEAFTTSVR 120
DB 61 DARPPPAAPSPQVSCLEKELVARVLQRLCERGAKNVLAFGFALLDGAAGGPPPEAFTTSVR 120

QY 121 SYLPTNTVTDALRGSGAWGLLRVCGDDVLVHLARCALFVLVAPSCAYQVCGPPLYQLGA 180
DB 121 SYLPTNTVTDALRGSGAWGLLRVCGDDVLVHLARCALFVLVAPSCAYQVCGPPLYQLGA 180

QY 181 ATQARPPPHASPRRLRCERAWNHSVREAGVPLGLPAPGARRRGSGASRSILPLPKRPRR 240
DB 181 ATQARPPPHASPRRLRCERAWNHSVREAGVPLGLPAPGARRRGSGASRSILPLPKRPRR 240

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QY 241 GAAPEPERTVPGQSWAHPPGRTGPRGFCVSPARPAEATSLGALSSTRHSHPSVG 300
DB 241 GAAPEPERTVPGQSWAHPPGRTGPRGFCVSPARPAEATSLGALSSTRHSHPSVG 300

QY 301 ROHHAGPSTSRPPRPWDTPCPVYATKHFYSSGDKQLRPSFLISSLPSTLTGARRL 360
DB 301 ROHHAGPSTSRPPRPWDTPCPVYATKHFYSSGDKQLRPSFLISSLPSTLTGARRL 360

QY 361 VETIFLGSRRPMPGTPRRLPRLPORYQWRPLFLELLGNHAQCPYGVLLKTHCPRLAAVT 420
DB 361 VETIFLGSRRPMPGTPRRLPRLPORYQWRPLFLELLGNHAQCPYGVLLKTHCPRLAAVT 420

QY 421 PAAGVCAREKPPQGSVAAPSEEDTPRRLVQLLRHSSPQWYVGVFVACRLRLVPPGLMGS 480
DB 421 PAAGVCAREKPPQGSVAAPSEEDTPRRLVQLLRHSSPQWYVGVFVACRLRLVPPGLMGS 480

QY 481 RHNERFLRNTKKEFISLGKAKLSLOELTWKMSVRDCAKLRRSPGVCVPAAEHRLBEI 540
DB 481 RHNERFLRNTKKEFISLGKAKLSLOELTWKMSVRDCAKLRRSPGVCVPAAEHRLBEI 540

QY 541 LAKELHLMMSVYVVELLRSFPYVTTTFQKNRLFYFKSVMSKLSQSIGIRQHLKRVQLRE 600
DB 541 LAKELHLMMSVYVVELLRSFPYVTTTFQKNRLFYFKSVMSKLSQSIGIRQHLKRVQLRE 600

QY 601 LSEAEVQHRHREARPAALLTSRLRFPKPDGLRPIVNMVYVVGARTFRREKRAERLTSRVA 660
DB 601 LSEAEVQHRHREARPAALLTSRLRFPKPDGLRPIVNMVYVVGARTFRREKRAERLTSRVA 660

QY 720 LFSVLNTERARRPGLLGASVLGLDDIHRAWRTFVLVRAQDPPPELVKVDVTGAYDTI 720
DB 720 LFSVLNTERARRPGLLGASVLGLDDIHRAWRTFVLVRAQDPPPELVKVDVTGAYDTI 720

QY 780 PQDLTEVIASIIKPONTYCVRRYAVVQKAAGHVRKAFKSHVSTLTLDQPYMQFVAHL 780
DB 780 PQDLTEVIASIIKPONTYCVRRYAVVQKAAGHVRKAFKSHVSTLTLDQPYMQFVAHL 780

QY 781 QETSPLRDADVIEOSSSLNEASSGLFDVFLRFMCHHAVIRNGKSYVQCQGIPOQSILSTL 840
DB 781 QETSPLRDADVIEOSSSLNEASSGLFDVFLRFMCHHAVIRNGKSYVQCQGIPOQSILSTL 840

QY 841 LCSLCYGDMEKMLFAGIRRDGLLRVDDLLVTPHLLTHAKTFLRTLVRGVPEYGCVVNL 900
DB 841 LCSLCYGDMEKMLFAGIRRDGLLRVDDLLVTPHLLTHAKTFLRTLVRGVPEYGCVVNL 900

QY 901 RKTVVNPFVEDEALGGTAFVQMPAHGLFPWCGLLLDTRTLEVSQSDYSYARTSIRASLTF 960
DB 901 RKTVVNPFVEDEALGGTAFVQMPAHGLFPWCGLLLDTRTLEVSQSDYSYARTSIRASLTF 960

QY 961 NRGFKAGNNMRKLFGLVLRKCHSLFLDLQVNSLQTVCTNIYKILLQAYRFHACVLOLP 1020
DB 961 NRGFKAGNNMRKLFGLVLRKCHSLFLDLQVNSLQTVCTNIYKILLQAYRFHACVLOLP 1020

QY 1021 PHQOVWKNPTFFLRVSDTASLCYSILKAKNAGSLGAKGAAGPLPSEAVOMLCHOAPLL 1080
DB 1021 PHQOVWKNPTFFLRVSDTASLCYSILKAKNAGSLGAKGAAGPLPSEAVOMLCHOAPLL 1080

QY 1081 KLTRHRVTVYVPLLGSLRTAQTLRSKLPGLTTLTALEAAANPALPSDFKTIIL 1132
DB 1081 KLTRHRVTVYVPLLGSLRTAQTLRSKLPGLTTLTALEAAANPALPSDFKTIIL 1132

RESULT 2
Q8NG46
ID Q8NG46 PRELIMINARY; PRT; 1069 AA.
AC Q8NG46;
DT 01-OCT-2002 (TReMBLrel. 22, Created)
DT 01-OCT-2002 (TReMBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE Telomerase reverse transcriptase.
GN Name=hTERT;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

```


OC Mammalia, Eutheria, Primates; Catarrhini; Hominoidea; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Hisatomi H., Ohyaishiki K., Ohyaishiki J.H., Nagao K., Kanamaru T.,
 RA Hirata H., Hibi N., Tsukada Y.,
 RT "Expression profile of a gamma-deletion variant of the human
 RT telomerase reverse transcriptase gene.";
 RL Neoplasia 5:193-197(2003).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Nagao K., Katumata K., Aizawa Y., Saito N., Hirata H., Sasaki H.,
 RA Yamamoto S., Hikiji K., Koike T., Hisatomi H.,
 RT "Differential alternative splicing expressions of telomerase reverse
 RT transcriptase in gastrointestinal cell lines.";
 RL Oncol. Rep. 11:127-131(2004).
 DR EMBL; AB085628; BAC11010.1; -;
 DR GO; GO:0005634; C:nucleus; IEA.
 DR GO; GO:0003677; F:DNA binding; IEA.
 DR GO; GO:0003964; F:RNA-directed DNA polymerase activity; IEA.
 DR GO; GO:0003721; F:telomeric template RNA reverse transcriptase...; IEA.
 DR InterPro; IPR003545; Telomerase_RT.
 DR PRINTS; PR01365; TELOMERASERT.
 DR RNA-directed DNA polymerase.
 SQ SEQUENCE 1069 AA; 120046 MW; BE1E77A653B1C666 CRC64;
 Query Match 93.7%; Score 5583.5; DB 2; Length 1069;
 Best Local Similarity 94.4%; Pred. No. 0;
 Matches 1069; Conservative 0; Mismatches 0; Indels 63; Gaps 1;
 OY. 1 MPAPRCRAVRSLRSHYREVLPLATFVRRLPGQWRLVQRGDPAAFRALVAQCLVCPW 60
 DB 1 MPAPRCRAVRSLRSHYREVLPLATFVRRLPGQWRLVQRGDPAAFRALVAQCLVCPW 60
 OY 61 DARPPAPSPROVCLKELVARLQRCERAKNVLAFGFPALLDGCARGPPEATTSVR 120
 DB 61 DARPPAPSPROVCLKELVARLQRCERAKNVLAFGFPALLDGCARGPPEATTSVR 120
 OY 121 SYLPTNTVDALGSGAWGLLRVGGDVLVHLLARCALFVLVAPSCAVQCGPPLVQLGA 180
 DB 121 SYLPTNTVDALGSGAWGLLRVGGDVLVHLLARCALFVLVAPSCAVQCGPPLVQLGA 180
 OY 181 ATOARPPPHASGPRRLRCERAWNHSVREAGVPLGLPAPGARRRGGASRSPLPKPRR 240
 DB 181 ATOARPPPHASGPRRLRCERAWNHSVREAGVPLGLPAPGARRRGGASRSPLPKPRR 240
 OY 241 GAAPERTPVQGSWAHPGRTGSDRGFCVSPAPAEATSLGALSGTRHSHPSVG 300
 DB 241 GAAPERTPVQGSWAHPGRTGSDRGFCVSPAPAEATSLGALSGTRHSHPSVG 300
 OY 301 ROHAGPPTSPRPPWDTPCPVVAETKHFYSSGDKQLRPSFLLSRLSLTGARRL 360
 DB 301 ROHAGPPTSPRPPWDTPCPVVAETKHFYSSGDKQLRPSFLLSRLSLTGARRL 360
 OY 361 VETIFLGRPMWPGTFRPLRPLQRYWQMRPLFLELLGNHACQPGVLLKTHCPLRAVT 420
 DB 361 VETIFLGRPMWPGTFRPLRPLQRYWQMRPLFLELLGNHACQPGVLLKTHCPLRAVT 420
 OY 421 PAAGVCAREKPGSVAAPPEEDTPRRLVQLLRQHSSPMQVYGFVRACLRLVPPGLWGS 480
 DB 421 PAAGVCAREKPGSVAAPPEEDTPRRLVQLLRQHSSPMQVYGFVRACLRLVPPGLWGS 480
 OY 481 RNERERFLNTKFFISLGHAKLSLOELTWKMSVRDCAWLRSRPGVCPAAEHLRSEI 540
 DB 481 RNERERFLNTKFFISLGHAKLSLOELTWKMSVRDCAWLRSRPGVCPAAEHLRSEI 540
 OY 541 LAKFLHLMVSVVILLRFFVYTTTFOKNLFFYRKSVMKLSQIGIRQHLKRVQRE 600
 DB 541 LAKFLHLMVSVVILLRFFVYTTTFOKNLFFYRKSVMKLSQIGIRQHLKRVQRE 600
 OY 601 LSEAEVRQHREARPAALLTSLRFLPKPDGLRPIVNDYVVGARTFRREKRAELTSLRVA 660
 DB 601 LSEAEVRQHREARPAALLTSLRFLPKPDGLRPIVNDYVVGARTFRREKRAELTSLRVA 660

661 LFSVLNTERARRPGLLGASVLGLDDIHRARWTFVLVRVAQDPPPELYFKVDVTCAYDTI 720
 DB 661 LFSVLNTERARRPGLLGASVLGLDDIHRARWTFVLVRVAQDPPPELYFKVDVTCAYDTI 720
 OY 721 PODRLTEVIASIIKPNQTYCVRRYAVVQKAAHGHVRKAFKSHVSTLTDLQPTMRQFVAHL 780
 DB 721 PODRLTEVIASIIKPNQTYCVRRYAVVQKAAHGHVRKAFKSHVSTLTDLQPTMRQFVAHL 780
 OY 781 QETSPLRDVAVTEQSSSINEASSGLDFVLRPMCHHVRIRKSVVQCGIFQGSSTLSTL 840
 DB 781 QETSPLRDVAVTEQSSSINEASSGLDFVLRPMCHHVRIRKSVVQCGIFQGSSTLSTL 840
 OY 841 LCSLCYGMENKLFAGIRRDGLLLRLVDDFLVTPHLTHAKTFLTRLVGRVPEYGCWNL 900
 DB 841 LCSLCYGMENKLFAGIRRDGLLLRLVDDFLVTPHLTHAKTFLTRLVGRVPEYGCWNL 900
 OY 901 RKTUVNPFVEDEALGGTAFVQMPAHGLFPWCGLLDDTLTLEVSQSYSSVARSIRASLTFF 960
 DB 885 -----SYARTSIRASLTFF 897
 OY 961 NRGFKAGNRMRKLFGLVLRKCHSLFLDLQVNSLQVCTNIYKILLQAYRHACVQLQ 1020
 DB 961 NRGFKAGNRMRKLFGLVLRKCHSLFLDLQVNSLQVCTNIYKILLQAYRHACVQLQ 1020
 OY 958 FHQQVWKNPFTFLVIRVISTASLCYSLKAKNAGMSLGAAGPLPSEAVQWLCHQAFLL 1017
 DB 958 FHQQVWKNPFTFLVIRVISTASLCYSLKAKNAGMSLGAAGPLPSEAVQWLCHQAFLL 1017
 OY 1021 KLTHRVTVYVPLLSGLRTAQLSRKLPGLTTLTALEAAANPALPSDFKTILD 1132
 DB 1018 KLTHRVTVYVPLLSGLRTAQLSRKLPGLTTLTALEAAANPALPSDFKTILD 1069

RESULT 3
 ID TERT CANFA STANDARD; PRT; 1123 AA.
 AC Q6A548;
 DT 25-OCT-2004 (Rel. 45, Created)
 DT 25-OCT-2004 (Rel. 45, Last sequence update)
 DT 25-JAN-2005 (Rel. 46, Last annotation update)
 DE Telomerase reverse transcriptase (EC 2.7.7.-) (Telomerase catalytic subunit).
 GN Name=TERT;
 OS Canis familiaris (Dog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
 OX NCBI_TaxID=9615;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX PubMed=15225880; DOI=10.1016/j.gene.2004.03.032;
 RA Nasir L., Gault E., Campbell S., Veeramalai M., Gilbert D.,
 RA McFarlane R., Munro A., Argyle D.J.;
 RT "Isolation and expression of the reverse transcriptase component of
 RT the Canis familiaris telomerase ribonucleoprotein (dogTERT).";
 RL Gene 336:105-113(2004).
 CC -!- FUNCTION: Telomerase is a ribonucleoprotein enzyme essential for
 CC the replication of chromosome termini in most eukaryotes. It
 CC elongates telomeres. It is a reverse transcriptase that adds
 CC simple sequence repeats to chromosome ends by copying a template
 CC sequence within the RNA component of the enzyme.
 CC -!- SUBUNIT: Component of the telomerase ribonucleoprotein complex at
 CC least composed of TEP1, EST1A, POT1 and a telomerase RNA template
 CC component (TER). Interacts with PINX1 (by similarity).
 CC -!- SUBCELLULAR LOCATION: Nuclear.
 CC -!- SIMILARITY: Belongs to the reverse transcriptase family.
 CC -!- SIMILARITY: Contains 1 reverse transcriptase domain.
 CC -----
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 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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 CC use by non-profit institutions as long as its content is in no way

Db	858	VDDFLVTHLTQAQAFRLTLVKGVPEYCCGRANLQKTAVNPFVEDGALSGAAAPLQIPAHK	917
Qy	927	LPFWCGLLDTRTLEVSQDSYSSYARTSIRASLTFNRGFKAGRNRRLKLVGLRLKCHSLF	986
Db	918	LPFWCGLLDTRTLEVSQDSYSSYARTSIRASLTFNQAKPGRNRRLKLVGLRLKCCALF	977

D _b	LDLVNGGIHTYVMNVYKIFLLQAYRHACVQLQFPNQFVRKNPSFFRLRVIADTASCCYSL	1037
	978	
	LDLVNSLQTVCTNITKILLQAYRHACVQLQFPHQGVWKNPTFFKRVISDIATSLCYSI	1044
Q _Y	987	

QY 1047 LKAKNAGMSLGAKGAAGPLPSEAVQWLC HQAFLLKLTRHRTVTVPLGSLRQTACTQLSRK 1106
|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:
Db 1038 LKARNAGLSIGAKGASGLFPSEARWLCLHFAFLKLAAHSHTYRCLLLGGALQAQKAHLRSQ 1097

Qy 1107 LPRGTTTLTALEAAANPALPSDFKTILD 1132
|| || || || || : | : || || ||
Dd 1098 LPRGTTLALEAAADPSLTADFXTILD 1123

RESULT 4	
Q8N6C3	
ID Q8N6C3	PRELIMINARY; PRT; 807 AA.

AC Q8N6C3;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)

DE Beta and gamma deletion isoform of telomerase reverse
DE transcriptase.
GN Name=hTERT;
OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]

RP SEQUENCE FROM N.A.
RC TISSUE=Gastric cancer;
RA Hisatomi H., Ohyashiki K., Ohyashiki J.H., Negao K., Kanamaru T.,
RA Hirata H., Hibi N., Tsukada Y.;

RT "Expression profile of a gamma-deletion variant of the human
RT telomerase reverse transcriptase gene.";
RL Neoplasia 5:193-197(2003).
RN [2]
RN

RP SEQUENCE FROM N.A.
RC TISSUE=Gastric cancer;
RA Nagao K., Katsumata K., Aizawa Y., Saito N., Hirata H., Sasaki H.,
RA Yamamoto S., Hikiiji K., Koiwa T., Hiyatomi H.

RT "Differential alternative splicing expressions of telomerase reverse
RT transcriptase in gastrointestinal cell lines.";
RL
RL Oncol. Rep. 11:127-131(2004).
DR EMRI., AR086379. BAC11014 1. -

DR	GO:0005634	C:nucleus; IEA.
DR	GO:0003677	F:DNA binding; IEA.
DR	GO:0003964	F:RNA-directed DNA polymerase activity; IEA.
DR	GO:0003721	F:telomeric template DNA reverse transcriptase activity; IEA.

CO, GP, 00003221, Telomerase template RNA reverse transcriptions: ., 100.
DR InterPr: IPR003545; Telomerase_RT.
DR PRINTS; PR01365; TELOMERASERT.
KW RNA-directed DNA polymerase. 1006644500P00703 CD064.

Query Match 68.0%; Score 4052; DB 2; Length 807;
Best Local Similarity 100.0%; Pred. No. 3.6e-241;
SQ SEQUENCE 807 AA; 50225 MW; 1590644800CE0D783 CRC64;

[illegible][illegible]

Db 61 DARPPAAPSFQVSCLEKELVARVLQRLCERGAKNVLAFGFALLDGAAGGPPPEAFTTSVR 120
 QY 121 SYLNTVNTDALTGSGGAWGLLRRVGGDVLVHLLARCALFVLVAPSCAYQVCGPPPLYQLGA 180
 Db 121 SYLNTVNTDALTGSGGAWGLLRRVGGDVLVHLLARCALFVLVAPSCAYQVCGPPPLYQLGA 180
 QY 181 ATQARPPPHASGPRRLCERAWNHISVRAGVPLGLPAPGARRRGGASRSILPKRPPR 240
 Db 181 ATQARPPPHASGPRRLCERAWNHISVRAGVPLGLPAPGARRRGGASRSILPKRPPR 240
 QY 241 GAAPPERTPVQGSWAHPGRTGSDRGFCVVSPPARPAEATSLGALSGRHSHPSVG 300
 Db 241 GAAPPERTPVQGSWAHPGRTGSDRGFCVVSPPARPAEATSLGALSGRHSHPSVG 300
 QY 301 RQHAGPPSTSRPPRPMWTPCPVVAETKHFLYSSGDKBQLRPSFLLSLRSLTGARL 360
 Db 301 RQHAGPPSTSRPPRPMWTPCPVVAETKHFLYSSGDKBQLRPSFLLSLRSLTGARL 360
 QY 361 VETIFLGSRPWMPGTPRRLPRLPQRYWQMRPLFLELLGNHAOCQYGVLLKTHCPLRAAVT 420
 Db 361 VETIFLGSRPWMPGTPRRLPRLPQRYWQMRPLFLELLGNHAOCQYGVLLKTHCPLRAAVT 420
 QY 421 PAAGVCAREKPGQSVAAPEEEDTDPRLLVQLLRHSSPMQVYGFVRACLRRLVPPGLMGS 480
 Db 421 PAAGVCAREKPGQSVAAPEEEDTDPRLLVQLLRHSSPMQVYGFVRACLRRLVPPGLMGS 480
 QY 481 RHNERFLRNTKFFISLGHAKLSLOELTWKMSVRDCAWLRSPGVGCVPAAEHRLREBI 540
 Db 481 RHNERFLRNTKFFISLGHAKLSLOELTWKMSVRDCAWLRSPGVGCVPAAEHRLREBI 540
 QY 541 LAKFLHLMSSVYVVELLSRFFVTTFQKNRLLFFYRKSVWSKLSQSIGIRQHLKRVQRE 600
 Db 541 LAKFLHLMSSVYVVELLSRFFVTTFQKNRLLFFYRKSVWSKLSQSIGIRQHLKRVQRE 600
 QY 601 LSEAEVROHREARPAALLTSRLRPIPKDGLRPIVNM DYVVGARTFRREKRAERLTSRVKA 660
 Db 601 LSEAEVROHREARPAALLTSRLRPIPKDGLRPIVNM DYVVGARTFRREKRAERLTSRVKA 660
 QY 661 LFSVLNYERARRPGLLGASVLGLDDIHRARWTFVLVRVRAQDPPPELYFVKVDVTGAYDTI 720
 Db 661 LFSVLNYERARRPGLLGASVLGLDDIHRARWTFVLVRVRAQDPPPELYFVKVDVTGAYDTI 720
 QY 721 PODRLTEVIASIIKPQNTYCVRRYAVVQKAAHGHVKAFAKSHV 763
 Db 721 PODRLTEVIASIIKPQNTYCVRRYAVVQKAAHGHVKAFAKSHV 763

RESULT 5

Q8NG38 PRELIMINARY; PRT; 795 AA.
 AC Q8NG38;
 DT 01-OCT-2002 (TremBLrel. 22, Created)
 DT 01-OCT-2002 (TremBLrel. 22, Last sequence update)
 DT 01-OCT-2003 (TremBLrel. 25, Last annotation update)
 DE ABG-deleted variant of telomerase reverse transcriptase.
 GN Name=TER1;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Stomach;
 RA Hisatomi H., Ohyaashiki K., Ohyaashiki J.H., Nagao K., Kanamaru T.,
 RA Hirata H., Hibi N., Tsukada Y.;
 RT "Expression profile of a gamma-deletion variant of the human
 RT telomerase reverse transcriptase gene."
 RL Neoplasia 5:193-197(2003).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Stomach;
 RA Nagao K., Katsumata K., Aizawa Y., Saito N., Hirata H., Sasaki H.,
 RA Yamamoto S., Hikiji K., Koiba T., Hisatomi H.;

RT "Differential alternative splicing expressions of telomerase reverse
 RT transcriptase in gastrointestinal cell lines.";
 RL Oncol. Rep. 11:127-131(2004).
 DR EMBL: AB086950; BAC11015.1; -;
 DR GO: GO:0005634; C:nucleus; IEA.
 DR GO: GO:0003677; F:DNA binding; IEA.
 DR GO: GO:0003964; F:RNA-directed DNA polymerase activity; IEA.
 DR GO: GO:0003721; F:telomeric template RNA reverse transcriptase.; IEA.
 DR InterPro: IPR003545; Telomerase_RT.
 DR PRINTS: PR01365; TELOMERASERT.
 KW RNA-directed DNA polymerase.
 SQ SEQUENCE 795 AA; 88964 MW; 6BEAC8A6D1A2E8CB CRC64;
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 Best Local Similarity 98.4%; Pred. No. 2.6e-236;
 Matches 751; Conservative 0; Mismatches 0; Indels 12; Gaps 1;
 QY 1 MPAPRCANVRSLLRSHYREVLPATFVRRLLGPOQWRLVQRGDPAAFRALVAQCLVCVPM 60
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 Db 61 DARPPAAPSPROVSCLEKELVARVLQRLCERGAKNVLAFGFALLDGAAGGPPPEAFTTSVR 120
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 Db 121 SYLNTVNTDALTGSGGAWGLLRRVGGDVLVHLLARCALFVLVAPSCAYQVCGPPPLYQLGA 180
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 Db 721 --DRLTEVIASIIKPQNTYCVRRYAVVQKAAHGHVKAFAKSHV 751

RESULT 6

Q9QX24
 ID Q9QX24 PRELIMINARY; PRT; 1128 AA.

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AC Q0X24;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE Telomerase catalytic subunit.
OS Mesocricetus auratus (Golden hamster).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
OC Mesocricetus.
OX NCBI_TaxID=10036;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21240330; PubMed=11342218; DOI=10.1016/S0167-4781(00)00306-7;
RA Guo W., Okamoto M., Lee Y.M., Baluda M.A., Park N.H.;
RT "Enhanced activity of cloned hamster TERT gene promoter in transformed
RT cells.";
RL Biochim. Biophys. Acta 1517:398-409 (2001).
DR EMBL; AF149012; AAF17334.1; -.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR GO; GO:0003723; F:RNA binding; IEA.
DR GO; GO:0003964; F:RNA-directed DNA polymerase activity; IEA.
DR GO; GO:0003721; F:telomeric template RNA reverse transcriptase. .; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0006278; P:RNA-dependent DNA replication; IEA.
DR InterPro; IPR000477; RVTse.
DR InterPro; IPR003545; Telomerase_RT.
DR Pfam; PF00078; RVT.1; 1.
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DR RNA-directed DNA polymerase; Transferase.
DR SEQUENCE 1128 AA; 128393 MW; 1D4F81249012174E CRC64;

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Matches 736; Conservative 124; Mismatches 238; Indels 64; Gaps 16;

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DB 181 TAETWPSVSRIRYRTPVGRNPTHLGSTHVRNSHQBAWKPPPLPSREAKRSLSITNRS 240
QY 232 LPLKPRRGAPEPERTPVGQGSWAHPGRTGRSDRGFCVVSPPAR-----PAEATSLEG 287
DB 241 VPPSKKACDLAPLEKGPYRQA-----VPTPSDKTW-VNPAKSHAVISRITK-ED 291
QY 288 ALSGTRHSHSPVGRQ-----HHAGPSTS-RPP-----RPWDPFCPPVVAETHFLYS 334
DB 292 LSSGVK--APGLSRGSGVCYKHKPSSTLSQSLPCQNAFQLRP-----YTETKRFlys 341
QY 335 -SGDKEQLRPSLLSSLSPLTGARLVETITFLGSRPMPGTPRPLRPORYWQMRPLF 393
DB 342 REGGERLNPSPLLNQLPSLTGAERLVEILFLGMRPTSGPLCGRRRLSKRYQMREPLF 401
QY 394 LELIGNHAQCQGVLLKTHCPURAATVPAAGCAREKPGQGSVAAPDEEDTDPRLVOLLR 453
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QY 454 QHSSPWQVYGFVACLRLLVPLGLMGSRHNERFLRNTKFTSLGKHAKLSLQELTWQMS 513
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QY 514 VRDCAWLRRSPGVCPVPAEHLRREILAKFLHLMLSVVVVVELLSRFFVTTTTFQKNRL 573

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QY 518 AWRRLSPGVGCVPAEAHRLREILAKFLHMLSVVVVLLRSFFVYVTTFTTQKRLFFYR 577
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QY 698 RAQDPPPELYFVKVDVTGAYDTIPQDRLTEVIASII-KPQNTYCVRRYAVVQKAAHGHR 756
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QY 935 LDRTRLEVQSDVSSVARTSIRASLTFRNGFKAGRNRRKLFGLVRLKCHSLFLDLQVNSL 994
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QY 1055 SIGAKGAAGPLPSEAVOMLCHQAFLLKLTIRHRTVYVPLLSGLSRTAQTLSRLKFTTLTA 1114
Db 1042 SLRAXGAGFPPEATRWLCYQAFLLKLAHVSVYKCLLGLPLRTAQKLCRKLPEATWTL 1101
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Db 1102 LKTAADPALSTDFQILD 1119

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RESULT 9

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TERT_MOUSE
ID TERT_MOUSE STANDARD; PRT; 1122 AA.
AC 070372; O35432;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Telomerase reverse transcriptase (EC 2.7.7.-) (Telomerase catalytic subunit).
GN Name=Tert;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98241176; PubMed=95802020; DOI=10.1038/sj.anc.1201933;
RA Greenberg R.A., Allsopp R.C., Chin L., Morin G.B., DePinho R.A.;
RT "Expression of mouse telomerase reverse transcriptase during development, differentiation and proliferation."
RL Oncogene 16:1723-1730(1998).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=98393668; PubMed=9724727; DOI=10.1073/pnas.95.18.10471;
RA Martin-Rivera L., Herrera E., Albar J.P., Blasco M.A.;

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RT "Expression of mouse telomerase catalytic subunit in embryos and adult tissues.";
RL Proc. Natl. Acad. Sci. U.S.A. 95:10471-10476(1998).
RN [3]
RA SEQUENCE OF 550-616 FROM N.A.
RT "Partial sequence of Mus musculus telomerase catalytic subunit homolog.";
RL Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Telomerase is a ribonucleoprotein enzyme essential for the replication of chromosome termini in most eukaryotes. It elongates telomeres. It is a reverse transcriptase that adds simple sequence repeats to chromosome ends by copying a template sequence within the RNA component of the enzyme.
CC -!- SUBUNIT: Component of the telomerase ribonucleoprotein complex at least composed of TEP1, EST1A, POT1 and a telomerase RNA template component (TER). Interacts with PINK1 (By similarity).
CC -!- SUBCELLULAR LOCATION: Nuclear.
CC -!- SIMILARITY: Belongs to the reverse transcriptase family. Telomerase subfamily.
CC -!- SIMILARITY: Contains 1 reverse transcriptase domain.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.ebi.ac.uk/ebis/ or send an email to license@ebi.ac.uk).
CC -----
DR EMBL; AF051911; AAC09323.1; -
DR EMBL; AF073311; AAC34821.1; -
DR EMBL; AF029235; AAB84200.1; -
DR MGD; MGI:1202709; Tert.
DR InterPro; IPR000477; RVTse.
DR InterPro; IPR003545; Telomerase_RT.
DR Pfam; PF00078; RVT; 1
DR PRINTS; PR01365; TELOMERASERT.
DR PROSITE; PS50878; RT_POL; 1.
KW DNA-binding; Nuclear protein; Ribonucleoprotein;
KW RNA-binding; Nuclear protein; Telomerase; Reverse transcriptase.
FT DOMAIN 595 928 Reverse transcriptase.
FT CONFLICT 553 553 I -> V (in Ref. 3).
SQ SEQUENCE 1122 AA; 127977 MW; F85266905DD6558C CRC64;

Query Match 58.8%; Score 3505; DB 1; Length 1122;
Best Local Similarity 62.4%; Pred. No. 2.8e-207;
Matches 719; Conservative 122; Mismatches 260; Indels 52; Gaps 13;

QY 1 MPAPRCRAVRSLRSHYREVLPATFVRLRGLPGQWLVQGDPAAPRALVAOCLVCPW 60
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QY 181 ATQARPPPHAS-GPRRLG-----CERAWNHSVREAGVPLGLPAPCARRRGGSARS 231
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Db 241 VPSAKKARCVPVPRVEGP-----HRQVLPFTSGKSW-VPSAPRSEVETAEDKLSK 292
QY 287 GALSCTRHSHPVSGRQHAGPSTSRPRPMDTFCPPVYAEKHFLYSSGD-KEQLRPSF 345
Db 293 GKVDLSLS-GSVCKKPKSPSTSLSPRQNAFLRP-FIETRIFLYSGDQERLNPFSF 350

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QY 346 LLSSLRPSITGARRLVETITFLGSRPMPGTPRLPLPQRYWQMRPLFLLELGNHAQCPY 405
Db 351 LLSLNQPNLTGARRLVEIIFLGSRPSTSGPLCKTRLSRRYQMRPLFQOLLVNAECQY 410
QY 406 GVLKTHCPRAA---VTPAAGVCAREKPGQSVAPAEEDTDPRLVOLLRHSSPWQY 462
Db 411 VLLKSHCHFRFANQVTDAL-----NTSPPHLMDLLRLHSSPWQY 452
QY 463 GFVRACLRRLVPPGLGWSRHRNRRFLRNTKFKISLGKHAQLSLQELTWKQSVRDCAWLRR 522
Db 453 GFRLACLRCKVVSASLWGTNRNRRFPKLLKFKISLGKYSKLSQLQELWKKVDEDCWILRS 512
QY 523 SPGVGCPAAERLRBEILAKFLHMLMSVYVVELLRSPFYVTTTFQKRLFFYKSVMS 582
Db 513 SPGRDVPAAERLRERILATFLMLMDTYVYVQLLRSPFYVTTTFQKRLFFYKSVMS 572
QY 583 KLSQIGIRHLKRVOLRLESEAEVQHRREARALLTSRLRFTPKDGLRPIVNMDDYVGA 642
Db 573 KLSQIGVROHLRVRLELQSEVRRHQDTWLAMPICRLRFIPKNGRPIVNMYSMTG 632
QY 643 RTFREKRAERLTSRVKALFSVLYNERARRPGLGASVLGLDDIHRWRTFVLRVRAODP 702
Db 633 RALGRKQAOHTQRLKTLFSLMNLVETKPHLMGSSVLGMNDIYRTWRAFVLRVRLDQ 692
QY 703 PPELTVKVDVTGAVDTTPQDRLTEVIAIISK-PONTYCVRRYAVVQKAAHGVKAFKS 761
Db 693 TPRMYFVKADVTCAYDAIPQGLVEVAVNMIRHSESTYCIROYAVVRDSDQGVHKSFR 752
QY 762 HYSTLTDLQPNYRQFVAHLOET--SPLRDVAVIEKSSLINEASSGLFDVFLRPMCHAVR 819
Db 753 QVTTLSDDQPNYRQGLKHLQSDASALRNSVVIEQSSISMNSSSLFDFFLHFLRHSVVK 812
QY 820 IRGKSYVOCQIPQSGISLTLCSLCYGDMEKFLPAGIRRDGLLRLLVDDFLLVPLHLTH 879
Db 813 IGDRCTYCCQIGIPQSSSLTLCSLCFGDMENKLFVQVQDGLLRFLVDDFLLVPLHLDO 872
QY 880 AKTFRLTVRGVPEYGCVVNLRKTVVNFPEVEALGGTAFVQMPAHGLFPWCGLLDTRT 939
Db 873 AKTFRLTVHGVPEYGCVMINLQTVVNFPEVEPTLGGAAAYQLPAHCLFPWCGLLDTRT 932
QY 940 LEVQSDYSYARTSIRASITFNRGFKAGNMRKLPGLVLRKCHSLFDLQVNSLOTVCT 999
Db 933 LEVFCDSYGYACTSIRKTSITFOSVFKAGTKMNKLLSVLRKCHGLFDLQVNSLOTVCI 992
QY 1000 NIYKILLQAYRFHACVQLQPHQVWKNPTFFLRVISTASLCYSILKAKNAGMSLGA 1059
Db 993 NIYKIFLQAYRFHACVQLQPHQVWKNPTFFLRVISTASLCYSILKAKNAGMSLGA 1052
QY 1060 GAAGPLPSEAVOMLCHQAFLLKLTTRHRTVTVPLGLSLRTAQTLQSRKLPGLTTLTAAEA 1119
Db 1053 GS---FPPEAAHWLCVQAFLLKLAHSHVYIKCLGLPLRTAQTLQSRKLPGLTTLTAAEA 1109
QY 1120 NPALPSDFKTLID 1132
Db 1110 DPALSTDFQTLID 1122

RESULT 10
QY 9996 PRELIMINARY; PRT; 524 AA.
AC QY 9996;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 05-JUL-2004 (Tremblrel. 27, Last annotation update)
DE Telomerase reverse transcriptase (fragment).
GN Name=TERT;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99144726; PubMed=10022128; DOI=10.1038/sj.onc.1202669;
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RA Greenberg R.A., O'Hagan R.C., Deng H., Xiao Q., Hann S.R., Adams R.R.,
RT Lichtsteiner S., Chin L., Morin G.B., Depinho R.A.;
RT "Telomerase reverse transcriptase gene is a direct target of c-Myc but
RT is not functionally equivalent in cellular transformation.";
RN Oncogene 18:1219-1226 (1999).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=99140777; PubMed=9988278; DOI=10.1038/6010;
RA Wu K.J., Grandori C., Anacker M., Simon-Vermot N., Polack A.,
RA Lingner J., Dalla-Favera R.;
RT "Direct activation of TERT transcription by c-MYC.";
RN Nat. Genet. 21:220-224 (1999).
RN [3]
RP SEQUENCE FROM N.A.
RA Ducrest A.-L., Anacker M., Reichenbach P., Nabholz M., Lingner J.;
RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RA Szutorisz H., Palmquist R., Roos G., Stenling R., Schorderet D.,
RA Reddel R., Lingner J., Nabholz M.;
RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF121948; AAD24464.1; -
DR EMBL: AF114847; AAD17210.1; -
DR GO: GO:0003964; F:RNA-directed DNA polymerase activity; IEA.
KW RNA-directed DNA polymerase.
FT NON TER 524
SQ SEQUENCE 524 AA; 57932 MW; 5F47DEFD01832B1B CRC64;

Query Match 47.4%; Score 2825; DB 2; Length 524;
Best Local Similarity 100.0%; Pred. No. 8.4e-166;
Matches 524; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPAPRCARVSLRSLSHYREVLPPLATFVRRLGPOQWRVLRQGDPAAFRALVAQCLVCPW 60
Db 1 MPAPRCARVSLRSLSHYREVLPPLATFVRRLGPOQWRVLRQGDPAAFRALVAQCLVCPW 60
QY 61 DARPPAAPSPFQVSCSLKELVARVQLRCLERGAKNVLAFFGALLDGAAGGPPPEAFTTSVR 120
Db 61 DARPPAAPSPFQVSCSLKELVARVQLRCLERGAKNVLAFFGALLDGAAGGPPPEAFTTSVR 120
QY 121 SYLNTVTDALRGSGAWGLLRVGGDDVLVHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180
Db 121 SYLNTVTDALRGSGAWGLLRVGGDDVLVHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180
QY 181 ATQARPPPHASGPRRLGCERAWNHSVREAGVPLGLPAPGARRRGSASRSLPLKRRPR 240
Db 181 ATQARPPPHASGPRRLGCERAWNHSVREAGVPLGLPAPGARRRGSASRSLPLKRRPR 240
QY 241 GAAPEPERTPVQGSWAHPGTRGFSDRGFCVWSPARPAEATSLEGALSCTRHSHPVSG 300
Db 241 GAAPEPERTPVQGSWAHPGTRGFSDRGFCVWSPARPAEATSLEGALSCTRHSHPVSG 300
QY 301 RQHAGPSTSRPRPMDTPCPVVAETKHFYSSGDKQLRPSFLLSLRSLTGARRL 360
Db 301 RQHAGPSTSRPRPMDTPCPVVAETKHFYSSGDKQLRPSFLLSLRSLTGARRL 360
QY 361 VETIFLGSRPMPGTPRELPRLPORYWQMRPLFLLELGNHAQCPYGVLLKTHCPRAAVT 420
Db 361 VETIFLGSRPMPGTPRELPRLPORYWQMRPLFLLELGNHAQCPYGVLLKTHCPRAAVT 420
QY 421 PAAGVCAREKPGQSVAPAEEDTDPRLVOLLRHSSPWQYVGFVRACLRLVPPGLMGS 480
Db 421 PAAGVCAREKPGQSVAPAEEDTDPRLVOLLRHSSPWQYVGFVRACLRLVPPGLMGS 480
QY 481 RHNERRFLRNTKFKISLGKHAQLSLQELTWKQSVRDCAWLRRSP 524
Db 481 RHNERRFLRNTKFKISLGKHAQLSLQELTWKQSVRDCAWLRRSP 524

RESULT 11
QY 9996 PRELIMINARY; PRT; 1346 AA.
AC QY 9996;
ID Q6RD80
RX MEDLINE=99144726; PubMed=10022128; DOI=10.1038/sj.onc.1202669;
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DT 05-JUL-2004 (Tremblrel. 27, Created)
DT 05-JUL-2004 (Tremblrel. 27, Last sequence update)
DT 05-JUL-2004 (Tremblrel. 27, Last annotation update)
DE Telomerase reverse transcriptase.
GN Name=TERT;
OS Gallus gallus gallus.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=208526;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=15363846;
RA Delany M.E., Daniels L.M.;
RT "The chicken telomerase reverse transcriptase (chTERT): molecular and
RT cytogetic characterization with a comparative analysis.";
RL Gene 339:61-69(2004).
DR EMBL; AY502592; AAS75793.1; -.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR GO; GO:0003964; F:RNA-directed DNA polymerase activity; IEA.
DR GO; GO:0003721; F:telomeric template RNA reverse transcriptase. .; IEA.
DR InterPro; IPR000477; RVTse.
DR InterPro; IPR003545; Telomerase_RT.
DR Pfam; PF00078; RVT_1; 1.
DR PRINTS; PR01365; TELOMERASERT.
DR RNA-directed DNA polymerase; Transferase.
KW SEQUENCE 1346 AA; 155316 MW; E93A8B64FB6A4D40 CRC64;

Query Match 43.4%; Score 2590; DB 2; Length 1346;
Best Local Similarity 44.1%; Pred. No. 8.4e-151;
Matches 593; Conservative 159; Mismatches 350; Indels 242; Gaps 29;

QY 9 AVRSLLRHRYEVLPLATFVRL--GPGQWRLVQSGDPA-AFRALVAQCLVCVPWDARPP 65
DB 25 AVLGAALGCYAEEXTLEAFVRLQSGGTGEVLEGGDQAQCYRTFVSCVCPVGRGAI 84
QY 66 PAAPSFQVSCLELVARVQLCRGAKNVLAFGALLDGAAGPPPAFTTSVRSYLPN 125
DB 85 PRPICFOQLSSQSEVITRIVQRLCEKKKKKILAYGSLDENSCHFRVLPSSCIYSLSN 144
QY 126 TVTDLALGSGAWLLRRVGDVVLHLLARCALFVLVAPSCAYQVCGPPLVOLGATQAR 185
DB 145 TVTETIRISGLWEILLRIGDDVMYLLHLCALFMLVPPSNQYVCGQPIYEL-ISRNVG 203
QY 186 PPP-----HAS---GPRRLGGERAWNHSVREAGVPLGLPAPGARRRGGSASR- 230
DB 204 PSPGPFVRRYSRFKNSLLDYVKELVFR---HVLKSQWKKCP-----RRRGVSSRR 256
QY 231 -----SLPLP-----SLPLP-----KPRRGAA 243
DB 257 KRRSHRIQSLRSGYQPSAKVNFQAGRQISTVTARLEKQSCSSCLIPARAPSLKRRDGEQ 316
QY 244 PE-----PERTPVGG-----SW----- 256
DB 317 VEITAKRVKIMEKETEEQACSIVPD---VNQSSORHGTSMHVPRAVGLIKEHYISERS 373
QY 257 -----AHFGR-----TRG----- 264
DB 374 NSEMSGPSVHSHFGKRPVADKSSFPQGVQGNKRIKTGAEKRAESNREGIEMVINPIHK 433
QY 265 PSDRGF-CVVSAPPAE-----EATSLGALGSTRHSHPSVGRQKHAGPPSTSRPPRWD 319
DB 434 PNRRGIERRINPTKPELNSVQTEPMEGASSDRKQE-----NPPAHLAKQLPNTL 484
QY 320 PCPPVYATKTHLYSSGDKQLRPSFLSLRPSLTGARRLVETIFLGRPW-----M 372
DB 485 SRSTVIFKKFLYLSRSYQEVFPFKSILSRQCGQAGRRRLIETIFLSQNLKQSQNOSL 544
QY 373 FGTGPRRLPLRQRYQMRLPFLFLGNHQAQCPYGVLLKTHCP-----LRAA 418
DB 545 FQKWKRRKRLPKRYQWQMEIEI FQKLVKNEHKCPYLVLFRKNCVLLSEACKKKTETLQAA 604

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QY 419 VTPAAGV-----CAREKPGQ-----SVAA-----PEE-----EDTDPRRLVOLLRQ 454
DB 605 LPGEAKVHKHTEHGKSTEGTAPNSFLAPPVSLACGQPERGEQHPAEGSDP-LLERLRQ 663
QY 455 HSSPMQVYGVFVRACLRLRPPGLWSRNNRRPURNTKPISLKGHAKLSLQELTWKMSV 514
DB 664 HSSHQVYGVFVRECLERVIPAEELWGSSHNKCRFFKNVKAFLSMGKYAKLSLQQLMWKRV 723
QY 515 RDCAWLRSRSGVGCVPAAEHLREEILAKFLHLMWSVYVVELLSFFVYVTTTQKRLF 574
DB 724 NDCVWLRLAKGNHSPVAPVAYEHYREEILAKFLYWLMDSVIELLAKSFFVITETMQKNLF 783
QY 575 FYRKSVMWSKLSQIGIROHLKRVQLRELSEAEVROHREARPAALLTSRLRFPKPGDLRPV 634
DB 784 YTRKFIWGLQNLGIRDHFAKVLHRLALSSBEMEVIROKVPPIASRLRFPKNNGLRPV 843
QY 635 NMDVYVGARTF---RREKRAERLTSRVKALFSLVLYNERARRPGLLGASVLGLDDIHRAR 691
DB 844 RLSRVSEGQKLKSKESREKKIQRVNTQKNLFSVLYNERTVNTSIIIGSVFGRDDIYRKNK 903
QY 692 TFVLRV-RAQDPPPELYFVVDVTGAYDTIPQDRLTEVIAIIPK--QNTYCVRRYAVVQ 748
DB 904 EFVTKVPFESGEMPHFYFVGDVSRADFDTIPHKLVEVISQVLKPESTVYVIGRWYAVIM 963
QY 749 KAAHGHVRKAFKSHVSTLTLQPYMRQFVAHLQTSPLRDVAVIEQSSLSNEASSGLFDV 808
DB 964 ITPTGKARKLYKRVHSTFEDFIPDMKQFVSKLQERTSLRNAIVVEQCLTFNENSTLFTF 1023
QY 809 FLRFMCHHAVIRKGSYVQCGIPQGSILSTLCLSCYGDWENKLFAGIRDGLLLRLVD 868
DB 1024 FLQMLHNIIEIGHRYVYQCSGIPQGSILSTLCLSCYGDWENKLLCGIQDGVLRILVD 1083
QY 869 DFLVTPHLTHAKTFLTLVRGVPYCGVNLKRTVYVNFVVEDEALGSGTAFVQMPAHGLF 928
DB 1084 DFLVTPHLMAQARTFLTAAGIPEYGLINAKTVVNFV-DI PGCSKFKHLPDCRLI 1142
QY 929 PWGLLLDTLTLEVQSDYSSYARTSIRASLTFRNGFVAGRMRRKLFGVLKCHSLPLD 988
DB 1143 SWCGLLADVQTLVEYCYDYSSYAFTSIRSSLSFNSIRAGNMCKLTAVLKLCCHPLLD 1202
QY 989 LOVNSLQVCTNVIKILLQAYRHACVLOLPFHQVYWKNPFTFLRVISDTASLCYSTLK 1048
DB 1203 LKINSQTLVINIYKIFELQAYRHACVLOLPFHQVYWKNPFTFLRVISDTASLCYSTLK 1262
QY 1049 AKNAGMSLGAKGAGPLPSEAVOWLCHQAFLLKLTTHRVTVYVPLLSLRTAQTLQSLRP 1108
DB 1263 AKNPGVSLGSKDASGMFPFEAAEWLCYHAFIVKLSNHKVIYKLLKPLKVKYKHLFGKIP 1322
QY 1109 GTTLTALAAANPALPSDFKTILD 1132
DB 1323 RDTMELLKTVTPEPSLCQDFKTILD 1346

RESULT 12
Q9DE32 ID Q9DE32 PRELIMINARY; PRT; 1191 AA.
AC Q9DE32;
DT 01-MAR-2001 (Tremblrel. 16, Created)
DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE Telomerase reverse transcriptase.
GN Name=TERT;
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21488334; PubMed=11602347; DOI=10.1016/S0378-1119(01)00684-9;
RA Kuramoto M., Ohsumi K., Kishimoto T., Ishikawa F.;
RT "Identification and analyses of the Xenopus TERT gene that encodes the
RT catalytic subunit of telomerase.";

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RL Gene 277:101-110(2001).
DR EMBL; AF212299; AAG43537.1; --
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003677; P:DNA binding; IEA.
DR GO; GO:0003723; P:RNA binding; IEA.
DR GO; GO:0003964; P:RNA-directed DNA polymerase activity; IEA.
DR GO; GO:0003721; P:telomeric template RNA reverse transcriptase. . ; IEA.
DR GO; GO:0016740; P:transferase activity; IEA.
DR GO; GO:0006278; P:RNA-dependent DNA replication; IEA.
DR InterPro; IPR00477; RVTse.
DR InterPro; IPR003545; Telomerase_RT.
DR Pfam; PF00078; RVT_1_2.
DR PRINTS; PRO1365; TELOMERASERT.
DR RNA-directed DNA polymerase; Transfexase.
SQ SEQUENCE 1191 AA; 138016 MW; 98D9D76869A57D6 CRC64;

Query Match 38.9%; Score 2316.5; DB 2; Length 1191;
Best Local Similarity 42.4%; Pred. No. 5.1e-134;
Matches 518; Conservative 201; Mismatches 381; Indels 123; Gaps 25;

QY 1 MPAPRCRAVRLSHRYREVLPATFVRRLG-POGWR--LVQRGDPAAFRALVAQCIVC 57
DB 1 MPLRTGGATLILQRLVQVGLVYETDTLQVPGIKVPVLLGDSKFRSFAELVVC 60
QY 58 VPMWARPAPPAAPSPQVSCLEKELVARVLQRLCERGAKNVLAFGFALLDGAAGGPPAEFTT 117
DB 61 IPRGKPLPSPVFLQSTQREVVARVQRIKCKKKNVLAFGYGLVD-EKNSLIRLTP 119
QY 118 SVRSYLPNTVTDALRGSGAWGLLRVGGDVLVHLLARCALFVLVAPSCAYQVCGPPLY- 176
DB 120 NICNYFPNPTTITSTILWETLLTRVGDVMMYWLQCSIFVFVPPRCYQITQPIYT 179
QY 177 -----QLGAATQAR-----PPPHASGPRRLRCGERAWNSVRE 209
DB 180 LPSDDVFLFQSFQSTQSNVLLRYIKRVFHLKYLKPKXHTSM-----LWRRNKSP 234
QY 210 AGVPLGLPAPGARRRGSGASRL-----PLPKRPRRGAAP-----PERTFVGQ 254
DB 235 SGLLRSKTSMAVTEIHSKRKLCSDKICVDPKKRRNLKDDTVDFHDLPMCRSVSL 294
QY 255 SWAHPGR-----TRG-PSDRGFCVSPAPAAEATSLGALSGRH----- 294
DB 295 SNMYPKTNVQVTLTSGYKTKTQCKQKPSCEQKTTAFYSVAGDCNLSLKNVNKLI 354
QY 295 SHPSVGRQHAGPPTSPPRPWDPCPPVVAETKFLY-SSGDEQLRPPSLLSLRPS 353
DB 355 TNASV-----PTAQR-----LPSNIFIDFQRTLYLSYKKGFSSEFILNSLST 401
QY 354 LTGARRLVETIFLGS-----RPWMPGTTPRLPRLPQRYWQMRPLFLELIGNHAQCPY 405
DB 402 PSGSKLVETIFLSNLAEQNPDQPKRDENCHY--KLPKRYWKMKPHQELIQNHKKFPY 459
QY 406 GVLLKTHCPRAAVTPAAGVCAREKPOGQSVAAPEED-----TDPRLVQLLRQHS 457
DB 460 LVYLNKHCPRSSM-----ACSEKR---SLQKNRIENDGKQLKHTTKANLLSLKQHS 511
QY 458 PMQVYGFVRACLRRLVPPCLMGSRNRRFLRNTKFFSL-CKHAKLSLOELTWQMSYRD 516
DB 512 IQWVYFVRECLNNVVPDMMWSSNKKRFPNKSFLFFSGFKGFKISLSLWMSMRVED 571
QY 517 CAWLRSRPGVGVCPAAEHLREILAKFLHLMSSVVVVELLRSFFVYTTTFQKRLFFY 576
DB 572 CSWIRLQSDHVPASEHLRLKILAKFVFWLMDYIVQLLSFFVYTTTFQKRLFFY 631
QY 577 KXSVNKLQSIGIRQHLRVQLRELSAEVRQREARPALLTSRLRFPKPDGLRPIVM 636
DB 632 KXSVNKLQNLGRKHLKLVKLSLSSDELENQKQNVPLVSLRFLPKTNGLRPISKI 691
QY 637 DYVVGARTF--REKRAELTSRVKALFSLVNYERARPGLLGASVGLDIDHRAWRTFV 694
DB 692 SSTLSQQOSKENQEKIHFSSQIRNLFVSLNRYEWNRCSLTSSVFGMDDIYKKKGFV 751
QY 695 LRV-RAQDPPPPELYFVKVDVTGAYDTIPQDRLTEVIASIIKP--QNTYCVRRYAVVQKAA 751

DB 752 LDFEKPQVEKLFYFVKTDVKGAYDTIPHSKLDDEVISKVINPANEVYCIIRYATVSDP 811
QY 752 HGHVRKAPKSHVSTLTDLQPYMROFVAHLOETSPLRDAVAVLEQSSSLNEASSGLDFVFLR 811
DB 812 TGRRIKSPFRHVSBLADVLPMNKQFVSNQOEKLLRLTILVEQNLLNESSVKLLAVFQQ 871
QY 812 FMCHEAVRIRKSYVQCGIPQSGSILSTLLCSLCYGDMMENKLFAGIRRDGLLRVDDPL 871
DB 872 IIRSHILRIKORYYWCQCGIPQSGSMLSTILCSLCYGDMMENAMGGIKNGVLMRLDDPL 931
QY 872 LVTHPLTHAKTFLTRVGRVPEYGCVMRLKTVNVPVED--EALGGTAFVMPAHGLPP 929
DB 932 LVTHPLDQAKTFLTRLAEGIPQYGCISFPQKTVNVPVDDIPEC---SEVEQLPSHCLFR 988
QY 930 WCGLLDTRTLEVOSSYARTSTRASLTNRGFKAGRNMRKLFGVLRKCHSLFLDL 989
DB 989 WCGLLDTRTLDVYDYSSYACTSIRSWTFSCHSAAAGKYMKKQKUIRVLRUKCHSLFLDL 1048
QY 990 QVNSLQTVCTNIYKILILQAYRFHACVQLQLPFHQQVWKNPTFFLRVISTASLCYSILKA 1049
DB 1049 KVNLSRTVCINTYKILFLQAYRFHACVQLQFPFGQVWNNPPFFLTVISDMAPCFYTFKA 1108
QY 1050 KNAGWSLGAAGAAGPLPSEAVOMLCHOAFLKLTRHRYVYVPLGLSLRTAQTQSLRKLPG 1109
DB 1109 KNKDLTRGYKDVSCQFNFEAVQWLSYQAFLTCLHNNKLVYKCLIGPLQNCMKQLSRRLSQ 1168
QY 1110 TTLTALEAANPALPSPDKTILD 1132
DB 1169 DTIELLSVTDSLHKDFSCIMD 1191

RESULT 13
Q94807 PRELIMINARY; PRT; 523 AA.
ID O94807
AC O94807
DT 01-MAY-1999 (Tremblrel. 10, Created)
DT 01-MAY-1999 (Tremblrel. 10, Last sequence update)
DT 01-OCT-2000 (Tremblrel. 15, Last annotation update)
DE Telomerase transcriptase (Fragment).
GN Name=hTERT;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99137484; PubMed=9973199;
RA Takakura M., Kyo S., Kanaya T., Hirano H., Takeda J., Yutsudo M.,
RA Inoue M.;
RT "Cloning of human telomerase catalytic subunit (hTERT) gene promoter
RT and identification of proximal core promoter sequences essential for
RT transcriptional activation in immortalized and cancer cells.";
RL Cancer Res. 59:551-557(1999).
RL EMBL; AB016767; BAA74724.1; --
FT NON TER 523
SQ SEQUENCE 523 AA; 56555 MW; 8FDE562DDECC93DA CRC64;

Query Match 37.0%; Score 2207.5; DB 2; Length 523;
Best Local Similarity 78.7%; Pred. No. 9.4e-128;
Matches 435; Conservative 3; Mismatches 56; Indels 59; Gaps 6;

QY 1 MPAPRCRAVRLSHRYREVLPATFVRRLGPOGWRVLRQDPAAPFALVAQCIVCPW 60
DB 1 MPAPRCRAVRLSHRYREVLPATFVRRLGPOGWRVLRQDPAAPFALVAQCIVCPW 60
QY 61 DARPPAPSPQVSCLEKELVARVLQRLCERGAKNVLAFGFALLDGAAGGPPAEFTTSVR 120
DB 61 DARPPAPSPQVSCLEKELVARVLQRLCERGAKNVLAFGFALLDGAAGGPPAEFTTSVR 120
QY 121 SYLPTNTVTDALRGSGAWGLLRVGGDVLVHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180
DB 121 SYLPTNTVTDALRGSGAWGLLRVGGDVLVHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180

QY 181 ATQARPPPHASGPRRLGCRANWHSVREAGVPLGLPAPGARRRGGSSASRLPLPKRRR 240
 DB 181 ATQARPPPHASGPRRLGCRANWHSVREAGVPLGLPAPGARRRGGSSASRLPLPKRRR 240
 QY 241 GAAPPERTPVCGQSWAHPTGRGSDRGFCVSPARPAEATSLEGALSCTRSHSPSVG 300
 DB 241 GAAPPERTPVCGQSWAHPTGRGSDRGFCVSPARPAEATSLEGALSCTRSHSPSVG 300
 QY 301 RQHAGPSTSRPPRPMDTPCPVVAETKHFYSSGDKQELRPSFLLSSLRPSLTGARRL 360
 DB 301 RQHAGPSTSRPPRPMDTPCPVVAETKHFYSSGDKQELRPSFLLSSLRPSLTGARRL 360
 QY 361 VETIFLGRPMWGTTPRLPLRPLQRYWQMRPLFLELLGNHACQPGVLLKTHCPRAAVT 420
 DB 361 VETIFLGRPMWGTTPRLPLRPLQRYWQMRPLFLELLGNHACQPGVLLKTHCPRAAVT 420
 QY 421 PAAGVCAREKQGSVAAPPEEDTPRRLVQLLRQHSPPQVYGFVRACLRRLVPLGLW-- 478
 DB 421 PAAGVCAREKQGSVAAPPEEDTPRRLVQLLRQHSPPQVYGFVRACLRRLVPLGLW-- 478
 QY 479 -----GSRHNERFLRNTKFFISLGHAKLSLQELTWK 511
 DB 479 -----GSRHNERFLRNTKFFISLGHAKLSLQELTWK 511
 QY 512 MSVRDCAWLRRSP 524
 DB 512 MSVRDCAWLRRSP 523

RESULT 14
 ID Q9JK99 PRELIMINARY; PRT; 575 AA.
 AC Q9JK99;
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Telomerase catalytic subunit (fragment).
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22860253; PubMed=13679242; DOI=10.1016/S0024-3205(03)00670-2;
 RA Wong S.C., Ong L.L., Er C.P., Gao S., Yu H., So J.B.;
 RT "Cloning of rat telomerase catalytic subunit functional domains,
 RT reconstitution of telomerase activity and enzymatic profile of pig and
 RT chicken tissues".; 2760 (2003).
 RL Life Sci. 73:2749-2760 (2003).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Wong S., Gao S., Xu X., Yu H.;
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF247818; AAF62177.1; -.
 DR GO: GO:0005634; C:nucleus; IEA.
 DR GO: GO:0003677; F:DNA binding; IEA.
 DR GO: GO:0003723; F:RNA binding; IEA.
 DR GO: GO:0003964; F:RNA-directed DNA polymerase activity; IEA.
 DR GO: GO:0003721; F:telomeric template RNA reverse transcriptase. .; IEA.
 DR GO: GO:0016740; F:transference activity; IEA.
 DR GO: GO:0006278; F:RNA-dependent DNA replication; IEA.
 DR InterPro: IPR000477; RVFse.
 DR Pfam: PF00078; RVT_1; 1.
 DR PRINTS: PR01365; TELOMERASRT.
 DR RNA-directed DNA polymerase; transferase.
 FT NON_TER 1
 SQ SEQUENCE 575 AA; 65672 MW; F80C81BD7F6A91A3 CRC64;

Query Match 33.8%; Score 2016; DB 2; Length 575;
 Best Local Similarity 67.6%; Pred. No. 6.7e-116;
 Matches 391; Conservative 71; Mismatches 110; Indels 6; Gaps 3;

QY 558 RSPFYVTETTFQKNRLFFYRKSVMSKLSQSIGIRHOLKRVQLRELSEAVRQHRARPALL 617
 DB 1 RSPFYITESTTFQKNRLFFYRKSVMSKLSQSIGIRHOLKRVQLRELSEAVRQHRARPALL 60
 QY 618 TSLRLEFIPKDGRLPIVNMDDYVVCARTFRKRAERLTSRKALFSLVLYERARRPGLLG 677
 DB 61 ICRURFIPKNGRLPIVNMDSYSGMTRALGRKKQAHFTQRLKTLFSLMLNERTKHPLHMG 120
 QY 678 ASVLGLDDIHRAMTFVRLVRAQDPPPELFPVKVDVTGAYDTIPQDRTEVIASTIK-PQ 736
 DB 121 SSVLGMDIYTRWAFVRLVRAQDPPPELFPVKVDVTGAYDAIPQGLVEVVAWNRHSE 180
 QY 737 NTYCVRYAVVQKAAHGHVAKFKSHVSTLTDLQPYMRQFVAHQET--SPLRDVAVIEQ 794
 DB 181 STYCIQYAVVRDSQGVHKSFRQVTTLSDLQPYMGQFLKHLQDSASALRNSVIEQ 240
 QY 795 SSSINEASSGLFDVFLPFMCHAVIRGKSVVQCGIPQGSILSTLLCSLCYGDWENKLF 854
 DB 241 SISNNESSLSDFLFLHFLRHVVVKIGDRCTQCQIPQGSSTLTLCSLCYGDWENKLF 300
 QY 855 AGIRRDGLLRLLVDDFLVTPHLLTHAKTFLRTLVRGVPEYGVVNLKRTVNVFVDEAL 914
 DB 301 AEVQDGLLRLLVDDFLVTPHLLTHAKTFLRTLVRGVPEYGVVNLKRTVNVFVDEAL 360
 QY 915 GGTAFVQMPAHGLFPWCGLLLDTRTLEVSQDSYARTSIRASLTFRNGFKAGNRMRKL 974
 DB 361 GGAAPYQLPAHCLFPWCGLLLDTRTLEVSQDSYARTSIRASLTFRNGFKAGNRMRKL 420
 QY 975 FGVLRLKCHSLFLDLQVNSLQTVCTNIYKILLQAYRHFACVLOLPHHQVWKNPTPELR 1034
 DB 421 LSVLRKCHGLFLDLQVNSLQTVCTNIYKILLQAYRHFACVLOLPHHQVWKNPTPELR 480
 QY 1035 VISDTASLCYSILKAKNAGMSLGAKGAGPLPSSEAVOWLCHQAFLLKTLHRVTVVPLLG 1094
 DB 481 IISQASCCVALLKVKPGMTLKASG---PPPEAAHWLCYQAFLLKTLHRVTVVPLLG 537
 QY 1095 SLRTAQTLRSKLPGLTTLTALEAAANPALPSDFKTIID 1132
 DB 538 PLRTAQKLLCKLPEATWTILKAAADPALSTDFQTIID 575

RESULT 15
 ID Q673L3 PRELIMINARY; PRT; 615 AA.
 AC Q673L3;
 DT 25-OCT-2004 (TrEMBLrel. 28, Created)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
 DE Telomerase reverse transcriptase catalytic subunit splice variant c
 DE (telomerase reverse transcriptase catalytic subunit splice variant
 DE b).
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BN;
 RA Kaneko R., Hirabayashi T., Yagi T.;
 RT "Predominant expression of rTERB, an inactive splicing variant of
 RT telomerase reverse transcriptase, in the adult rat brain and heart".;
 RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AY539720; AAT09127.1; -.
 DR EMBL: AY539719; AAT09126.1; -.
 DR GO: GO:0003964; F:RNA-directed DNA polymerase activity; IEA.
 DR RNA-directed DNA polymerase.
 KW SEQUENCE 615 AA; 68614 MW; 2892840D86620B63 CRC64;

Query Match 23.6%; Score 1408; DB 2; Length 615;
 Best Local Similarity 55.8%; Pred. No. 2.1e-78;
 Matches 305; Conservative 51; Mismatches 135; Indels 56; Gaps 10;

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QY 1 MPAPRCRAVRSLLSHYREVLPATFVRRLGPGQWRLVQRGDPAAFRALVAQCLVCVPM 60
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1 MPAPRCRAVRSLLSHYREVLPATFVRRLGPGQWRLVQRGDPAAFRALVAQCLVCVPM 60
QY 61 DARPPAAPSPQVSCLEKELVARVLORLCERCAKNVLAEGFALLDQARGGPEATTSTVR 120
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
61 GSQPPADLSFHQVSKELVARVQVRLCERNERNVLAEGFALLDQARGGPEATTSTVR 120
QY 121 SYLPTNTVDALRGSGAWGLLRRVGGDDVLVHLLARCALFVLVAPSCAYQVCCPPYQLGA 180
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
121 SYLPTNTVETLRVSGAWMLLSRVGDDLLVLLSHCALVLLVPPSCAYQVCCPPYQLGA 180
QY 181 ATQA-----RPPHAGPRLRG-CERAWNHVREAGVPLGAPGARRRGGSASRS 231
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
181 TTDWSSVAGYRPTRPVGNFTNLRSAGHQIKNSGHQEAQPKALPSRGTKRLSLITSTN 240
QY 232 LPLKPRRGAPEPERTPVGGSWAHPCGTRGSDRGFCVVP-ARPAEATSLEG--- 287
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
241 VPSAKARPEALRVKGRHQVPTPSGKTWAPSP-----AASPKVPPAKNLSLKGKAS 296
QY 288--ALSCTRSHSPSVGRQH-----AGPPTSRRPPMDTPCPPVYAETHFLYS-SCD 337
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
297 DFLSG-----SVCKKHKPSSTLSLSPQDAEKLRP-----FTTRHFLYSRGGG 342
QY 338 KEOLRPSFLSLTGARLVETIFLGSRPMPGTPRRRLPRLPQRYWQMRPLFLELL 397
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
343 OBEIPLNSFLNLSLTPSLTGARLVETIFLGSRPMPGTPRRRLPRLPQRYWQMRPLFQQL 402
QY 398 GNHACPCVGLKTHCPLRAAVTPAAGVCAREKPGSVAAPEEDTDPRLLVQLRHSS 457
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
403 MNAKQCVYRFLRSHCRFTA-----NQRVPAMDTPSHLTSLLRHSS 447
QY 458 PQVYGFVRACLRLVPPGLWGRHNRERFLRNTKFKISLGKHAQLSLQELTWKMSVRDC 517
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
448 PQVYGFVRACLRLVPPGLWGRHNRERFLRNTKFKISLGKHAQLSLQELTWKMSVRDC 507
QY 518 AMLRSP 524
Db |||||
508 HMLRSP 514

RESULT 16
Q9R266 PRELIMINARY; PRT; 514 AA.
AC Q9R266;
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)
DE Telomerase reverse transcriptase (fragment).
GN Name=Term;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99144726; PubMed=10022128; DOI=10.1038/sj.onc.1202669;
RA Greenberg R.A., O'Hagan R.C., Deng H., Xiao Q., Hann S.R., Adams R.R.,
RA Lichtsteiner S., Chin L., Morin G.B., DePinho R.A.
RT "Telomerase reverse transcriptase gene is a direct target of c-Myc but
RT is not functionally equivalent in cellular transformation.";
RL Oncogene 18:1219-1226(1999).
DR EMBL; AF121949; AAD24465.1;
DR GO; GO:0003964; F:RNA-directed DNA polymerase activity; IEA.
KW RNA-directed DNA polymerase.
FT NON_TER 514
SQ SEQUENCE 514 AA; 58382 MW; 3096599776D9BBFD CRC64;

Query Match 23.0%; Score 1373; DB 2; Length 514;
Best Local Similarity 56.1%; Pred.No. 2.4e-76;
Matches 304; Conservative 50; Mismatches 142; Indels 46; Gaps 10;

QY 1 MPAPRCRAVRSLLSHYREVLPATFVRRLGPGQWRLVQRGDPAAFRALVAQCLVCVPM 60

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RESULT 17
Q9SE99 PRELIMINARY; PRT; 1123 AA.
AC Q9SE99;
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)
DE Telomerase reverse transcriptase catalytic subunit.
GN Name=TER;
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsia.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=Landsberg erecta;
RX MEDLINE=20079564; PubMed=10611295; DOI=10.1073/pnas.96.26.14813;
RA Fitzgerald M.S., Riha K., Gao F., Ren S., McKnight T.D., Shippen D.E.;
RT "Disruption of the telomerase catalytic subunit gene from Arabidopsis
RT inactivates telomerase and leads to a slow loss of telomeric DNA.";
RL Proc. Natl. Acad. Sci. U.S.A. 96:14813-14818(1999).
DR EMBL; AF172037; AAD54276.1;
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR GO; GO:0003723; F:RNA binding; IEA.
DR GO; GO:0003964; F:RNA-directed DNA polymerase activity; IEA.
DR GO; GO:0003721; F:telomeric template RNA reverse transcriptase; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0006278; F:RNA-dependent DNA replication; IEA.
DR InterPro; IPR000215; Prot_inh_serpin.
DR InterPro; IPR000477; RVTse.
DR InterPro; IPR003545; Telomerase_RT.

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Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1 MTRAPRCRAVRSLLSHYREVLPATFVRRLGPGQWRLVQRGDPAAFRALVAQCLVCVPM 60
QY 61 DARPPAAPSPQVSCLEKELVARVLORLCERCAKNVLAEGFALLDQARGGPEATTSTVR 120
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
61 GSQPPADLSFHQVSKELVARVQVRLCERNERNVLAEGFALLDQARGGPEATTSTVR 120
QY 121 SYLPTNTVDALRGSGAWGLLRRVGGDDVLVHLLARCALFVLVAPSCAYQVCCPPYQLGA 180
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
121 SYLPTNTVETLRVSGAWMLLSRVGDDLLVLLSHCALVLLVPPSCAYQVCCPPYQLGA 180
QY 181 ATQA-----RPPHAGPRLRG-CERAWNHVREAGVPLGAPGARRRGGSASRS 231
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
181 TTDWSSVAGYRPTRPVGNFTNLRSAGHQIKNSGHQEAQPKALPSRGTKRLSLITSTN 240
QY 232 LPLKPRRGAPEPERTPVGGSWAHPCGTRGSDRGFCVVP-ARPAEATSLEG--- 286
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
241 VPSAKARPEALRVKGRHQVPTPSGKTWAPSP-----AASPKVPPAKNLSLKGKAS 292
QY 287 GALSGTRSHSPSVGRQH-----AGPPTSRRPPMDTPCPPVYAETHFLYS-SCD 345
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
293 KGVSDLSL-SVCKKHKPSSTLSLSPQDAEKLRP-----FTTRHFLYSRGGG 350
QY 346 LLSSLRPSLTLGARLVETIFLGSRPMPGTPRRRLPRLPQRYWQMRPLFLELL 405
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
351 LLNLQPLNLTGARRLVETIFLGSRPMPGTPRRRLPRLPQRYWQMRPLFLELL 410
QY 406 GVLLKTHCPLRAA---VTPAAGVCAREKPGSVAAPEEDTDPRLLVQLRHSS 462
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
411 VRLRSHCRFTAQNVQVTDAL-----NTSPHLMOLLRLHSSPWQVY 452
QY 463 GFVRACLRLVPPGLWGRHNRERFLRNTKFKISLGKHAQLSLQELTWKMSVRDC 522
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
453 GFVRACLRLVPPGLWGRHNRERFLRNTKFKISLGKHAQLSLQELTWKMSVRDC 512
QY 523 SP 524
Db |||||
513 SP 514

RESULT 17
Q9SE99 PRELIMINARY; PRT; 1123 AA.
AC Q9SE99;
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)
DE Telomerase reverse transcriptase catalytic subunit.
GN Name=TER;
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsia.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=Landsberg erecta;
RX MEDLINE=20079564; PubMed=10611295; DOI=10.1073/pnas.96.26.14813;
RA Fitzgerald M.S., Riha K., Gao F., Ren S., McKnight T.D., Shippen D.E.;
RT "Disruption of the telomerase catalytic subunit gene from Arabidopsis
RT inactivates telomerase and leads to a slow loss of telomeric DNA.";
RL Proc. Natl. Acad. Sci. U.S.A. 96:14813-14818(1999).
DR EMBL; AF172037; AAD54276.1;
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR GO; GO:0003723; F:RNA binding; IEA.
DR GO; GO:0003964; F:RNA-directed DNA polymerase activity; IEA.
DR GO; GO:0003721; F:telomeric template RNA reverse transcriptase; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0006278; F:RNA-dependent DNA replication; IEA.
DR InterPro; IPR000215; Prot_inh_serpin.
DR InterPro; IPR000477; RVTse.
DR InterPro; IPR003545; Telomerase_RT.

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Pfam: PF00078; RVT_1; 1.

DR PRINTS; PRO1365; TELOMERASE.T.
DR PROSITE; PS00284; SERPIN; UNKNOWN_1.
KW RNA-directed DNA polymerase; Transference.
SQ SEQUENCE 1123 AA; 130551 MW; 44f248295817B7F6 CRC64;

Query Match 12.2%; Score 724.5; DB 2; Length 1123;
Best Local Similarity 23.8%; Pred. No. 6e-36;
Matches 294; Conservative 192; Mismatches 506; Indels 237; Gaps 39;

Qy 1 MPRAPRCRAVRSLLRSHYEVLPATFV-----RLGPGQWR-----L 38
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1 MPKPRHVRPEILWLRFNGRNRLNDAIVDLIPNRNIQEPCRCRGCGCLGSSDKPAFL 60
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Qy 39 VQRGDPAARFALVAQCVCVPWDARPAPPAEPFRQVSCLELVARVLORL---CERGAKN 95
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Db 61 LRSDDIPIHYKLHLRCFV-VLHEQTPLDPSFTSMWSOREIVERIEMMQSGCD--CON 117
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Qy 96 VLAFGFALLDGARGGPPEATTSVRSYLNTVDALRGSGAWGLLRVGDDVLVHLLAR 155
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Db 118 VICARDVKDOS-----SPIELLT-SSSEFWFLKRVGHVDMVILQQ 159
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Qy 156 CALFVLVAPSCAYOVCPPLYQLGAAT-----QARPPPHASGPRRRLCGERAMNHVSRE 209
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Db 160 TSIFLPLLGKHQGVSPPLCIKHRTLSVHENKKRDDNDVQPPTKRQWLSAVDDCPKD 219
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Qy 210 AGVPLGLPAG-----ARRGGASRSLSLPKPRPCA-----APEPETPVQGSA 257
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Db 220 DSATI-TPIVEDVDQHRBKTKTTSRIYIKRRRKQKVNFKKVDCNACPITP----- 271
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Qy 258 HPQTRGPSDRGPCVSVPARPAEATSLEGALSGRTHSHSPSVGRQHAGPSTSRPRPW 317
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Db 272 ---STNGKYSTG-----NDENMLHGIGSLTDVPOAKO----- 303
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Qy 318 DTCPPVYATKFLYS-SGDKEQLRPSLSLPSLTGARLVETTFLSGRPMWPOTP 376
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Db 304 -----VKRNKNFKGLSETYSVIPNNHILKTRPNCSDSLKMNNHIFGEVNVMSSTPS 356
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Qy 377 RLRLPLPO----RYWMRPULFLELNHAQCPGVLLKTHCP-----LRAAVTPAAG 424
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Db 357 HGKNCPSGISCLYHSLLSKNLKLIKTKSSHLMKLDKHCPLLQEDALKSGTSSOS 416
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Qy 425 VCAREK-----POGSVAA-----PEEBTDRLRLVQLRHQSHPQVYGFVRACLRRLVPPG 476
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Db 417 --BRQADKLPHGSSSSGTQPKCPSVERKL-----YCTMDQVVSWFIWAIACRIVDES 468
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Qy 477 LWSRNERREFLNTKFTSLGHAKLSIQELTWKMSVRDCAWLRRSPGVGCVPAAEHRL 536
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Db 469 LLGITHQMRVLRKNIWFVSRNRNECKTVNQFLHKVKSDFPFPAKE--LCVMVNGHEL 526
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Qy 537 REE-----ILAKFLHLMSSVYVELLRSFFYTTFQKRLFFPYRKSVWSLKSIG 588
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Db 527 QSESIRSTQMCLCTKWISMLFEIVKLVHFNFYATESQGGRLNIYYIRKRSWERLISKE 586
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Qy 589 IROHLKXVOLRELSEAEVRQREARPALITSRLRIPKPDGLRPIVNDYVVGARTFRE 648
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Db 587 ISKALDGYVLDDAEAESRKK-----LSKRFPLKANGVRMVL-----FSSS 630
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Qy 649 KRAERTLSRKALFSVLNTERARRPGLGASVLGLDDIHRAWRTFVLVRQAQDP-PELY 707
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Db 631 SRSQSL-----RDTHAVLKIQLKEPVLGSSFDHDDFYRNLCPLYLIHRSQSGELPLY 686
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Qy 708 FVKVDVTGAYDTIPQDRLTEVIASIIKPONTYCVRYAVVQKAHH-----VRKAPKS 761
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Db 687 FVYADVFKAFDSVDQKGLAHVQSFLKDE--VILANCRILVCCGKRNSWNKILVSSDKNS 744
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Qy 762 HVSTLTLDQPMYRMQFAVHQETSPLRADVVEQSSSLNEASSGLFDVFLRFWCCHAVRIR 821
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Db 745 NFRPFTSTPYNA-----IQ-----SIIVDKGNHRVRKDLMMVIGNMLKNMLQDD 792
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Qy 822 GKSYVOCGGIPOGSIILSTLCSLCYGMENKULFAGI-----RRDGL----- 862
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Db 793 KSPYVITAGIPQGRHLSLLCCFYFGHLBERTIYPFLEBASKDVSSKECSREEELIPTS 852
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Qy 863 --LLRLVDDFLVTPHLTHAKTLFTRVGRPEYGCVMNLRKTVMNFPVEDE----- 912
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Db 853 YKLLREIDDDYLFVSTRDQASFYHRLKHGFDYCNCFMNETKFICINFEDKBHRCSSNM 912
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Qy 913 --ALGCTAFVQMPAHGLFMCGLILDTRTEVQSDYSVYARTSIRASLTFRNGFKAGRNM 970
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Db 913 FVGDNGVFFVR-----WTGLINSRTFPEQVDITRYSLSGHISTFVSVAWQNKPVRML 964
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Qy 971 RRKLFGLRLKCHSLFDLQVNSLOTVCTNIYKILLQARYFHACVQLQFPFQQVMK-NP 102
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Db 965 ROKLYCYLFPVKCHPILFSDNSINSGEIVRLNIYOIFLLAAKMFHCYVEV---SREWKLP 102
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Qy 1030 TFFLRVISTASLCYCISILKAKNAGMSLGA-KAAGPLPSEAOWMLCHOAFLKLTFRHRT 108
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Db 1022 QTLFXKTTISVRYMFLINRRVRRINTSSFRPVLKYKEEWITWGLDAYIOVLKKONS 108
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Qy 1089 YVPLLGSLRTA-----QTOLSRKLPGETT 1111
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Db 1082 YRMLLIYLKALSUKHLSLSQLSELKYAT 1110
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 18
Q9SPU7

ID Q9SPU7 PRELIMINARY; PRT; 1123 AA.
AC Q9SPU7;
DT 01-MAY-2000 (T-EMBLrel. 13, Created)
DT 01-MAY-2000 (T-EMBLrel. 13, Last sequence update)
DT 05-JUL-2004 (T-EMBLrel. 27, Last annotation update)
DE Telomerase reverse transcriptase.
GN Name=AtTERT; Synonym=F5E19.190;
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eucots; rosids;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxId=3702;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=9402974; PubMed=10471830; DOI=10.1016/S0014-5793(99)01083-2;
RA Oguchi K., Liu H., Tamura K., Takahashi H.;
RT "Molecular cloning and characterization of AtTERT, a telomerase
reverse transcriptase homolog in Arabidopsis thaliana.";
RL FEBS Lett. 457:465-469(1999).
RN [2]
RP SEQUENCE FROM N.A.
RA Sato S., Nakamura Y., Kaneko T., Kato T., Asamizu E., Kotani H.,
RA Tabata S., Mewes H.W., Rudd S., Lem

Matches 294; Conservative 199; Mismatches 511; Indels 233; Gaps 39;

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QY 1 MPRAPRCRAVRSLLRSHYREVLPATFV-----RRLGPOGWR-----L 38
Db 1 MPRKPRHRVPEILWELFGNRRANLDAIVDLIPNENIQPEOCRCGQCLGSSDKPAFL 60
QY 39 VORGDPAAFRALVAOCLVCPWDARPPPAAPSFRQVSCLELVARVQLRL---CERGAN 95
Db 61 LRSDDPIHYRKLHLRCFV-VLHEQTPFLDPSPTSWNSQREIVERIIEMMQSGCD--CON 117
QY 96 VLAQFALLDARGGPPPEAFTTSVRSYLPNTVTDALRGSGAWGLLRRVGGDVLVHLLAR 155
Db 118 VICARYDKQS-----SPILELT-SSWEFLKRVGHVGVVYLQ 159
QY 156 CALFVLVAPSCAYQVCGPPLVOLGAAT-----QARPPPHASGPPRRRLGCERAMNHSVRE 209
Db 160 TSIPLLPLGKGHQVSGPPLCIKHKRTLVSHENKRRDNDVQPTTKRWLSSAVDDCPKD 219
QY 210 AGVPLGLPAG-----ARRGGSASRLPLPKRPRGA-----APEPTPVQGGSWA 257
Db 220 DSATI-TPIVGEDVDQHKETTKTSRIYLRKRRKQKVNFKVDCNAPCITP-----271
QY 258 HPGRTGSDGFCVVSARPAEATSLGALSCTHSHSPSVGRQHHAGPSTSRPPRPW 317
Db 272 ---STNGKVSTG-----NDENLHIGINGSLTDFVQAKQ-----303
QY 318 DTPCPVPVYAEAKHFLYS-SGDKEQLRPSFLSSLRPSLTGARRLVETIFLGSRPMMPGTP 376
Db 304 -----VKNKNPKFGLSEIYSVIPPNHILKTLRPNCSDSKLLMNHIFGEVNVWSTPS 356
QY 377 RRLPRLPO-----RYQMPLPFLLELGNHACPYGVLLKTHCP-----LRAAVTPAAG 424
Db 357 HGKGNCPGSGICLYHSLLSKLSKNLIGTKTSHSLKMLDKPCFVLLLOEDALSKGTTSQSS 416
QY 425 VCAREK-----POGSVAA-----PEEDTDPRLVOLLROHSSPQVYGFVRACLRLVPPG 476
Db 417 --RQKADKLPHGSSSSGTGPKCPSVEERKL-----YCNQDVSVFIWAICRYIPES 468
QY 477 LWSGRHNRRLNRTKFTISLKGAKLSIQELTWKMSVRDCAWLRRSPGVGCVPAAEHRL 536
Db 469 LLGTHQWRLKNIAMFVSRRENEKTVNQFLHKVPSDPPFPARKE--LCCWVNGHEL 526
QY 537 REE-----ILAKFLHLMVSVYVLLRFFYVTTTFQKNRLLFFYRKSVWSKLQSIG 588
Db 527 QSESTRSQMLCTKWISGLFLEIKVLVHFNFYATESQGGRLNIYYRKRSWERLISKE 586
QY 589 IRQHLKRVQLBELSEAVRQREARPAALLTSLRFLPKPDGLRPIVNMVYVVGARTFRE 648
Db 587 ISKALDGVYLVDDAEASSRKK-----LSKFRFLPKANGVRMVYLD-----FSSS 630
QY 649 KRAERLTSRKALFSLVLYERARRPGLLAGASVGLGDDITHRAWRTFVLVRVRAQDPP-PELY 707
Db 631 SRSQSL-----RDTHAVLDKIQLKEPDVLGSSVFDHDDFYRLMCPVLIHLRSQSSELPLY 686
QY 708 FVKVDVTGAYDTIPDRLTEVIASIIKPQNTYCVRRYAVVQKAAHGH-----VRKAPKS 761
Db 687 FVADVFAFADFSDQKLLHVIQSPKDE--YILNRCLVLCGKRKNVWVNLVSSDKNS 744
QY 762 HVTSLTDLQPYMRQFVAHLOETSPLRDAVLEQSSSLNEASSGLPDVFLRFWCHAVRIR 821
Db 745 NPSRTSTVPYNA-----LQ-----SIVVDKGENHRVRKDLMMVWITGNMLKNMLQ 792
QY 822 GKSYYVQCGIIPGSLTSLTCLSCYGDMEKLFAGI-----RRDGI-----862
Db 793 KSFYVQIAGIPQGHRLSLLCCFYVGHLERTLIIYFLEEASKDVSSKCSREEELIIPTS 852
QY 863 --LRLVDDFLVTPHLTHAKTFLRTLVRGVPEYGVVNLKRTVNVNPFVEDE-----912
Db 853 YKLLRFIDDLFVTSRDOASSFYHLKXGPKDYNCFWNETKFCINFEDKEHRCSNRM 912
QY 913 --ALGGTAFVQMPAHGLFPWCGLLDRTLLEVQSDSYSSYARTSTRASITFNRGFKAGNM 970
Db 913 FVGDNGVFPVR-----WTGLLINSRTFEVQVDYTRYLSGHISSTSFSAVQNKPVRL 964
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QY 971 RRKLFVGLRLKCHSLFELDLQVNSLQTVCTNIYKILLQVAFPHACVLOLPHQOQWK-NP 1029
Db 965 ROKLCYFLVPKCHPILFDSNINSGEIVRLNIYQIFLLAAKFHCYVYEV---SRFWKLHP 1021
QY 1030 TFFLRVISTASLCYSLKAKNAGMSLGAK-GAAGPLPSEAVQWLCHOAFLLKLTHRRVT 1088
Db 1022 QTLFKFTITISVRYMFRINRRRINTGSSFRPVLKYKEEVIMGLDAYIQVLKKONS 1081
QY 1089 YVPLLGSRRTAQTO--LSRKLPGTTLTAAEAAANPAL 1123
Db 1082 YRMILLIKSALSXKHSLSQQLSSELRLYATDRSNSSSL 1118

RESULT 19
Q9AU13 PRELIMINARY; PRT: 1259 AA.
AC Q9AU13;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Telomerase reverse transcriptase.
GN Name=TERT;
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaceae; Oryza.
OX NCBI_TaxID=4530;
RN [1]
RP SEQUENCE FROM N.A.
RA Oguchi K., Tamura K., Takahashi H.;
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF288216; AAK35007.1; -
DR Gramene; Q9AU13; -
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR GO; GO:0003723; F:RNA binding; IEA.
DR GO; GO:0003964; F:RNA-directed DNA polymerase activity; IEA.
DR GO; GO:0003721; F:telomeric template RNA reverse transcriptase. .; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0006278; P:RNA-dependent DNA replication; IEA.
DR InterPro; IPR001209; Ribosomal_S14.
DR InterPro; IPR00477; RVTse.
DR InterPro; IPR003545; Telomerase_RT.
DR Pfam; PF00078; RVT_1; 1.
DR PRINTS; PR01365; TELOMERASERT.
DR PROSITE; PS00527; RIBOSOMAL_S14; UNKNOWN_1.
KW RNA-directed DNA polymerase; Transferase.
SQ SEQUENCE 1259 AA; 143710 MW; 15B041789F2D5CAD CRC64;

Query Match 11.5%; Score 688; DB 2; Length 1259;
Best Local Similarity 23.9%; Pred. No. 1.2e-33;
Matches 305; Conservative 175; Mismatches 486; Indels 312; Gaps 45;

QY 36 W-RLVQRGDPAARFALVAOCLVCPWD---ARPPPAAPSPFRQVSCLELVARVQLRLC-- 89
Db 66 WEHLRDRDPIAYRRLITRAVCAJADLSDAPPPTPGNSGHSQARLVREMMKSIAD 125
QY 90 -ERGAKNVLAQFALLDARGGPPPEAFTTSVRSYLPNTVTDALRGSGAWGLLRRVGGDV 148
Db 126 QSHGTKNVLGNG--LHEGGQ-----SICISDLVSSSSWSILLHRIGDLL 167
QY 149 LVHLLARCALFVLVAPSCAYQVCGPPL-----YOLGAATOARPPPHASGPPRRRLGCERAW 203
Db 168 MCVLLRCTSLFPLVKKNNDYFQVSGVPLNVLRNPFIFASTVARKHQPOTTKAKHTC-YLM 226
QY 204 N-----HSVRAGVPLGLPAP-----GARRRGGS--ASRSLPLPKRP 238
Db 227 KSNAMENLSICHSSNSGNSVSSSTCKIVTQSCETCGSIRRAESKDPSEGCNCKPFP 286
QY 239 RRGAAPE-----PERTPVQGGSWAHFGR-----TRGHS- 266
Db 287 SDGRSGCCNCYTHNTRKRLKLYSQWRSSKKQVCVDSSESAEWSKLNGSNFNMSNGPSE 346
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QY	267		-----DRGFCV-----VSPARPABEATS-----LEGALSGTRHSHPSV-----GRQ----	302
Dd	347	NLAGKMNDAQSVBELTVDNTSLARSDNDSSEIKVINATILSSEKSPCSVFDIRGSQGLS	406	
QY	303	-HHAGPSTSRPRPWDTCPGVVAETKHFLYS-----SGDKQLRPSFLLSSLRP	352	
Dd	407	CHY-----SLUSEVOYSTCPCQGPFSYLHLNSCSICFNCFIISNASKHLSDLDSLIS--RN	458	
QY	353	SLTGARLAVETIF-----LGSRP-----	370	
Dd	459	GIFYNRRTTVSFVHCKHLSKRKEPDALSLVKHIFFGINSCCASILLKYNCHESTIRKSNCCL	518	
QY	371	--WNMGPTRLPLRPQPWQMRFLELLGNHAQCYPYGVLTKTCPRLAAAWTP--AAGVC	426	
Dd	519	CCWLPGSIKNLIR-----NSKRQCYKKLFHKCVSKKVAPDVTXNDG	561	
QY	427	AREKPOQSVAAPEREDTDPRLVOLLROQHSPWOVGTFVRACLRLRYPPGLNGSRHNERR	486	
Dd	562	KAHYPPEGKAAYD-----RSFRLEBAYSTHOQVASFMVAVLKRIIVPKPLLGNFGFKRS	615	
QY	487	PLRNTKFISLGKHAKLSLOBLTWKMVSRCAMLRR-----SPGVGCVPAAEH	534	
Dd	616	LRTNIWFILARRRETQOLSDICIDGLKVSHYSWLNSIEFSCNCFSAIIKGQTGSTGAEE	675	
QY	535	RLREBIILAFLUMLMSVVVELLSRSFFYTETTFOKNRLFYYRKSWMSKLQSIGIROHLK	594	
Dd	676	QEOKNILHCWSLWFSDIVPVVRTYFYVTERESKRDVDFYPYKSVWRDLTSNAIAS-LN	734	
QY	595	RVOLRELISEAEVROHRARPALLTSRLRFTPKDPGLRPIYNMDDVWGARTFREKRAERL	654	
Dd	735	KCNFRILI-RGEPR--KAVRHLCNSSRVRLFPAKDMPRLVDL-----RAKSK	778	
QY	655	TSRKVALFSLNYEARRPGILGASVLGLDDIHRAWRTFVLVARAQ-DPPPELYFVKVDV	713	
Dd	779	DANLNKCHLMKKURDEKPENMFSGSVFDYNNVHQNLNQFISSKRSQLMKKLKVYIVVADV	838	
QY	714	TGAYDTIPQDRLTEVIASIIPONTYCVRXYAVVQAAGAHHVRKAFKSHVS-----TLTD	768	
Dd	839	SKAFDCVSHDWMLWIIDDAFK-CDEYTVRKCSKVICNRSKNSLYRFPDSNAGINSIYD	897	
QY	769	LQPYMRQFVAHLQBSTPLRDAVITEQSSLSNEASSGLFDVFLRPMCHH-----AVR	819	
Dd	898	LS-----IQLSS-GGGIFVDQ-----GTICRIKBEQFHLLYEQIKCNLIK	937	
QY	820	IRGKSYYOCOGIPGOSTILTSLTLLCSLYCDMENKLFAGRIRDG-----LIILRL	866	
Dd	938	IGQKYIQQVGIAQGSKLPNLCSLYXGHLENSVLSKFLHDSKLNAGEAFSEPEYLLMRF	997	
QY	867	VDDPELLVPHLTHAKTFLRTLVRGVEPYCGVUNLRKTVMNF-----PVEDALGGTAUF	920	
Dd	998	IDDFIFSLSLAHQELNRMRGFVFVCMYMDNSKYGFNFCAGNSPFSSNRLYRGDDGV	1057	
QY	921	QMPAHLFPWCGLLDLTRTELEVQSDSYSIARTSTRALTNRGPKAGNMRRKLFGLVRL	980	
Dd	1058	-----SPMWSGLLINCETTEIOADYTRYLDITTIISTIV-KMHSSTKYHSKLCHYMRP	1111	
QY	981	KCHSLFLDLQVNSLOTCTNIYKILLQARYFACVLOLPHOOVWKNPFFFLAVISDTA	1040	
Dd	1112	KCHFIFYDNSINSPGITRVNIYOAFLLCAMKFH-CYIRSVDANVSK--LELLQVIRKTF	1168	
QY	1041	SLOCYSILKANAGMSGAKGAAGPLPSEAOWLCHOAF--LLKLTIRHVTVVPLLSLRT	1098	
Dd	1169	RYMHS LIVRMQDVDEL-----HYNVRPVLKRRKETIWGLGTAIRV	1210	
QY	1099	AQTOLSRKLPGETTITALALE	1116	
Dd	1211	LOQKOSRYKDMLTLLTAE	1228	
RESULT 20				
Q8LKW0		PRELIMINARY;	PRT; 1261 AA.	
ID Q8LKW0				

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Db 486 LSLVKHIFGINSCLLKYNCHESTIRKSNCLCCWLPKSKNKLIR- 531
QY 396 LIGNEAQCYPYGLLXTHCPRAAVTP--AAGVCAREKPGSVAAPEEDTDPRRLVQLLR 453
Db 532 ---NSKCOYKGLFLKHGCVCKVADPVTDNGKHAHPGGKAAAYD-----RSFSRL 582
QY 454 QHSSPWQYVGFVACILRLRVLPPGLWGSRHNERFLRNTKFFISLGHAKLSIQELTWKMS 513
Db 583 AVSTHQQVASFVAVLKRIVPKPLLGNISFGKSLRNIWKFLKRRFFQLSDICGDLK 642
QY 514 VRDCAWLR-----SPGVGCVPAABHRLREELAKFLHLMVSVVVELLRSPFF 561
Db 643 VSHVSLNIEFSNCFSCSALIGKQTSSTASAEQKQKILHCWISLWFSDIVIPVVTYF 702
QY 562 YVTEFTFQKRLFFYKRSWMSKLSIGIRHQLKRVQLRELSAEVQHQREARPAALLTSRL 621
Db 703 YVTERESKYDYFFYPKSVWRDLTNAIAS-LNKKNFRL-RGEPR--KAVRHLCSSRV 758
QY 622 RFPKPDGLRPVNDYVVGARTFRREKRAERLTGRVKALFVLNVARRRPGILGASVL 681
Db 759 RFLPKAKMRPLVDL-----RAKSKDANLKNCHLIMKKLDEKEMEGSSVF 805
QY 682 GLDDIHRAWRTFVLVRAQ-DPPPELYFYKVDVTGAYDTIPQDRLTVEVIASIKPQNTYC 740
Db 806 DYNVHONLSQFISKRSQMKKLKVIYVADVSKAFDCVSHDWLKMIDDAFK-CDEYT 864
QY 741 VRYAVVQKAAGHVRKAFKSHVS-----TLTDQPYMQFVAHQETSPDLDAVVISQS 795
Db 865 VRKSKVTCNRSKSLYRFDNSNASTGNGNSIYDLS-----IQLSS--GGGIFVDQ- 912
QY 796 SSLNEASSGLPVDVFLRFMCH-----AVRIRGKSVQCGIPQGSILSTLCSLCY 846
Db 913 -----GTICILKEQFHLHYEQIKNLKIGQKYLYQVGAQSKLSPNLCSLYY 964
QY 847 GDMENKLFAGIRRDG-----LLRLVDDFLVLTPTPLHPLTHAKTFLRTLVRGVE 893
Db 965 GHLENSVLKFLHDSKLNAGEAFSEPEVLLMRFIDDFIFISFSLHQAQFLNMRGFFV 1024
QY 894 YGVVNLKRTVNVF-----FVEDALGTAFTVQMPAHGLFPWCGLLLDTRTLEVSQDYS 947
Db 1025 YNCYMNDKSYGFNFCAGNSEPSNRLYRGDDGV-----SFMWSEGLLNCETLEIQADYT 1079
QY 948 SY-----ARTSIRASLTNRGFKAGNMRKLFGLVLRKCHSLFLDLQVNSLOT 996
Db 1080 RYLDTHVLPVLRCHLHQSTSK-----LCPLVAV--QNAHFIFDYSNINSPT 1129
QY 997 VCTNIYKILLQAYRPHACVLOLPPHQYQKNPTFFLRFVISTASLCYSILKAKNAGMSL 1056
Db 1130 IRVNIYQAFLLCAMKFH-CYIRSVSDANVSK--LELLQVIRKTFRYMHSLLVRRMQDV 1186
QY 1057 GAKGAAGPLPSAVOWLCHQAF--LLKTRHRVTVPVLLGSLRTAQTLRKLPOTTLTA 1114
Db 1187 -----HYNVRPVLKLRKETIWLGLTAYIRVLQQRKYQKMDLTLT 1228
QY 1115 LE 1116
Db 1229 AE 1230

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RESULT 21

TERT_SCHPO

ID TERT_SCHPO STANDARD; PRT; 988 AA.

AC O13339; O13338;

DT 30-MAY-2000 (Rel. 39, Created)

DT 30-MAY-2000 (Rel. 39, Last sequence update)

DT 25-OCT-2004 (Rel. 45, Last annotation update)

DE Telomerase reverse transcriptase (EC 2.7.7.-) (Telomerase catalytic subunit).

GN Name=trti; ORFNames=SPBC29A3.14c;

OS Schizosaccharomyces pombe (fission yeast).

OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;

OC Schizosaccharomycetales; Schizosaccharomycetaceae;

Schizosaccharomycetes.

NCBI_TaxID=4896;

[1] SEQUENCE FROM N.A.

STRAIN=972;

RX MEDLINE=97400623; PubMed=9252327; DOI=10.1126/science.277.5328.955;

RA Nakamura T.M., Morin G.B., Chapman K.B., Weinrich S.L., Andrews W.H.,

RL Lingner J., Harley C.B., Cech T.R.;

RT "Telomerase catalytic subunit homologs from fission yeast and human.";

Science 277:955-959(1997).

[2]

RN SEQUENCE FROM N.A.

RP STRAIN=972;

RX MEDLINE=21849401; PubMed=11859360; DOI=10.1038/nature724;

RA Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,

RA Sgouros J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,

RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,

RA Collins M., Connor R., Cronin A., Davis P., Fellwell T., Fraser A.,

RA Gentes S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,

RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,

RA James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,

RA Money P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,

RA Oliver K., O'Neill S., Pearson D., Quail M.A., Rabinowitsch E.,

RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,

RA Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,

RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,

RA Woodward J., Volkart G., Aert R., Robben J., Grymonprez B.,

RA Weltjens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,

RA Gabel C., Fuchs M., Fritz C., Holzer E., Moestl D., Hilbert H.,

RA Bozrym K., Langer I., Beck A., Leirach H., Reinhardt R., Pohl T.M.,

RA Eger P., Zimmermann W., Wedler H., Wambutt R., Purnelle B.,

RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,

RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,

RA Lucas M., Rochet M., Gallardin C., Tallada V.A., Garçon A., Thode G.,

RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,

RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,

RA Cerutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,

RA Shpakovski G.V., Usery D., Barrell B.G., Nurse P.;

RT "The genome sequence of Schizosaccharomycetes pombe.";

RL Nature 415:871-880(2002).

CC FUNCTION: Telomerase is a ribonucleoprotein enzyme essential for

CC the replication of chromosome termini in most eukaryotes. It

CC elongates telomeres. It is a reverse transcriptase that adds

CC simple sequence repeats to chromosome ends by copying a template

CC sequence within the RNA component of the enzyme.

CC SUBCELLULAR LOCATION: Nuclear.

CC ALTERNATIVE PRODUCTS:

CC Event=Alternative splicing; Named isoforms=2;

CC Name=1;

CC IsoId=O13339-1; Sequence=Displayed;

CC Name=2;

CC IsoId=O13339-2; Sequence=VSP_006395;

CC MISCELLANEOUS: Deletion causes telomere shortening and senescence.

CC SIMILARITY: Belongs to the reverse transcriptase family.

CC Telomerase subfamily.

CC SIMILARITY: Contains 1 reverse transcriptase domain.

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CC EMBL; AF015783; AAC49802.1; -

CC EMBL; AF015783; AAC49803.1; -

CC EMBL; AL022299; CAA18391.1; -

CC F01; T03838; T03838.

CC GeneDB SPombe; SPBC29A3.14c; -

CC InterPro; IPR000477; RVTse.

CC InterPro; IPR003545; Telomerase_RT.

CC Pfam; PF00078; RVT; 2.

543 MTNTKLSYSHLMKLTILNRMFKDPFGFAVNTDDVMRKYTEEFVLKWR--QVGRPKLVFVT 601
QY 711 VDVGTGYDTIPDRL-----TEVIASIIKPONTYCVRR-----YAVVQKAAGHVRKAFK 760
Db 602 MDIEKCYDSVDREKLSQLLGTTRLLSSEFRIMTVQAMKRNAEAVVDLDKARNQKCECFR 661
QY 761 ---SHVSTLTDLQPMRQFVAHLQETSPISPLDAAVVIEQSSLINEASSGLFDVFLRPMCHHA 817
Db 662 QRWKIALEGDQYPSLLNVLEDDQNDUNAKETLLVENVKRDPPYKKKALLDPVTKICRHNY 721
QY 818 VRIRGSYVOCQIGPOGSILSTLCSLYCGDMENKLFAGIRRDG-----LLRLVLD 868
Db 722 IEFNRKYKTKGIPQGLCVSSILSPFYASLEENALGYLKESMDANDPNITLLRLTD 781
QY 869 DFLVTPHLLTHAKTFUFTLRVGVPEYGCVVNLRTVVNFPVEBALG--GPAFV--QMPA 924
Db 782 DYLLITTKENNAILFTLEKLNIVSRQNKFKFNMKLQTNFLPDPSPKLNKYGWSVEDQVIA 841
QY 925 HGLFPWCGLLLDPTLETVQSDYSYARTSIRASITFN--RGFKAGRNWRKLVGVLRLLKCH 983
Db 842 HDVIDWIGISIDMSLTALMPNI--NLRRKGLTCLTNMNMOTKCAKSMWLKRKL-----K 892
QY 984 SLFLDLQVNSLOTVCTN-----IYKILLQVRPHACVQLQLPFFHQVWKNPTFFLRVI 1036
Db 893 SFLMNNITHFRKTIINRFSNKTILNKLYTAGAYKMQCCIEYKDHFT--NTEIHPQLD 950
QY 1037 SDTASLCYSILKA 1049
Db 951 KIICAIYVSVTRA 963

RESULT 24
Q7SD71 PRELIMINARY; PRT; 939 AA.
ID AC Q7SD71; 01-MAR-2004 (T-EMBLrel. 26, Created)
DT 01-MAR-2004 (T-EMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (T-EMBLrel. 26, Last annotation update)
DE Hypothetical protein.
OS Name=NCU02791.1;
GN Neurospora crassa.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.
OX NCBI_TaxID=5141;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=OR74A;
RA Galagan J.E., Calvo S.E., Borkovich K.A., Selker E.U., Read N.D.,
RA Jaffe D., Fitzhugh W., Ma L.-J., Smirnov S., Purcell S., Rehman B.,
RA Elkins T., Engels R., Wang S., Nielsen C.B., Butler J., Endrizzi M.,
RA Qui D., Iankiev P., Pedersen D., Nelson M., Washburne M.,
RA Selitrennikoff C.P., Kinsey J.A., Braun E.L., Zelter A., Schulte U.,
RA Koche G.O., Jedd G., Mewes W., Staben C., Marcotte E., Greenberg D.,
RA Roy A., Foley K., Naylor J., Thomann N., Barrett K., Gnerre S.,
RA Kamal M., Kamysseisen M., Mauceli E., Bielek C., Rudd S., Frishman D.,
RA Krystofova S., Rasmussen C., Metzberg R.L., Perkins D.D., Kroken S.,
RA Cogoni C., Macino G., Catchside D., Li W., Pratt R.J., Osmani S.A.,
RA DeSousa C.C., Glass L., Orbach M.J., Berglund J., Voelker R.,
RA Yarden O., Flannan M., Seiler S., Dunlap J., Radford A., Aramayo R.,
RA Natvig D.O., Alex L.A., Mannhaupt G., Esboole D.J., Freitag M.,
RA Paulsen I., Sachs M.S., Lander E.S., Nusbaum C., Birren B.,
RL "The Genome Sequence of the Filamentous Fungus Neurospora crassa.";
RT Nature 0:0-0(2003).
CC -i- CAUTION: The sequence shown here is derived from an
CC ENBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
CC ENBL; AABX01000062; EAA34711.1; -.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR GO; GO:0003723; F:RNA binding; IEA.
DR GO; GO:0003964; F:RNA-directed DNA polymerase activity; IEA.
DR GO; GO:0003721; F:telomeric template RNA reverse transcriptase; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.

```
DR GO:0006278; P:RNA-dependent DNA replication; IEA.
DR InterPro; IPR000477; Rvise.
DR InterPro; IPR003545; Telomerase_RT.
DR Pfam; PF00078; RVT_1; 1.
DR PRINTS; PR01365; TELOMERASERT.
KW Hypothetical protein; RNA-directed DNA polymerase; Transferase.
SQ SEQUENCE 939 AA; 104679 MW; 86F6B140E94056DC CRC64;

Query Match 7.9%; Score 469.5; DB 2; Length 939;
Best Local Similarity 27.3%; Pred. No. 2.5e-20;
Matches 148; Conservative 86; Mismatches 205; Indels 103; Gaps 15;

QY 430 KPOGSVAPEEDTDPRLVOLLQHSPPQVYGFVRACLRRLVPPGLWGS----- 480
Db 400 RPPSTAAVISNDSQSYSLDLATPISS---ISAFQAVLSKIIIPNDPWGSSDSEEGHPQ 456
QY 481 RHNERFLRNKTKFISLCHKAKLSLOELTWKMSVRDCAWLRSPQVGCVPAAEHRL--RE 538
Db 457 EHNSKSVFLKQDNFRLRRFESMTLHNLVQGMKSSISWL-ASAAISHKCSQPELNKRX 515
QY 539 EILAKFLHLMMSVYVELLRSPFYVTTTFOKNRLFFYRKSVMSKQSIGIROHLKRVOL 598
Db 516 EYLLEFLYTTFDSLIIPLIRSNFYVTESSAHRYLFFPRHDVMLSVTKPAL-ACLKVMKF 574
QY 599 RELSEAEVRQREARPAALLTSRLRPIKPDG--LRPIVNMVYVVGARTP-----RRE 648
Db 575 BEVGAAEAVKMLEGR-KLGFQSVRLPKGVGSNLRPIMNLRRRLVRLGLSGKIGWKQKQ 633
QY 649 KRAERLTSRKVALFSVLNVEARRRPGGLGASVLGLDDIHRARWTFVLKRVRAQ----DPPP 704
Db 634 MLGFSINSVLGVNSMLFKERERPRGLGGMFAVDGIQVRKFRARVMSVSKKGGK 693
QY 705 ELYFVKVDVTGAYDTPIDRLTEVIASIKPQNTYCVRRYAVVQKAAHGV----- 755
Db 694 KFYFVKVDVQAADFIPQAAVVELLGI-----PGHGVYKSHVEVSLPLDVEHN 744
QY 756 -----RKAFKSHVSTLT-----DLQPMRFQVAHLQ 781
Db 745 PANNDTNTIDNPKYKLPKTRWHSTTTSFSPSTTTTTTTTTSASISLPOQDSVA--- 801
QY 782 ETSPLRDVAVTEQSSLSNEASGLFDVFLRFMCHAVRIGKSVYQCGIPQGSILSTLL 841
Db 802 -TTKNTLTFISHSTSKLHTSALLSLAKEHITQNLVIGIKGYRQTKGIPQGSVLSLT 860
QY 842 CSLCYGDMENKI-----FAGIRRDG--LLRLVDDFLVTPHLTHAKTFLR 885
Db 861 CNYFYADLERSQGLAFLGLGTEDDEGRGSRDGNLTMLRLIDDFFLLITTSKARRFVE 920
QY 886 TL 887
Db 921 VM 922

RESULT 25
QUN56 PRELIMINARY; PRT; 85 AA.
AC QUN56;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE Telomerase reverse transcriptase (Fragment).
GN Name=TERT;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99105927; PubMed=9887342; DOI=10.1093/hmg/8.1.137;
RA Cong Y.S., Wen J., Bacchetti S.;
RT "The human telomerase catalytic subunit hTERT: organization of the
RT gene and characterization of the promoter.";
RL Hum. Mol. Genet. 8:137-142 (1999).

DR EMBL; AF097365; AAD12057.1; -.
DR GO:0003964; F:RNA-directed DNA polymerase activity; IEA.
DR RNA-directed DNA polymerase.
KT NON TER 85
SQ SEQUENCE 85 AA; 9601 MW; 67A096FC9ECB53B3 CRC64;

Query Match 7.5%; Score 450; DB 2; Length 85;
Best Local Similarity 100.0%; Pred. No. 1.8e-20;
Matches 85; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPRAPRCRAVRSLLRSHYREVLPLATFVRLPGQWELVQGDPAAFRALVAOCLVCVPW 60
Db 1 MPRAPRCRAVRSLLRSHYREVLPLATFVRLPGQWELVQGDPAAFRALVAOCLVCVPW 60
QY 61 DARPPPAAPSFQVSCCLKELVARVL 85
Db 61 DARPPPAAPSFQVSCCLKELVARVL 85

RESULT 26
Q6C9D0 PRELIMINARY; PRT; 940 AA.
AC Q6C9D0;
DT 25-OCT-2004 (TREMBLrel. 28, Created)
DT 25-OCT-2004 (TREMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TREMBLrel. 28, Last annotation update)
DE Yarrowia lipolytica chromosome D of strain CLIB99 of Yarrowia
DE lipolytica.
OS ORENAMES=VALI0D121889;
GN Yarrowia lipolytica CLIB99;
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Dipodascaceae; Yarrowia.
OX NCBI_TaxID=284591;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CLIB99;
RG Genolevures;
RA Dujon B., Sherman D., Fischer G., Durrens P., Casaregola S.,
RA Lafontaine I., de Montigny J., Marck C., Neuveglise C., Talia E.,
RA Goffard N., Frangeul L., Aigle M., Anthouard V., Babour A., Barbe V.,
RA Barnay S., Blanchin S., Beckerich J.M., Beyne E., Bleykasten C.,
RA Boisrame A., Boyer J., Cattolico L., Confaniolieri F., de Daruvar A.,
RA Despons L., Fabre E., Fairhead C., Ferry-Dumazet H., Groppi A.,
RA Hantraye F., Hennequin C., Jauniaux N., Joyet P., Kachouri R.,
RA Kerezi A., Koszul R., Lemaire M., Lesur I., Ma L., Muller H.,
RA Nicaud J.M., Nikolski M., Oztas S., Ozier-Kalogeropoulos O.,
RA Pellenz S., Potier S., Richard G.F., Straub M.L., Suleau A.,
RA Swennene D., Tekia F., Wesolowski-Louvel M., Westhof E., Wirth B.,
RA Zeniou-Meyer M., Zivanovic I., Bolotin-Fukuhara M., Thierry A.,
RA Bouchier C., Caudron B., Scarpelli C., Gaillardin C., Weissenbach J.,
RA Wincker P., Souciet J.L.;
RT "Genome evolution in yeasts.";
RL Nature 430:35-44 (2004).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=CLIB99;
RG Genoscope;
RA EMBL; CR382130; CAG80920.1; -.
RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
DR GO:0005634; C:nucleus; IEA.
DR GO:0003677; F:DNA binding; IEA.
DR GO:0003721; F:telomeric template RNA reverse transcriptase. .; IEA.
DR InterPro; IPR000477; RVTse.
DR InterPro; IPR003545; Telomerase_RT.
DR Pfam; PF00078; RVT_1; 1.
DR PRINTS; PR01365; TELOMERASERT.
KW RNA-directed DNA polymerase; Transferase.
SQ SEQUENCE 940 AA; 108087 MW; 4EA86CEFF00811FFC CRC64;

Query Match 7.5%; Score 450; DB 2; Length 940;
Best Local Similarity 25.6%; Pred. No. 3.9e-19;
Matches 159; Conservative 115; Mismatches 238; Indels 110; Gaps 24;
```


Qy	445	PRRLVOLLQKHS--PWOVYGFVR-----ACRLRLVPP 475
Db	314	PKRLVFPVQIASTIVKCKCOQYNFLRLDADWFLPRLDYEDGHSDVNDVVSFCFAASHLLFFH 373
Qy	476	GLWGRSHNERRFLNRKTFISLGKHAKLQELATWKSVRDCAWLRSPGCVGCPAAEHR 535
Db	374	VLFGSADNWAULRSKVYYVYLNLPSTSPHLDTMTGGFLRLTEINWLFIS--DNULKSRDDM 432
Qy	536	LR-BEILAKFLHLMVYVVELLSFFYVTTTFQKRLPFYKRSVMSKLOSIGIRHLK 594
Db	433	LKARELFEQLMTWVNRFLPQLIRSFYFTDSLTSQD--IYRHPVQR-KTRASTLOELK 489
Qy	595	RVLQ--RELSEAEVRQREARPALTSRLRIFKPDGLRPTVNMVYVVGARTFRREKRAE 652
Db	490	RTQFSSKVLTPSD-----LGISKFRLMPKKSGFRPIVSLGRPVQS---PRKKPI 536
Qy	653	RLTSRYKALFSLVNIYERARRPGLLGASVLGLDDIH--RAWRTPLVLRVAQDPPELYFV 709
Db	537	SVNNKSLKYL-KYQEFR--LGGNNKGLDSVHLKLVGKEYAKIQQ--LOGLKPV 590
Qy	710	KVDVTGAYDTIIPQDLRTEVIA-----SIHKPONTYCVRRYAVVQAAHGHR 756
Db	591	KIDVTAAFDTIPASKVKQDISKRELLDCESYSLHSHSRILPMSSKTVLRFWFTTSRACNRS 650
Qy	757	KAFKSHSVTLTLOQPMRQFVAHLQETSPDLADAVVIEQSSSLNEASSGLDFVFLRMCHH 816
Db	651	GA-----LQAFRLIG-----NKGIVIDENKSDSVGKQLLYKJLNDHLFRN 690
Qy	817	AVRIRGKSVQOCGIPQGSILSTLCSLCYGMENKLPAGI--RRDGLLRLVDDFLVLT 874
Db	691	DVFDIQVHRQVRGIPQGSILSSLFCSMVYEEMVREKFSDLVDRPDTCLMRFVDDFMLIT 750
Qy	875	PLHTAKTFLRTLVRGVPYGCYNLRTVNVFPVEDEALGGTAQVOMPAGHLPFGCGLL 934
Db	751	TDTATATEFINRALKGLPDYGVSVNRSKCLYNFPL---SVGGVRIAQLGEEGEMPFGLMK 807
Qy	935	LDRTRLTEVQSDSYSSYARTSIRASTFNFRGFK--AGRNWRKRLFGVLRKCHSLFDLOVN 992
Db	808	IBPCNLQIHRDY-PYS-----SALLWVDKGVKLAVRHRAKEYFSA---RFRLLINKSV 859
Qy	993	SLQTVCTNI---YKILLQAVR 1011
Db	860	E-AVLKKNVSAFFRYVFLRAIR 880

RESULT	27
Q80SUS	
ID	Q80SUS PRELIMINARY; PRT; 116 AA.
AC	Q80SUS;
DT	01-JUN-2003 (TReMBLrel. 24, Created)
DT	01-JUN-2003 (TReMBLrel. 24, Last sequence update)
DT	05-JUL-2004 (TReMBLrel. 27, Last annotation update)
DE	Telomerase reverse transcriptase (Fragment).
GN	Name=tert;
OS	Rattus norvegicus (Rat).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI	TaxID=10116;
[1]	
RP	SEQUENCE FROM N.A.
RC	STRAIN=Fischer;
RA	MEDJLNNB-22615084; PubMed=12729609; DOI=10.1016/S0003-2697(03)00091-5;
RX	Holzmann K., Berger W., Meiji D., Cerni C., Sasgary S.;
RT	"Detection and quantification of transcripts for the catalytic subunit
RT	TERT and the RNA component of telomerase in rat tissue.";
RL	Anal. Biochem. 317:120-123(2003).
ENBL	AJ440965; CAD29524.1; -.
DR	ENBL; AJ440966; CAD29525.2; -.
DR	EMBL; AJ440966; CAD29525.2; -.
GO	GO: 0003964; F:RNA-directed DNA polymerase activity; IEA.
KW	RNA-directed DNA polymerase.
FT	NON TER 1
FT	NON TER 116
SQ	SEQUENCE 116 AA; 12634 MW; BAA7F12F6B23DB35 CRC64;

	Query Match	7.5%;	Score 449;	DB 2;	Length 116;		
	Best Local Similarity	74.8%;	Pred. No. 3.2e-20;				
	Matches	86;	Conservative	15;	Mismatches	14;	
				Indels	0;	Gaps	0;
Qy	47	FRLVAQLVCVPWDARPPPAASFRVSCIKELVARVLQRLCBGRKKNVLAFGFALLDG	106				
			:	:	:	:	:
			:	:	:	:	:
			:	:	:	:	:
Dd	2	FRTLVAQLVCVPWGSQPDPADLSFHQVSLLKELVSRVQKLCEBGERNVLAFGFALLNG	61				
			:	:	:	:	:
			:	:	:	:	:
Qy	107	ARGGPPPEAFTTSVRSYLPNTVTDALRGSGAWGLLRRVGDDVLVHILARCALFVL	161				
			:	:	:	:	:
			:	:	:	:	:
Dd	62	ARGGPPMAFTTSHVHSYLIPNSVTSTCVSAGWMILLSRVGDDLIVYLLASHCALYLL	116				
			:	:	:	:	:
			:	:	:	:	:

RESULT 28

ID	TERM_EUPAE	STANDARD;	PRT;	1031 AA.
AC	000939;			
DT	30-MAY-2000 (Rel. 39, Created)			
DT	30-MAY-2000 (Rel. 39, Last sequence update)			
DT	25-OCT-2004 (Rel. 45, Last annotation update)			
DE	Telomerase reverse transcriptase (EC 2.7.7.-) (Telomerase catalytic subunit) (Telomerase subunit P123).			
DE	subunit (Telomerase subunit P123).			
OS	Eukaryota; Alveolata; Ciliophora; Spirotrichea; Hypotrichia;			
OC	Euplotida; Euplotidae; Euplotes.			
OX	NCBI_TaxID=5940;			
OX	[1]			
RN	SEQUENCE FROM N.A.			
RP	MEDLINE=97274210; PubMed=9110970; DOI=10.1126/science.276.5312.561;			
RX	Langner J., Hughes T.R., Shevchenko A., Mann M., Lundblad V.,			
RA	Cach T.R.;			
RA	"Reverse transcriptase motifs in the catalytic subunit of			
RT	telomerase.";			
RL	Science 276:561-567(1997).			
CC	-1- FUNCTION: Telomerase is a ribonucleoprotein enzyme essential for			
CC	the replication of chromosome termini in most eukaryotes. It			
CC	elongates telomeres. It is a reverse transcriptase that adds			
CC	single sequence repeats to chromosome ends by copying a template			
CC	sequence within the RNA component of the enzyme.			
CC	-1- SUBCELLULAR LOCATION: Nuclear.			
CC	-1- SIMILARITY: Belongs to the reverse transcriptase family.			
CC	Telomerase subfamily.			
CC	-1- SIMILARITY: Contains 1 reverse transcriptase domain.			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration			
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -			
CC	the European Bioinformatics Institute. There are no restrictions on its			
CC	use by non-profit institutions as long as its content is in no way			
CC	modified and this statement is not removed. Usage by and for commercial			
CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/			
CC	or send an email to license@isb-sib.ch).			
CC	EMBL; U95964; AAC47515.1; -.			
DR	InterPro; IPR000477; RVTse.			
DR	InterPro; IPR003545; Telomerase_RT.			
DR	Pfam; PF000078; RVT; 1.			
DR	PRINTS; PR01365; TELOMERASERT.			
DR	PROSITE; PS50878; RT_POL; 1.			
KW	DNA-binding; Nuclear protein; RNA-directed DNA polymerase; Telomere;			
KW	transferase.			
FT	DOMAIN 498 852 Reverse transcriptase.			
FT	SEQUENCE 1031 AA; 122562 MW; 57B87A63A1FED60F CRC64;			
QY	Query Match 7.5%; Score 448.5; DB 1; Length 1031;			
Db	Best Local Similarity 22.2%; Pred. No. 5.4e-19;			
QY	Matches 138; Conservative 125; Mismatches 303; Indels 57; Gaps 16;			
QY	464 FVRACLRRLVPPGLGWSGRNREFLNTKFTSLGKHKLISLQELTWKMSVRDCAWLRRS 523			
Db	361 FINEFFYNILPKDFTLGR-NRKNFQKKVKYVELNKHLELHKMLLEKINTREISWQVE 419			
QY	524 PGVGCVPAAEHLUREBEILAKFLHLMSSVTVVLELLRSFFVTVTTTFOGRLFFYRKSVWSK 583			

Db 420 TSAKHFFYPDHE-NIYVLMKLLRWIFEDLVVSLIRCFYFTEQOQSXYSTKYRKNIMDV 478
 Qy 584 LQSIGIRQHRLKVQLRELSEAEVRQHREARPALITSLRLPIKPDGLRPVNMDYVVVGAR 643
 Db 479 IMKMSIAD-LKKETLAEVQEKEVEWKKSL-GFAPGKLRLIPKTTFRPMTFN----KK 532
 Qy 644 TFRREKRAERLTSTRVKALFVLNVERARR- -PGLLGASVGLDDIHRAWRTFVLRVRAQ 700
 Db 533 IVNSDRXTTKTLTNTKLLNSHLMLKTLKRNMFKDPFGFAVFNYVDVMKKYEFEVCWK-K 591
 Qy 701 DPPPELYFVKVDVTGAYDTTPQDELTEVI-----ASIIPONTYCVRRYAV 746
 Db 592 VGQPKLFPAFWMDBEKCYDSVNREKLSFTFLTKLLSSDFWIMTAQILKRKNNIVIDSKNF 651
 Qy 747 VQKAAGHGVAKAFKSHYSTLTLDLPYMRFQVAHLQETSPLRDADVIBQSSSLEASSGLF 806
 Db 652 RKKEMKDYPQKFQOK-TALEGGQPTFLSVLENQDNLNKKTLLIVEAKQRNVFKDNLL 710
 Qy 807 DVFLRFMCHHAVIRGRKSYQCQIGIPGSGISLTLLCSLCYGDMMENKLFAGRIRD- ---- 860
 Db 711 QPVINICQYNVINENGKRYFKQTGIPQGLCVSSILSSFYATLBESSIGFLRDESMNPEN 770
 Qy 861 ---GLLRLLVDDFLLVTPHLTHAKTFPLTVRGVPYGCVVNLKRTVNVFPVEDEALGGT 917
 Db 771 PNVNLLMRLLTDYLLITQENNAVLFIETKLINVSRNGFKPNMKKLOTSPFLSPSKPAKY 830
 Qy 918 AFVOMPAGHLGF- - - - -PWCGILLDRTELVSQSDYSYARTSIRASLTEN-RGFKAGRNWR 972
 Db 831 GMDSVESQNIVQDYCDMIGISDMKTLALMPNINRIE-GILCTNLNMOTKASMWLKK 889
 Qy 973 KLGVLRLKCHSLFDLQVNSLOTVCT- - - - -NIYKILLIQAYRFHACVLQLPFHQQVM 1026
 Db 890 KLSFLMNNTHYF- - - - -RKTIITTEDFANKTLNKLFISGGYKYMQCAKEYDKHFK-- 940
 Qy 1027 KNPTFFFLRVISDTASLCYSILKA 1049
 Db 941 KNLAMSSMIDLVSIIYSVTRA 963

RESULT 29
 Q7Z1L0 PRELIMINARY; PRT; 1032 AA.

ID	Q7Z1L0	PRELIMINARY;	PRT;	1032 AA.
AC	Q7Z1L0;			
DT	01-OCT-2003 (TREMBLrel. 25, Created)			
DT	01-OCT-2003 (TREMBLrel. 25, Last sequence update)			
DT	01-MAR-2004 (TREMBLrel. 26, Last annotation update)			
DE	Telomerase reverse transcriptase.			
GN	Name=TERF-3;			
OS	Euplotes crassus.			
OC	Eukaryota; Alveolata; Ciliophora; Spirotriches; Hypotrichia;			
OC	Euplotida; Euplotidae; Moneuplotes.			
OX	NGBI_taxid=5936;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RP	MEDLINE=42671093; PubMed=12787498; DOI=10.1016/S0092-8674(03)00363-5;			
RA	Karamysheva Z., Wang L., Shrode T., Bednenko J., Hurley L.A.,			
RA	Shippen D.E.;			
RT	"Developmentally programmed gene elimination in Euplotes crassus			
RT	facilitates a switch in the telomerase catalytic subunit.";			
RL	Cell 113:565-576(2003).			
DR	EMBL; AY267544; AAP42279.1; -			
DR	GO; GO:0003723; F:RNA binding; IEA.			
DR	GO; GO:0003964; F:RNA-directed DNA polymerase activity; IEA.			
DR	GO; GO:0016740; F:transferase activity; IEA.			
DR	GO; GO:0006278; P:RNA-dependent DNA replication; IEA.			
DR	InterPro; IPR000477; RVTrse.			
DR	Pfam; PF00078; RVT_1; 2.			
XW	RNA-directed DNA polymerase; Transferrase.			
SQ	SEQUENCE 1032 AA; 122842 MW; 006D9C6CE32EF472 CRC64;			

Query Match 7.4%; Score 441; DB 2; Length 1032;
 Best Local Similarity 24.0%; Pred. No. 1.6e-18;

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Db      635  -VSQSIHGLGINFKEKQMESFGLGEEHLKAASSISELSKHKHSMKITNAPVGMCGTKIYS 693
Qy      938  RTLEVSQSYSS-YARTSIRASILTFRNGFKAGRNMRKLFGLVRLKCHSLFLDLQVNSLOT 996
Db      694  DGFSIKQQTADPYLPFSIAHST-----KPGRALESRRKLLQNMRSRIYD---PNNKK 745
Qy      997  VCTNIYKILLQAVRFHACVLQLPFPHQQWKNPTFFLRVISDTASLCYSILKAKNAGMSL 105
Db      746  AYENIYDTFL-----FYGKGLGLLGRMDFNRSFARTLEHSKRFAPRI--CRKHGISI 798
Qy      1057 GAK 1059
Db      799  TRK 801

RESULT 31
Q9JLM1
ID Q9JLM1 PRELIMINARY; PRT; 104 AA.
AC Q9JLM1;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Telomerase reverse transcriptase (Fragment).
GN Name=Terf;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Hatakeyama S., Ishikawa F.;
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF157502; AAF42984.1; --
DR MGD; MGI.1202709; Tert.
DR GO; GO:0005515; F:protein binding; TFI.
DR DR GO; GO:0003720; F:telomerase activity; IDA.
KW RNA-directed DNA polymerase.
FT NON TER 104
SQ SEQUENCE 104 AA; 11598 MW; 4B649B63476D3D44 CRC64;

Query Match 6.7%; Score 397; DB 2; Length 104;
Best Local Similarity 76.0%; Pred. No. 4.4e-17;
Matches 79; Conservative 7; Mismatches 18; Indels 0; Gaps 0

Qy      1  MPRAPRCVRSLLRSYREVLPATFVRRLLPGQWRVLVQGDPAAFRAVLAQCLVCVFW 60
Db      1  MTRAPRCVRSLLRSYREVLPATFVRRLLPGQWRVLVQGDPAAFRAVLAQCLVCVFW 60
Qy      61  DARPPPAAPSPQVSCCLKELVARVLQRLCERGAKNVLAFGFALL 104
Db      61  GSQPPPADLSFHQVSSKLVARVVQRLCERNRVLAFGFELL 104

RESULT 32
Q818Z7
ID Q818Z7 PRELIMINARY; PRT; 1135 AA.
AC Q818Z7;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Telomerase.
OS Sterkiella sp. Aspen.
OC Eukaryota; Alveolata; Ciliophora; Spirotrichea; Stichotrichia;
OC Stichotrichida; Oxytrichidae; Sterkiella.
OX NCBI_TaxID=200599;
RN [1]
RP SEQUENCE FROM N.A.
RA Marandi S.S., Prescott D.M.;
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY116501; AAN87866.1; --
DR DR GO; GO:0005634; C:nucleus; IEA.
DR DR GO; GO:0003677; F:DNA binding; IEA.

```


QY 952 TSIRASLTFRNGFKAGRNMRRLFGVLRKCHSLFLDLQVNSLQVCTNYYKILLQAVR 1011
 Db 972 EGILCTLVNMVQTNESILWKKLKSFLMNNISFYFKSTINTKQFANITLSKLYAAAEK 1031
 QY 1012 FHACVLQLP-FHQ 1023
 Db 1032 YVACCOEKFREFHE 1044
 RESULT 34
 Q9UNR4 PRELIMINARY; PRT; 73 AA.
 ID Q9UNR4
 AC Q9UNR4; 01-MAY-2000 (TReMBLrel. 13, Created)
 DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
 DT 01-MAY-2004 (TReMBLrel. 26, Last annotation update)
 DE Telomerase reverse transcriptase (Fragment).
 GN Name=TERT;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99151529; PubMed=10029071;
 RA Horikawa I., Cable P.L., Afshari C., Barrett J.C.;
 RT "Cloning and characterization of the promoter region of human
 telomerase reverse transcriptase gene.";
 RL Cancer Res. 59:826-830(1999).
 DR EMBL; AF098956; AAD12786.1; -
 DR GO; GO:0003964; F:RNA-directed DNA polymerase activity; IEA.
 FT RNA-directed DNA polymerase.
 KW NON TER 73
 SQ SEQUENCE 73 AA; 8290 MW; 20097F24B3035134 CRC64;

Query Match 6.6%; Score 394; DB 2; Length 73;
 Best Local Similarity 100.0%; Pred. No. 4.3e-17;
 Matches 73; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MPRAPRCRAVRSLLSHYREVLPPLATFVRRLLPQGWRLVQRGDPAAFRALVAQCLVCPW 60
 Db 1 MPRAPRCRAVRSLLSHYREVLPPLATFVRRLLPQGWRLVQRGDPAAFRALVAQCLVCPW 60
 QY 61 DARPPPAAPSPRQ 73
 Db 61 DARPPPAAPSPRQ 73

RESULT 35
 Q91826 PRELIMINARY; PRT; 1108 AA.
 ID Q91826
 AC Q91826;
 DT 01-MAR-2003 (TReMBLrel. 23, Created)
 DT 01-MAR-2003 (TReMBLrel. 23, Last sequence update)
 DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
 DE Telomerase (Fragment).
 OS Sterkiella sp. Aspen.
 OC Eukaryota; Alveolata; Ciliophora; Spirotrichea; Stichotrichia;
 OC Stichotrichida; Oxytrichidae; Sterkiella.
 OX NCBI_TaxID=200599;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Marandi S.S., Prescott D.M.;
 RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY116502; AAN87867.1; -
 DR GO; GO:0005634; C:nucleus; IEA.
 DR GO; GO:0003677; F:DNA binding; IEA.
 DR GO; GO:0003721; F:telomeric template RNA reverse transcriptase. . .; IEA.
 DR InterPro; IPR003545; Telomerase_RT.
 DR PRINTS; PR01365; TELOMERASERT.
 FT NON TER 1
 SQ SEQUENCE 1108 AA; 131535 MW; EC8262E01B8E0FAD CRC64;

Query Match 6.6%; Score 392; DB 2; Length 1108;
 Best Local Similarity 22.2%; Pred. No. 1.8e-15;
 Matches 136; Conservative 112; Mismatches 307; Indels 58; Gaps 15;
 QY 450 QLLROHSSFWQVYGFVRACLRLRPPGLWGSRRERRFLRNTKFKISLGHAKLSLQELT 509
 Db 427 QLFHEYQDQRQISNLFTEFVANVPFKNFLEGG-NKKIFNKKMLQFVKFNRFSTKISLL 485
 QY 510 WKMSVRDCAWLRRSPGVCVPAAEH---RLREIILAKFLHLMWSVVVVVLLRSFFVVTET 566
 Db 486 NKFRVNEVSWL-----SFCKDENKXFFMNEHVFVKLKWVFDLAIITLMCYFSTBK 541
 QY 567 TFQKNRFFYKRSVMSKLSQIGIRQHLKRVQLRSEAEVRRHREARPALLTSRLRPIPK 626
 Db 542 AKEYQRIFFYKRIWNIMRLSIDLLAQ-NLKQVEKKEMRIFCESQ-NFAPGKLRLEPK 599
 QY 627 PDGLRPIVMMDYVVCARTFRE-----KRAERLTSRVK---ALFSVLNVEARPPGLLG 677
 Db 600 GDTFRPIM-----TFNRKIPNQVGKFSQSRMTTNKLTQTAHMLKMLKSHSFG 650
 QY 678 ASVLGLDDIHRARWTFVLRVRAQDPPPELYFVKVDVTGAYDTIPODRLTEVIAS----- 731
 Db 651 FAVENYDDIMKRYENFVQKW-KQINSPKLYFVAMDIKCYDNDVCERVVNFLOKSDLMDK 709
 QY 732 -----IIRPONTYCVRRYAVVQAAHGHVRKAFKSHVSTLTDLQPYMRQFVAHQET 783
 Db 710 EYFILTNTFVLRKNNIIVERSNFRKLPKIQVFRYKQK-IGIDGSSYPTLPEILEDFND 768
 QY 784 SPLRDANVIEQSSLSNEASSGLFDVLRPMCHAVIRGKSVQCGIPIQGSILSTLLCS 843
 Db 769 LMKRTIIIAEQEQRKKFPKNDLLQVPLKICNNYVTFNKKQYKMGKIPQGLVCVPYILSS 828
 QY 844 LCYGDMEKNLFAPIRRD-----GLLLRLVDDFLVTPHLTHAKTFLRLTVRGVPEY 894
 Db 829 FYANLEENALQFLRKESMDPEKPEINLMLRUTDYLMTTEKNAMLFIEKLYQSLGN 888
 QY 895 GCVVNLRTVNVFPVEDEALGTAFTVQ---MPAHGLFPWCGLLLTDLTRTLEVSQSYSSAR 951
 Db 889 PFKENMKKLTNFALNLQKIGCTNTTQDIDSINDDLFWHIGISIDIKTLNIQNI-NICK 947
 QY 952 TSIRASLTFRNGFKAGRNMRRLFGVLRKCHSLFLDLQVNSLQVCTNYYKILLQAVR 1011
 Db 948 EGILCTLVNMVQTNESILWKKLKSFLMNNISFYFKSTINTKQFANITLSKLYAAAEK 1007
 QY 1012 FHACVLQLP-FHQ 1023
 Db 1008 YVACCOEKFREFHE 1020

RESULT 36
 Q6CSS0 PRELIMINARY; PRT; 861 AA.
 ID Q6CSS0
 AC Q6CSS0;
 DT 25-OCT-2004 (TReMBLrel. 28, Created)
 DT 25-OCT-2004 (TReMBLrel. 28, Last sequence update)
 DT 25-OCT-2004 (TReMBLrel. 28, Last annotation update)
 DE Kluyveromyces lactis strain NRRL Y-1140 chromosome C of strain NRRL Y-1140 of Kluyveromyces lactis.
 GN ORFNames=KLLA0C1831g;
 OS Kluyveromyces lactis NRRL Y-1140.
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Saccharomycetaceae; Kluyveromyces.
 OX NCBI_TaxID=284590;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=NRRL Y-1140;
 RG Genolevures;
 RA Dujon B., Sherman D., Fischer G., Durrens P., Casaregola S.,
 RA Lafontaine I., de Montigny J., Marck C., Neuvéglise C., Tallia E.,
 RA Goffard N., Frangeul L., Aigle M., Anthouard V., Babour A., Barbé V.,
 RA Barnay S., Blanchin S., Beckerich J.M., Beyne E., Bleykasten C.,
 RA Boisarane A., Boyer J., Cattolico L., Confaniolero F., de Daruvar A.,

Db 563 QYHNILSSSSHLNCKSLVDKTKTIALQKGNILEVCRSQYDVV-----GSVKDARG 616
 QY 823 K--SVVQCGIPQSGILSLCLSCVGMENKLFAGI---RDGALLRLVDDFLAVTPEHL 877
 Db 617 NLHLYKRGVQGSLSIFCDIILYSAMVHDCQFOLWKSQDFLVRVLDVDFLVTDPD- 675
 QY 878 THAKTFLRLVRG--VPEYGCYVNLKTKTVNPFVDEALGGTAFAVQMPAHGLFPWCGLLL 935
 Db 676 SNIYQVHNILSGKILESAGFVNKDKTV---VNVQTTTKTS-----I 715
 QY 936 DTRTEVQSDYSYARTSIRASLTNRGFKAGNMRKLFGLVRLKCHSLFLDLQVNSLQ 995
 Db 716 DFVGLVNTDLSIKRNSGSLV-TTNFRTFKTLVKYKLPYQLNLEGFLDCSFGVLE 774
 QY 996 TVCTNIYKILLQAVRFHACVQLPFPHQVWKNPTFFELRVISDTSASLCSYLK 1048
 Db 775 NVLENMGSLRLVLRFP-----KTKFTSIVKYDTFHCYKFIK 811

RESULT 38

Q9GRCS PRELIMINARY; PRT; 895 AA.
 ID Q9GRCS
 AC Q9GRCS
 DT 01-MAR-2001 (TremBLrel. 16, Created)
 DT 01-MAR-2001 (TremBLrel. 16, Last sequence update)
 DT 01-OCT-2003 (TremBLrel. 25, Last annotation update)
 DE Telomerase reverse transcriptase.
 GN Name=PcTERT;
 OS Paramacium caudatum.
 OC Eukaryota; Alveolata; Ciliophora; Oligohymenophorea; Peniculida;
 CC Paramacium.
 OX NCBI_TaxID=5885;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=KNZ-5 and KNZ-2;
 RX MEDLINE=21147925; PubMed=11250070; DOI=10.1016/S0378-1119(01)00337-7;
 RA Takenaka Y., Matsuura T., Haga N., Mitsui Y.;
 RT "Expression of telomerase reverse transcriptase and telomere
 RT elongation during sexual maturation in Paramacium caudatum.";
 RL Gene 264:153-161(2001).
 DR EMBL; AB035309; BAB18587.1; --
 DR GO; GO:0005634; C:nucleus; IEA.
 DR GO; GO:0003677; F:DNA binding; IEA.
 DR GO; GO:0003723; F:RNA binding; IEA.
 DR GO; GO:0003964; F:RNA-directed DNA polymerase activity; IEA.
 DR GO; GO:0003721; F:telomeric template RNA reverse transcriptase. . .; IEA.
 DR GO; GO:0006278; F:RNA-dependent DNA replication; IEA.
 DR InterPro; IPR000477; RVTse.
 DR Pfam; PF00078; RVT_1; 2.
 DR PRINTS; PR01365; TELOMERASERT.
 KW RNA-directed DNA polymerase; Transferase.
 SQ SEQUENCE 895 AA; 107086 MW; 130C0DB32FD11C76 CRC64;

Query Match 6.1%; Score 364; DB 2; Length 895;
 Best Local Similarity 22.2%; Pred. No. 7.3e-14;
 Matches 142; Conservative 113; Mismatches 274; Indels 110; Gaps 21;
 QY 448 LVQLRQSSPWQVGFYRACLRRLVPPGLWGSRRNRRFLNRTKKFISLGHAKLSLOE 507
 Db 277 LDHLYLNIHQYTSVNVNFRLEIIPDLFG-QQNLFETLDSDFITLRFEDQSVD 335
 QY 508 LTWKMVRDCAWLRSPGCVGCPAAEHLR-----REEILAKFLHMLVYVVELLSFFYV 563
 Db 336 YIKMNVFEPWLNK-----YFNKKQRLLIIKRQNMPLMKFWQBIIPFLRHNFYI 390
 QY 564 TETTFQKRLFPYKSVNSKLSQISGIRQLKRVQLRELSEAEVROHREARPALLSRLRF 623
 Db 391 TERMKDDKFLFYKEIWHILQLSLTS-LTKNFFEISVNSIK-----TPYVGKLR 442
 QY 624 IPKPDGLRPIVNDYVVGARTFRREKRAERLTSRVKALFSVLNVERARRPGLLGASVLG- 682

Db 443 VPKECTFRPIV-----TYNRKAKTSISLRNK-LVDIKYILNRLIQPLGYSVFN 492
 QY 693 -----LDDIHRAMFTFVLVRADOPPELFFVKVDVTGAVDTIPQDRLTEVIASIIKPO 736
 Db 493 PEVFSRLEEFKKLM-----IKLQO--PKTYITMDIOKCYDTIILQLLQLESKQFS 544
 QY 737 NTYCVRRYAVVQKAAHGHVRKAFKSHVSTLADL-----QPYMRQ--EVAHLQ 781
 Db 545 SIYAINKYHIVSR-NNRMLKPSF-----SMKDLFILORTCAIPENKQLLKQGYIEHIQ 598
 QY 782 ETSPLRDVAWTEQSSLSNEASGLFDVFL-----RFMC-HHAFIRKSKSVQCGIPOGSL 837
 Db 599 KN--KOTIIINQGFQ-----NSVTFSEFLNSIKNIQNNIVQFENRYFRQTLGIPQGLNI 651
 QY 838 STLLCSLCYGMENKLFAGIRRDGALLRLVDDFLAVTPEHLTHAKTFLRLVRGVPYGCV 897
 Db 652 SGILCSFVLANLEOKLTNKLIGDILIMRLTDDYCCCLAFSDSSIKILNFTQIEQYQIR 711
 QY 898 VNLKRTVVNPFVDEALGGTAFAVQMPAHGLFPWCGLLDDTRTLEVSQDSYSSYARTSIRAS 957
 Db 712 LNHDKTOHNERSDR-----YFKWIGKIIDIETLTLPKPAFYLESDTKFQVQ 757
 QY 958 LTFNRGFKAGNMRKLFGLVRLKCHSLFLDLQVNSLQVCTVCTNIYKILLQAYRHACVL 1017
 Db 758 INVNLPTKVTYIKSKLSLILNQKFFFNSKLNDDKPTMK-----VL 801
 QY 1018 QLPHQVQWKNPTFFELRVISDTSASLCSYLKAKKAGMSL 1056
 Db 802 KIFVHSGLVKLISFLKRL-----KYNYGASKLRNQKSI 835
 RESULT 39
 TERT_TERTH STANDARD; PRT; 1117 AA.
 ID AC 077448;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE Telomerase reverse transcriptase (EC 2.7.7.-) (Telomerase catalytic
 DE subunit) (Telomerase subunit P133).
 GN Name=TERT;
 OS Tetrahymena thermophila.
 OC Eukaryota; Alveolata; Ciliophora; Oligohymenophorea; Hymenostomatida;
 CC Tetrahymenina; Tetrahymenidae; Tetrahymena.
 OX NCBI_TaxID=5911;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=B7;
 RX MEDLINE=98337940; PubMed=9671703; DOI=10.1073/pnas.95.15.8479;
 RA Bryan T.M., Sperger J.M., Chapman K.B., Cech T.R.;
 RT "Telomerase reverse transcriptase genes identified in Tetrahymena
 RT thermophila and Oxytricha trifallax";
 RL Proc. Natl. Acad. Sci. U.S.A. 95:8479-8484(1998).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98337941; PubMed=9671704; DOI=10.1073/pnas.95.15.8485;
 RA Collins K., Gandhi L.;
 RT "The reverse transcriptase component of the Tetrahymena telomerase
 RT ribonucleoprotein complex";
 RL Proc. Natl. Acad. Sci. U.S.A. 95:8485-8490(1998).
 CC -!- FUNCTION: Telomerase is a ribonucleoprotein enzyme essential for
 CC elongates telomeres. It is a reverse transcriptase that adds
 CC simple sequence repeats to chromosome ends by copying a template
 CC sequence within the RNA component of the enzyme.
 CC -!- SUBCELLULAR LOCATION: Nuclear.
 CC -!- SIMILARITY: Belongs to the reverse transcriptase family.
 CC Telomerase subfamily.
 CC -!- SIMILARITY: Contains 1 reverse transcriptase domain.
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -

Db 405 KLIPKRSFRVTCVPIKRSKLKLLKLELDLTKLEKCR-----EFERYRKE 449
 QY 674 GL-----LGASVLGLDDIHRARWTFV-----LRVRAQD-----PPPELVFKVD 712
 Db 450 VLSVPGQILRLKLSKLRDYESYRASVHSSSDVAEKISDYRDSLLTRGCEIPKILKFD 509
 QY 713 VTGAYDTTPDRLTEVIASIKPON---TYCVRRYAVQKAAHVRKAFKSHVSTLTDL 769
 Db 510 MKECYDRLSQPVLMKLEELFENQDNKTSYYVRYA--QLDASHKLKK-----VKTITDT 562
 QY 770 QYMQRFVA---HLQETSPDR--AVVIEQSSSINEASSGLFDFLRFMCHHVR-IRG 822
 Db 563 QYHNILNLSHSLNCKSLVDKTKTIALQKNILEVCRSQYDVV-----GSVDARG 616
 QY 823 K--SYVQCGIPQGSILSTLLCSLCYGDMEKLFAGI---RDGGLLLRLVDLFLVTPHL 877
 Db 617 NLHLKRGKGVFGFSLISFCIDILYSAMVHDCQFLMKSKQDFLFLVRLVDLFLVTPD- 675
 QY 878 THAKTFLRLVRG--VPEYGCVVNLRKTVNPFVDEALGGTAQVOMAHGLFPWCGLL 935
 Db 676 SNIYQVHNILSGKILESYGAFVNDKTVW-----VNOQTTTKPSIDFVGLV 722
 QY 936 DRTLEQSDYSSYARTSIRASLTFRGFKAGRNMRKLFGLVRLKCHSLFLDLQVNSIQ 995
 Db 723 NTDLISK-----RNSGSLV-TTNFRTKTLVKYKLTQYQNLNLEGFLDCSFGVLE 774
 QY 996 TVCTMIYKILLQAYRFHACVQLQFPHQQVKNPTFFLRVSDTASLCVSLK 1048
 Db 775 NVLENMGSLLRLVREF-----KTKFTSIVKYDTHCYKFK 811

RESULT 41

TERT YEAST
 ID TERT YEAST STANDARD; PRT; 884 AA.
 AC Q06153.
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE Telomerase reverse transcriptase (EC 2.7.7.-) (Telomerase catalytic subunit).
 DE subunit).
 GN Name=EST2; OrderedLocusNames=YLR318W; ORFNames=L8543.12;
 OS Saccharomyces cerevisiae (Baker's yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
 OX NCBI_TaxID=4932;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=S288c / AB972;
 RX MEDLINE=97313267; PubMed=9169871;
 RA Johnston M., Hillier L., Riles L., Albermann K., Andre B., Ansoorge W.,
 RA Benes V., Brueckner M., Delius H., Dubois E., Duesterhoeft A.,
 RA Entian K.-D., Floeth M., Goffeau A., Hebling U., Heumann K.,
 RA Heuss-Neitzel D., Hilbert H., Hilger F., Kleine K., Koetter P.,
 RA Louis E.J., Messenguy F., Mewes H.-W., Miosga T., Moestl D.,
 RA Mueller-Auer S., Nentwich U., Obermaier B., Piravandi E., Pohl T.M.,
 RA Portetelle D., Purnelle B., Rechmann S., Rieger M., Rinke M., Rose M.,
 RA Scharfe M., Scherens B., Scholler P., Schwager C., Schwarz S.,
 RA Underwood A.P., Urrestazu L.A., Vandenbol M., Verhasselt P.,
 RA Vierendeels F., Voet M., Volckaert G., Voss H., Wamburt R., Wedler E.,
 RA Wedler H., Zimmermann F.K., Zollner A., Hani J., Hobeisel J.D.;
 RT "The nucleotide sequence of Saccharomyces cerevisiae chromosome XII.";
 RL Nature 387:87-90(1997).
 RN [2]
 RP CHARACTERIZATION.
 RX MEDLINE=97274210; PubMed=9110970; DOI=10.1126/science.276.5312.561;
 RA Lingner J., Hughes T.R., Shevchenko A., Mann M., Lundblad V.,
 RA Cech T.R.;
 RT "Reverse transcriptase motifs in the catalytic subunit of
 RT telomerase."
 RL Science 276:561-567(1997).
 CC -!- FUNCTION: Telomerase is a ribonucleoprotein enzyme essential for
 CC the replication of chromosome termini in most eukaryotes. It
 CC elongates telomeres. It is a reverse transcriptase that adds

CC simple sequence repeats to chromosome ends by copying a template
 CC sequence within the RNA component of the enzyme.
 CC -!- SUBCELLULAR LOCATION: Nuclear.
 CC -!- MISCELLANEOUS: Deletion causes telomere shortening and senescence.
 CC -!- SIMILARITY: Belongs to the reverse transcriptase family.
 CC Telomerase subfamily.
 CC -!- SIMILARITY: Contains 1 reverse transcriptase domain.
 CC
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 CC or send an email to license@isb-sib.ch).
 CC
 CC EMBL; U20618; AAB64520.1; --
 CC PIR; S53396; S53396.
 CC Germonline; I42382; --
 CC SGD; S000004310; EST2.
 CC GO; GO:0005730; C:nucleolus; IDA.
 CC GO; GO:0005697; C:telomerase holoenzyme complex; IDA.
 CC InterPro; IPR000477; RVTse
 CC InterPro; IPR003545; Telomerase_RT.
 CC Pfam; PF00078; RVT; 1.
 CC PRINTS; PR01365; TELOMERASERT.
 CC PROSITE; PS00878; RT_POL; 1.
 KW DNA-binding; Nuclear protein; RNA-directed DNA polymerase; Telomere;
 KW Transference.
 FT DOMAIN 422 725 Reverse transcriptase.
 SQ SEQUENCE 884 AA; 102663 MW; 788334BB49592340 CRC64;
 Query Match 6.0%; Score 356.5; DB 1; Length 884;
 Best Local Similarity 22.1%; Pred. No. 2.1e-13;
 Matches 167; Conservative 127; Mismatches 309; Indels 151; Gaps 28;
 QY 329 KHFYSSGDKBQLRPS--FLLSSLRPSLTGARRLV---ETIFLGSRRPMWPTGPRRLPLRP 383
 Db 185 KQFLH---KLNINSSSPFPYKILPSSSSIKLTDLEAIF-----PTNLVKIP 230
 QY 384 QRYQWMLFLE-LLGNHAQCPYGVLLKTHCPRAVTPAAGVCAREKPGQSVAAPEED 442
 Db 231 QRLKVRINLTQKLLKHKRLNLYVILNSICP-----PLEGTVL----- 269
 QY 443 TDPRLVQLRQHSPPWVGVFVRACLRLVPPGLWGRHNERRLRTKFKISLGKHA 502
 Db 270 ----DLSHLSQ-SPKERVLFPIVILQKLPQEMFGSKKNGKIKNLNLLSPLNGY 324
 QY 503 LSLQELTWKMSVRDCAMLRSPGVGCVPAAEHRLR--EEILAKFLHLMVSVVVELLRSP 560
 Db 325 LPFDSLLKRLKDFRWL---FISDIWFTKHNPENLQALCFISLWFRQLIPKIIQTF 380
 QY 561 FYVTETTFQKRLFFYKRSVWSKLSQIGIROHLKRVQLRELSEAV-RQREARFALLT- 618
 Db 381 FYCTEIS-STVTIVYFRHDTNKLITPFIFYFTKY----LVENNVCNHNSTYTSNFH 435
 QY 619 SRLRFPKPGDLRPLVNMVYV-----GARTFRREKRAERLTSRKALFVNLVYERARR 672
 Db 436 SKMRLPKS-----NNEFRILAIIPCEGADEEFTYKHNHNAIQOTQKILEVLRNKR 489
 QY 673 PGLLGASVLGLDDIHRARWTFVLRV--RAQPPPELYFVKVDVTGAYDTIPQDRLTEVIA 730
 Db 490 PTFP-TKIYSPQIADRIKEFKQRLKKFNPNVPELYFMKFDVKSCYDSIPRMECMRLK 548
 QY 731 SIIPQNTYCVRRYAVVQKAAHVRKAFKSHVSTLTDLPYMQQFVAHLQETSPDRV 790
 Db 549 DALKNENGFFVRYSQYFFN--TNTGLKLF-NVNVASRVKPEY-----EL 589
 QY 791 VIEQSSSINEASSGLFDFLRFMCHHVRIRGKSVQCGIPQGSILSTLLCSLCYGD- 849
 Db 590 YIDNVRTVHLSNQDVINVVEMEIPKTAUWDEKCIREDGLPQGSLSAPIVDLVDDLL 649
 QY 850 --ENKLFAGIRRDGLLLRLVDLFLVTPHLTHAKTFLRLVGRVPEYGCVVNLRKT-VN 906

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Db 650 EFYSEFKASQDYLILKLADDFLIISTDOQQVINIKKLANGGFKQNAKANRDKILAVS 709
Qy 907 FPVDEALGGTAQVQMPAHGLFPWCGLLDTRTLEVOSSYARTSIRASLTFRNGFKA 966
Db 710 SOSDDT-----VIQFCAMHIFVKELEVWKSSTMNPHIRS-----KS 748
Qy 967 GRNMRKLVGVRLKCHSLFLDLQVNSLQTVCTWI-----YK-----ILLQA 1009
Db 749 SKGIFRSIALFTRISYKTTIDTILNSTNTVLMQIDHVVKNISECYKSAFKDLSINVTQN 808
Qy 1010 YREHACVQLPFPHQVWKNPTFFLRVSDTASLC 1043
Db 809 MQFH-----SFLRIIEMTVSGC 826

RESULT 42
Q6BUP6 PRELIMINARY; PRT; 894 AA.
AC Q6BUP6;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Similar to sp|Q06163 Saccharomyces cerevisiae YLR318w EST2.
GN ORFNames=DEHA0C12045g;
OS Debaryomyces hansenii CBS767.
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Debaryomycetes.
OX NCBI_TaxID=284592;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CBST767;
RG Genolevures;
RA DuJon B., Sherman D., Fischer G., Durrens P., Casaregola S.,
RA Lafontaine I., de Montigny J., Marc C., Neuvéglise C., Talla E.,
RA Goffard N., Frangoul L., Aigle M., Anthouard V., Babour A., Barbe V.,
RA Barnay S., Blanchin S., Beckerich J.M., Beyne E., Bleykasten C.,
RA Boisarane A., Boyer J., Cattolico L., Confanioleri F., de Daruvar A.,
RA Despons L., Fabre E., Fairhead C., Ferry-Dumazet H., Groppi A.,
RA Hantraye F., Hennequin C., Jauniaux N., Joyet P., Kachouri R.,
RA Kerrest A., Koszul R., Lemaire M., Lesur I., Ma L., Muller H.,
RA Nicaud J.M., Nikolski M., Oztas S., Ozier-Kalogeropoulos O.,
RA Pellenz S., Potier S., Richard G.P., Straub M.L., Suleau A.,
RA Swennene D., Tekala F., Wesolowski-Louvel M., Westhof E., Wirth B.,
RA Zeniou-Meyer M., Zivanovic I., Bolotin-Fukuhara M., Thierry A.,
RA Bouchier C., Caudron B., Scarpelli C., Gaillardin C., Weissenbach J.,
RA Wincker P., Souciet J.L.;
RT "Genome evolution in yeasts.";
RL Nature 430:35-44(2004).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=CBST767;
RA Genoscope;
RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; CR382135; CAG86234.1; -.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR GO; GO:0003721; F:telomeric template RNA reverse transcriptase. .; IEA.
DR InterPro; IPR000477; RVTse.
DR InterPro; IPR003545; Telomerase_RT.
DR Pfam; PF00078; RVT_1; 1..
DR PRINTS; PR01365; TELOMERASERT.
KW RNA-directed DNA polymerase; Transference.
SQ SEQUENCE 894 AA; 105407 MW; 37C705E712D9C8CE CRC64;

Query Match 6.0%; Score 355.5; DB 2; Length 894;
Best Local Similarity 20.6%; Pred. No. 2.4e-13;
Matches 166; Conservative 161; Mismatches 338; Indels 141; Gaps 32;

Qy 341 LRPSFLSLRPSLTGARRLV--ETIFLGRPMFGTPRRLL-----PR-----LPQR 385
Db 157 LLPSP-KSKISLLKSRMLYKQNTKVINSLRFFSDFLDIEDIVPRETFKYRNLPKK 215
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Qy 386 YWQMRPLFLELLGNHAQCPYGVLLKTHCPRLAAVTPAAGVCAREKPOGSVAAPREEDTP 445
Db 216 FRPLKRLCNQIIHNDSCNYSIYKE-----ICTSPQK-TIKTNFDYYTEI 261
Qy 446 RRLVOLLROHSSPQWVGYFRACLRRLRVLPPCLWGRHNRFRRLNRTKKFTSLGKHAKLSL 505
Db 262 SVIR-----FVLIVTGKIFPLNTWGTGTPKNKSEVIKVIYRFIKAGKNDKFLK 308
Qy 506 QELTWMKSVRDCAWLRSPGVGCVPAAEHRLREILAKFLHMLMSVYVVELLRFYVYTE 565
Db 309 DQLISSIQLSHIYWLKGTSEI--TSKODYKRLVSLFSFSEWFLSVVICKLVGSEFWYTE 366
Qy 566 TT--FQKRLFFYRKSVWSKLQSIGIRQHLKRVOLRSELSAEVQHQREARPALTSRLRP 623
Db 367 VSHGILSKDILHYPHNEWKRAITNKNLDNYVKNLVETTVSVEFNE-TSAFKYKYNIGRLRL 425
Qy 624 IPKPDGLRPI-VNMDYVVGARTFRREKRAERLTSRVKALFSLVLYNERARPPGLL--GASV 680
Db 426 LPKSNDFRALCIFIKIQIISNNLNK--EKEQKFOYLNHMMNNIRPIRELLLOKERDK 482
Qy 681 LGLDDIHRAWRTFVLR-----VRAQPPPELYFYKVDDVTGAVDTIPQDRLTE 727
Db 483 LRLDKKSHP-RCFSLRDIAHNICLFKHDLINKYTHIPKLFMLKFDKMKHCFDNVSODRILK 541
Qy 728 VIASIIKPQNT---YCVRYAVVQKAHGHVRKAFKSHVSTLTDLPYMRQFVAHLQETS 784
Db 542 SVEELFAEDSSDKVYIYRFQV-----ESSVFKQELKK---ORYVIKNESNVQEYN 588
Qy 785 PLR-----DAVIEQSSSLNEASSGLDPVFLRFMCHHAVIRG--KSYVOCOG 830
Db 589 ILEGQCSNFQPNRSPKLIIVDKATFRFRKSQVLETVREHVFHSTMVLPNNTEKFRRTKG 648
Qy 831 IPOGSLSTLLCSLCYGDMMENKLFAGI---RRDGLLRLVDDFLLVTPHLTHA-KTFLRT 886
Db 649 VFQGLPLATLCLNVLVNSLVDENFQFLNDNSDILLRLVDDFLVISTDRSQCKVVDIV 708
Qy 887 LVRGVPYGYCVNLRKTVVNFPPVEDEALGGTAQVQMPAHGLFPWCGLLDTRTLEVOSSDY 946
Db 709 LGQEFQSSGAPVNTSKTY-----WAETTMDEDSIKFVGLKINPSTLLEILPDA 756
Qy 947 SSVARTSIRASLTFNRGFKAGRNRRKLFGLVRLKCHSLFLDLQVNSLQTVCTNIYKIL- 1005
Db 757 DS---NSFSLSLKYKSKFSKSVLYLQWCYKV-RLADH--FKLELVFKAALKNAIILN 810
Qy 1006 -LIQAY--RFHACVQLQ-LPFIHQVWKNPTFFLRVSDTASLCYSLKAKXNAGMSLGAKGA 1061
Db 811 AIIESYVYVHFKEILMRLLGFEDEQPFQF--FLLSLLHMTLRK-YQLVNPKNKAGM----- 860
Qy 1062 AGPLPSEAVQWLCHQAFLLKLTTRHV 1087
Db 861 -----EEISTMPFRKVIISKLSKNSV 880

RESULT 43
Q8MUQ8 PRELIMINARY; PRT; 896 AA.
AC Q8MUQ8;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Telomerase reverse transcriptase.
OS Paramesium tetraurelia.
OC Eukaryota; Alveolata; Ciliophora; Oligohymenophorea; Peniculida;
OC Paramesium.
OX NCBI_TaxID=5888;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=22220131; PubMed=12234682; DOI=10.1016/S0378-1119(02)00790-4;
RE Ye A.J., Romero D.P.;
RT "A unique pause pattern during telomere addition by the error-prone
RL telomerase from the ciliate Paramesium tetraurelia.";
RL Gene 294:205-213(2002).
DR EMBL; AF515460; AAN03860.1; -.
```

DR	GO: 0005634; C:nucleus; IEA.
DR	GO: 0003677; F:DNA binding; IEA.
DR	GO: 0003723; F:RNA binding; IEA.
DR	GO: 0003964; F:RNA-directed DNA polymerase activity; IEA.
DR	GO: 0003721; F:telomeric template RNA reverse transcriptase. . .; IEA.
DR	GO: 00016740; F:transferase activity; IEA.
DR	GO: 0006278; F:RNA-dependent DNA replication; IEA.
DR	InterPro; IPR000477; RVISE.
DR	InterPro; IPR003545; Telomerase_RT.
DR	Pfam; PF00078; RVT 1; 2.
DR	PRINTS; PR01365; TELOMERASERT.
KW	RNA-directed DNA polymerase; Transferase.
SEQUENCE	896 AA; 107237 MW; 697031P9DD61A883 CRC64;

Query Match		5.7%;	Score 342;	DB 2;	Length 896;
Best Local Similarity		22.0%;	Pred. No. 1.7e-12;		
Matches 157;		Conservative 133;	Mismatches 310;	Indels 114;	Gaps 27;

Qy	384	ORYWQMPLEFLLCNHAQCPYGVLLKTHCPRAAVTPAGVCAREPQGSVAPEEDT	443
Dd	224	QEKQRLTKQLTKNNKFNPOAFKIFVLPFTNYLNKKEVSQIKNLYIPIPLYD-	282
Qy	444	DPRELVLRLQHSHPWYGVFVRACTRLRVPGLWGSRHNERFLRNTKFKISLGKHL	503
Dd	283	-----EYKNFLSYDQVISILRYFLRTIIPIDPLG-OSNDLYTFKDLSPFTRFEDQ	335
Qy	504	SLOELTWKMSVDCAMLRSPGVGCVPAAEHRLREEILAKFLHWMVYVVELLRSPFY	563
Dd	336	NYLDYINRLNVFOIPWNSVFSKKKILLKXKQQLPIF-REFLQIIIPFLRHNFYI	394
Qy	564	TETTFQKRLFFYRKSVWSKLQSIGIRQHLKRVQLRELSEAEVQHRREARPALTSRLRF	623
Dd	395	TERMKDDWKLFYRKEIWTIVLKLNLQ-LSSNNLKQISPEKITQ-----YIGKLRI	446
Qy	624	IKPDGLRPIVNDYVVGATFEREEKAERLTSRVKALFVLNVERARRPGLLGASVLG-	682
Dd	447	VPKPTFRPIV-----TYNKRISKU-SLNKKLDOIKYVLRNLSQQGLGFSVGN	496
Qy	683	-----LDDIHRAWRTFVLVRADQPPPELYFVKVDVTGAYDITPDQRLTEVTSIIKPQ	736
Dd	497	PQIFNRLEEFKGLWKYQF-----PQYFMSMDIHKCYDSIQLEFLKFTESNLIQ	548
Qy	737	NTVCRRYAVV-----QKAAGHVRAFKSHVST-----LTDLPYMRQFVAHLQETSPLR	787
Dd	549	SAYVINKYLIIRNRSGRSKQMRLEFNIFDRTCAIPINNPAQALQGYEYIQN---K	605
Qy	788	DAVIEOSSSINEASSGLDFVL---RFMC-HHAVIRGKSYVQCQIPGSGISLTLLCS	843
Dd	606	LAII-----ANLGIQTTFSEFLSISBELCONNIVQFEDRYFTIQTGLPGIUNISGLCS	661
Qy	844	LCYGDMENKLFAGIRRDGLLRLLRVDDFLVTPHLTHAKTFLRTLVRGVPYGCVVNLRT	903
Dd	662	FYANIEKNLTKRLIGTILWRLTDDYCCHTFDKQNLITIKNNPKEVEKQVSIHLNDDKT	721
Qy	904	VVAFPVEDEALGGTAFVQMPAHGLFPWCGLL--LDTRTL-----EVQSDYSSYARTSIR	955
Dd	722	QHNI--DQKIVS-----FKWIGKIINLDKLTLPAPAQEKDQKFSNQINVNLP	767
Qy	956	ASLTFNRGFKAGNRMRKLFQVLRKLCCHSIFLDLVNSLOTVCTNYIKILLQAYRHAC	1015
Dd	768	SRIN-SYFFKA-----KLXS-LMLNQFKFFNPKINDQPTL-----IKIAKTF-IHAG	812
Qy	1016	VLQLPFHQVQWK-----NPTFFFLRVLS---DTASLCYSILKAKNAGMSL	1056
Dd	813	LIKLINFEWAKLFKVSKQSKNKIDFKLIKQVQIEIANYCFQ--QAQERSEL	864

RESULT 44	
ID QYR69	PRELIMINARY; PRT: 79 AA.
AC QYR69	
DT 01-OCT-2003 (TrEMBLrel. 25, Created)	
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)	

DT	01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE	Telomerase reverse transcriptase (TERT) (Fragment).
GN	Name=TERT;
OS	Felis silvestris catus (Cat).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
OX	NCBI_TaxID=9685;
RN	[1]
RP	SEQUENCE FROM N.A.
RA	MEDLINE=22692837; PubMed=12808208;
RA	Yazawa M., Okuda M., Uyama R., Nakagawa T., Kanaya N., Nishimura R.,
RA	Sasaki N., Masuda K., Ohno K., Tsujimoto H.;
RT	"Molecular cloning of the feline telomerase reverse transcriptase
RT	(TERT) gene and its expression in cell lines and normal tissues.";
RL	J. Vet. Med. Sci. 65:573-577(2003).
DR	EMBL; AB094676; BAC78444.1; -
DR	GO; GO:0003964; F:RNA-directed DNA polymerase activity; IEA.
KW	RNA-directed DNA polymerase.
FT	NON_TER 1
FT	NON_TER 79
FT	NON_TER 79
SEQ	SEQUENCE 79 AA; 9086 MW; BSADCD207226308B CRC64;
Query Match 5.7%; Score 339; DB 2; Length 79;	
Best Local Similarity 81.0%; Pred. No. 1.2e-13;	
Matches 64; Conservative 6; Mismatches 9; Indels 0; Gaps 0;	
QY	627 PDGLRPIVNNMDYVGARTFRREKRAELTSFVKALFSVLNYERARRPGLIGASVLGDDI 686
Dd	1 PSGLRPIVNNMDYVGARTFRFDKKVRHLTSQVKNLFGVLNYERARRPGLIGASVLGDDI 60
QY	687 HRAWRTFVLRVRAQDPPE 705
Dd	1 HRVRSFVLRVRAQDPAPQ 79
RESULT 45	
QY	Q76K45 PRELIMINARY; PRT; 79 AA.
ID	AQ C76K45;
DT	05-JUL-2004 (TrEMBLrel. 27, Created)
DT	05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT	05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE	Telomerase reverse transcriptase (TERT) (Fragment).
GN	Name=TERT;
OS	Canis familiaris (Dog).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX	NCBI_TaxID=9615;
RN	[1]
RP	SEQUENCE FROM N.A.
RA	MEDLINE=22976522; PubMed=14620776;
RA	Yazawa M., Okuda M., Kanaya N., Hong S.H., Takahashi T., Ohashi E.,
RA	Nakagawa T., Nishimura R., Sasaki N., Masuda K., Ohno K.,
RA	Tsuji moto H.;
RT	"Molecular cloning of the canine telomerase reverse transcriptase gene
RT	and its expression in neoplastic and non-neoplastic cells.";
RL	Am. J. Vet. Res. 64:1395-1400(2003).
DR	EMBL; AB094677; BAD06179.1; -
DR	GO; GO:0003964; F:RNA-directed DNA polymerase activity; IEA.
KW	RNA-directed DNA polymerase.
FT	NON_TER 1
FT	NON_TER 79
FT	NON_TER 79
SEQ	SEQUENCE 79 AA; 9119 MW; 3C180172A78D4DBF CRC64;
Query Match 5.7%; Score 338; DB 2; Length 79;	
Best Local Similarity 77.2%; Pred. No. 1.3e-13;	
Matches 61; Conservative 12; Mismatches 6; Indels 0; Gaps 0;	
QY	627 PDGLRPIVNNMDYVGARTFRREKRAELTSFVKALFSVLNYERARRPGLIGASVLGDDI 686
Dd	1 PSGLRPIVNNMDYIGARTFRHDKQAHLTSQLTKLFSVLNYERARRPGLIGASVLGDDI 60
QY	687 HRAWRTFVLRVRAQDPPE 705


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DR EMBL; CR380947; CAG57699.1; --
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR GO; GO:0003721; F:telomeric template RNA reverse transcripts. . .; IEA.
DR InterPro; IPR000477; RVase.
DR InterPro; IPR003545; Telomerase_RT.
DR Pfam; PF00078; RV1_1; 1.
DR PRINTS; PR01365; TELOMERASERT.
DR RNA-directed DNA polymerase; Transferase.
DR GO; GO:0003964; F:RNA-directed DNA polymerase activity; IEA.
SQ SEQUENCE 851 AA; 98673 MW; CCB0F339CEB446BD CRC64;

Query Match
Best Local Similarity 5.2%; Score 309; DB 2; Length 851;
Matches 136; Conservative 117; Mismatches 235; Indels 156; Gaps 25;

QY 464 FVRACLRRLVPPGLMGRSRRNRRFLRNTKFKTSLGKHAKLSLOELTWKMSVDCAWLRSS 523
D 464 FVRACLRRLVPPGLMGRSRRNRRFLRNTKFKTSLGKHAKLSLOELTWKMSVDCAWLRSS 523
D 266 FIVILEKLIQLIGSRKNSFVLSKISQLKPLNGKINKEPFTKLNVNA---VRRY 322
QY 524 PGVGVCPAAHRLREILAKFLHMLSVVYVVELLSFFVYTTTFQKRLFFYRKSVMSK 583
D 524 PGVGVCPAAHRLREILAKFLHMLSVVYVVELLSFFVYTTTFQKRLFFYRKSVMSK 583
D 323 LSIIDPIGQKQSMR-LYLTCCVNYLLSKLIPSLKSFYCYTEVS-SYSKILYFRNDEMNS 380
QY 584 LOSIGIRQHLKRVQLRELSEAEVQHRARPALLTSR-----LRIPKPDGLRPVNDY 638
D 584 LOSIGIRQHLKRVQLRELSEAEVQHRARPALLTSR-----LRIPKPDGLRPVNDY 638
D 381 ISTPFLKEYLDKYLQ-----NTHCNSHFYSMESQFNHCNFRLLPKK----- 422
QY 639 VVGARTF-----REKRAERL-----TSRVKALFSLNYERARRPGL--LGASVLGL 683
D 639 VVGARTF-----REKRAERL-----TSRVKALFSLNYERARRPGL--LGASVLGL 683
D 423 --GNNEFRVIGIPYKGNNAEELQYKQNTKIVTPKLLDYLKRSQTTQKLLFSAMQI 480
QY 684 DP-----IHRWRTFVLVRAQDPPPELVFVVDVTGAYDTIPQDLTEVIAI1K- 734
D 684 DP-----IHRWRTFVLVRAQDPPPELVFVVDVTGAYDTIPQDLTEVIAI1K- 734
D 481 SDHICQYKCHLSKGYI-----PKLFYKFDIHCYDSIPIAKAKSVLNSLNN 530
QY 735 -PQNYCYVRVAV-----QXAAHGHRKAFKSHVSTLTDLPYMRQFVAHLQETS 784
D 735 -PQNYCYVRVAV-----QXAAHGHRKAFKSHVSTLTDLPYMRQFVAHLQETS 784
D 531 CGYEEFYVRVSTILNTKQNEVRYDTIVNGHIN----- 562
QY 785 PLRD-AVVEIQSSLEASSGLFDVFLRMCHAVIRKGSVVOCGIPOGSILTLCS 843
D 785 PLRD-AVVEIQSSLEASSGLFDVFLRMCHAVIRKGSVVOCGIPOGSILTLCS 843
D 563 -IRDFEIMVNDSTTTFLTKEDIMDLIEFEMEMTSIRLPDKYLRKXGLFQGLSATIVD 621
QY 844 LCYGDG--ENKLFAGI-RDGLLLRLVDLFLVTPH---LTHAKTFLRLVRGVEYGCV 897
D 844 LCYGDG--ENKLFAGI-RDGLLLRLVDLFLVTPH---LTHAKTFLRLVRGVEYGCV 897
D 622 ILYDMLKRNRFKDIILNDGLVLRHADDLLISPSKEIISVARLKN---EGFTEYNAQ 678
QY 898 VNLRTVNVFVEDEALGCTAFVQMPAHGLPWCGLLLDTRTLEVOSDYSSVARTSI--- 954
D 898 VNLRTVNVFVEDEALGCTAFVQMPAHGLPWCGLLLDTRTLEVOSDYSSVARTSI--- 954
D 679 VNRKIVFS---ESDNIAITA-----IPFCGVEIIPRTLEVIKRFPSAMNETDISH 726
QY 955 -----RASLTNRGFKAG-----RNRKRLFGVLRKCHSLFLDLQVNSLQ 995
D 955 -----RASLTNRGFKAG-----RNRKRLFGVLRKCHSLFLDLQVNSLQ 995
D 727 EGNIVSKAVLPKRLNLTGMNANLNSITMLKQVENATINVIILNSHIATSVSFS 786
QY 996 TVCTNIYKILLIQAQRFHACVQLQLPFPHQVKNKPTFFLRVSDT 1039
D 996 TVCTNIYKILLIQAQRFHACVQLQLPFPHQVKNKPTFFLRVSDT 1039
D 787 SPVNELYNICLLSRN-----LNLNHRDLQR----FLTSIKKT 821

RESULT 48
Q57EQ2
ID Q67BQ2 PRELIMINARY; PRT; 261 AA.
AC Q67BQ2;
DT 25-OCT-2004 (TREMBLrel. 28, Created)
DT 25-OCT-2004 (TREMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TREMBLrel. 28, Last annotation update)
DE Telomerase reverse transcriptase catalytic subunit (Fragment).
GN Name=TERT;
OS Hordeum vulgare (Barley).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae;
OC Triticeae; Hordeum.
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OX NCBI_TaxID=4513;
RN [1] SEQUENCE FROM N.A.
RP TISSUE=Root tips;
RC Sykorova E.;
RA "Comparison of protein subunits of plant telomerases.";
RT Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
RL EMBL; AY363163; AAR11376.1; -
DR GO; GO:0003964; F:RNA-directed DNA polymerase activity; IEA.
KW RNA-directed DNA polymerase.
FT NON_TER 1 261
FT NON_TER 261 261
SQ SEQUENCE 261 AA; 30247 MW; 70DC6AC97D2D0BFD CRC64;

Query Match
Best Local Similarity 4.2%; Score 250.5; DB 2; Length 261;
Matches 69; Conservative 52; Mismatches 126; Indels 29; Gaps 4;

QY 455 HSSPQVYGVFVACLRRLVPPGLMGRSRRNRRFLRNTKFKTSLGKHAKLSLOELTWKMSV 514
D 455 HSSPQVYGVFVACLRRLVPPGLMGRSRRNRRFLRNTKFKTSLGKHAKLSLOELTWKMSV 514
D 3 YSTHDQVSVFVAVLTRIIPQPLGNPSSKRALRMNIWKFIILRRPFTQVTDICELKA 62
QY 515 RDCAWLRSPGVGCVPAA-----EHLREEILAKFLHMLSVVYVVELLSRPFY 562
D 515 RDCAWLRSPGVGCVPAA-----EHLREEILAKFLHMLSVVYVVELLSRPFY 562
D 63 PEYSWLSKIGFTGCFCSVLLREETGLSNGMEEQKQNLHWCWISWLFSDIPLINTLYL 122
QY 563 VTETTFQKRLFFYRKSVMSKLSQSIGIRQHLKRVQLRELSEAEVQHRARPALLTSRLR 622
D 563 VTETTFQKRLFFYRKSVMSKLSQSIGIRQHLKRVQLRELSEAEVQHRARPALLTSRLR 622
D 123 VTERETKRYDYFYPKSVNRNLTSNTVAS-LNAQSFKLCGT---SRAIKHLYESSVR 178
QY 623 FIPKPDGLRPVNDYVVGARTFVRKRAERLTSRVKALFSLNYERARRPGLLGASVLG 682
D 623 FIPKPDGLRPVNDYVVGARTFVRKRAERLTSRVKALFSLNYERARRPGLLGASVLG 682
D 179 FLPAKDIRPLVNF-----KAQSKDGLTNKCHLVIKKLDDNPMFSGSSAPD 225
QY 683 LDDIHRWRTFVLVRAQDPPPELVFVVDVTGAYD 718
D 683 LDDIHRWRTFVLVRAQDPPPELVFVVDVTGAYD 718
D 226 YDGVTKNLSFMSVSRGQLKESKIYVIVADVSKAPD 261

RESULT 49
Q9ROB3
ID Q9ROB3 PRELIMINARY; PRT; 52 AA.
AC Q9ROB3;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update)
DE Telomerase catalytic subunit (fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1] SEQUENCE FROM N.A.
RP Drissi R., Cleveland J.L.;
RL Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF090439; AAD54013.1; -
FT NON_TER 1 52
FT NON_TER 52 52
SQ SEQUENCE 52 AA; 6479 MW; 41473425E44BDA9C CRC64;

Query Match
Best Local Similarity 3.4%; Score 200; DB 2; Length 52;
Matches 37; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

QY 567 TFQKRLFFYRKSVMSKLSQSIGIRQHLKRVQLRELSEAEVQHRHRE 611
D 567 TFQKRLFFYRKSVMSKLSQSIGIRQHLKRVQLRELSEAEVQHRHRE 611
D 1 TFQKRLFFYRKSVMSKLSQSIGIRQHLKRVQLRELSEAEVQHRHRE 45

RESULT 50
Q6W8T6
ID Q6W8T6 PRELIMINARY; PRT; 260 AA.
AC Q6W8T6;
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DT 05-JUL-2004 (TrenBLrel. 27, Created)
DT 05-JUL-2004 (TrenBLrel. 27, Last sequence update)
DE 05-JUL-2004 (TrenBLrel. 27, Last annotation update)
DE Telomerase reverse transcriptase (Fragment).
GN Name=TERT;
OS Euplotes raikovi.
OC Eukaryota; Alveolata; Ciliophora; Spirotrichea; Hypotrichia;
OC Euplotida; Euplotidae; Euplotes.
OX NCBI_TaxID=5938;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=13;
RA Mollenbeck M., Gavin M.C., Klobutcher L.A.;
RT "Evolution of Programmed Ribosomal Frameshifting in the TERT Genes of
RT Euplotes.";
RL J. Mol. Evol. 58:701-711(2004).
DR EMBL; AY303932; AAQ97306.1; -.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR GO; GO:0003964; F:RNA-directed DNA polymerase activity; IEA.
DR GO; GO:0003721; F:telomeric template RNA reverse transcriptase. .; IEA.
DR InterPro; IPR000477; RVTse.
DR InterPro; IPR003545; Telomerase_RT.
DR Pfam; PF00078; RVT.1.
DR PRINTS; PR01365; TELOMERASERT.
KW RNA-directed DNA polymerase; Transferase.
FT NON TER 1
FT NON TER 260
SQ SEQUENCE 260 AA; 30779 MW; CFDDF0421FB12PB CRC64;

Query Match 3.3%; Score 195; DB 2; Length 260;
Best Local Similarity 22.6%; Pred. No. 0.00039;
Matches 62; Conservative 49; Mismatches 105; Indels 58; Gaps 7;

Qy 705 ELYFKVDVTGAYDTIPQDRL-----TEVIAS---IIKPO-----NTYCVRR 743
Db 2 KLYFTMDIEKCYDSVDREKLASFYKTTQLLSPDFFINKPKILKXNNKVIDSNNHRRKK 61

Qy 744 YAVVQKAAHGHRKAFKSHVSTLTLDLPYMRQFVAHLQETSPLRDVAVVIEQSSSINEASS 803
Db 62 MSYFVKTKWRDIALEGGQYPSLLTVLEQEQNEINA-----KKTIVESKRDNYKCD 113

Qy 804 GLFDVFLRFPMCHAVRIRKSVQCGIPQGSILSTLLCSLCYGD MENKLFAGIRRD---- 860
Db 114 TLLKPEVIDICKHNYIQFNRFYKQKGIPOGLCVSSILSPFYASLEESALGYLRDESM 173

Qy 861 -----GLLLRLVDDFLVTLPHLTHAKTFLRTLVRGVPYGCVNLKRTVVNFPVDEAL 914
Db 174 KSDPNINLLMLTDDYLLVTTKEDNAVTFIERCINISRENNFKFMKKLQTNFFLDP--- 230

Qy 915 GGTAFOVQMPAHGL-----FPCGGLLD 936
Db 231 -----TRPKYGLSIRQNIVEDYCDWIGITID 259
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Search completed: August 5, 2005, 14:11:06
Job time : 205 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 5, 2005, 14:11:13 ; Search time 173 Seconds
(without alignments)
2554.511 Million cell updates/sec

Title: US-10-053-758-225
Perfect score: 5961
Sequence: 1 MPAPRCRAVRLSLRSHYRE.....TALZAAANPALPDSFKTILD 1132

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1752860 seqs, 390397842 residues

Total number of hits satisfying chosen parameters: 1752860

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:

- 1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	5961	100.0	1132	9 US-09-990-080-2	Sequence 2, Appli
2	5961	100.0	1132	9 US-09-749-728B-31	Sequence 31, Appl
3	5961	100.0	1132	9 US-09-843-676-225	Sequence 225, App
4	5961	100.0	1132	9 US-09-953-052-2	Sequence 2, Appli
5	5961	100.0	1132	11 US-09-788-110A-23	Sequence 23, Appl
6	5961	100.0	1132	14 US-10-053-758-225	Sequence 225, App
7	5961	100.0	1132	14 US-10-208-243-2	Sequence 2, Appli
8	5961	100.0	1132	14 US-10-054-295-225	Sequence 225, App
9	5961	100.0	1132	14 US-10-054-611-225	Sequence 225, App
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11	5961	100.0	1132	14 US-10-044-692-2	Sequence 2, Appli

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13	5961	100.0	1132	14	US-10-295-681-57	Sequence 57, Appl
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28	5961	100.0	1132	17	US-10-490-143A-19	Sequence 19, Appl
29	5961	100.0	1132	17	US-10-794-514A-3	Sequence 3, Appli
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35	5961	100.0	1154	16	US-10-877-022-611	Sequence 611, App
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39	5961	100.0	1189	15	US-10-325-810-613	Sequence 613, App
40	5961	100.0	1189	16	US-10-877-124-613	Sequence 613, App
41	5961	100.0	1189	16	US-10-877-022-613	Sequence 613, App
42	5961	100.0	1189	17	US-10-877-146-613	Sequence 613, App
43	5961	100.0	1200	14	US-10-044-692-324	Sequence 324, App
44	5961	100.0	1200	14	US-10-044-539-324	Sequence 324, App
45	5961	100.0	1200	15	US-10-325-810-612	Sequence 612, App

ALIGNMENTS

RESULT 1
US-09-990-080-2
; Sequence 2, Application US/09990080
; Patent No. US20020102686A1
; GENERAL INFORMATION:
; APPLICANT: Morin, Gregg B.
; APPLICANT: Genon Corporation
; TITLE OF INVENTION: Human Telomerase Catalytic Subunit Variants
; FILE REFERENCE: 018/258C
; CURRENT APPLICATION NUMBER: US/09/990,080
; CURRENT FILING DATE: 1998-08-03
; PRIOR APPLICATION NUMBER: US 09/052,864
; PRIOR FILING DATE: 1998-03-31
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: Patent in Ver. 2.0
; SEQ ID NO 2
; LENGTH: 1132
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-990-080-2

Query Match 100.0%; Score 5961; DB 9; Length 1132;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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RESULT 2

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US-09-749-728B-31
; Sequence 31, Application US/09749728B
; Patent No. US20020142457A1
; GENERAL INFORMATION:
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; APPLICANT: Umezawa, Akihiro
; APPLICANT: Hata, Jun-ichi
; APPLICANT: Fukuda, Keiichi
; APPLICANT: Ogawa, Satoshi
; APPLICANT: Sakurada, Kazuhiro
; APPLICANT: Gojo, Satoshi
; APPLICANT: Yamada, Yoji
; TITLE OF INVENTION: THE CELL HAVING THE POTENTIALITY OF DIFFERENTIATION INTO CARDIOMY
; FILE REFERENCE: 00766.000043
; CURRENT APPLICATION NUMBER: US/09/749,728B
; CURRENT FILING DATE: 2001-09-17
; PRIOR APPLICATION NUMBER: H11-372826
; PRIOR FILING DATE: 1999-12-28
; PRIOR APPLICATION NUMBER: PCT-JP00-01148
; PRIOR FILING DATE: 2000-02-28
; PRIOR APPLICATION NUMBER: PCT-JP00-07741
; PRIOR FILING DATE: 2000-11-02
; NUMBER OF SEQ ID NOS: 80
; SOFTWARE: PatentIn Ver.2.0
; SEQ ID NO 31
; LENGTH: 1132
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-749-728B-31
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Query Match 100.0%; Score 5961; DB 9; Length 1132;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 3

US-09-843-676-225

Sequence 225, Application US/09843676

Patent No. US20020164786A1

GENERAL INFORMATION:

APPLICANT: Cech, Thomas R.

Lingner, Joachim

Nakamura, Toru

Chapman, Karen B.

Morin, Gregg B.

Harley, Calvin

Andrews, William H.

TITLE OF INVENTION: No. US20020164786A1el Telomerase

NUMBER OF SEQUENCES: 225

CORRESPONDENCE ADDRESS:

ADDRESSEE: Townsend and Townsend and Crew LLP

STREET: Two Embarcadero Center, 8th Floor

CITY: San Francisco

STATE: California

COUNTRY: United States of America

ZIP: 94111

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/843,676

FILING DATE: 26-Apr-2001

CLASSIFICATION: 536

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/854,050

FILING DATE: 09-MAY-1997

APPLICATION NUMBER: US 08/846,017

FILING DATE: 25-APR-1997

APPLICATION NUMBER: US 08/844,419

FILING DATE: 18-APR-1997

APPLICATION NUMBER: US 08/724,643

FILING DATE: 01-OCT-1996

ATTORNEY/AGENT INFORMATION:

NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002930US
TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 576-0200

TELEFAX: (415) 576-0300

INFORMATION FOR SEQ ID NO: 225:

SEQUENCE CHARACTERISTICS:

LENGTH: 1132 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 225:

US-09-843-676-225

Query Match

Best Local Similarity 100.0%; Score 5961; DB 9; Length 1132;

Matches 1132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 901 RKTWNFFVEDEALGGTAFVQMPAHGLFPWCGLLLDTRTLEVSQSDYSSYARTSIRASLTFF 960
Qy 961 NRGFKAGNMRKLFVGLRLKCHSLFDLQVNSLQTVCTNIIKYILLQAYRPHACVLQLP 1020
Db 961 NRGFKAGNMRKLFVGLRLKCHSLFDLQVNSLQTVCTNIIKYILLQAYRPHACVLQLP 1020
Qy 1021 FHQQVWKNPTFFLRVISDTASLCYSILKAKNAGMSLGAKGAAGPLPSEAVQWLCHQAFLL 1080
Db 1021 FHQQVWKNPTFFLRVISDTASLCYSILKAKNAGMSLGAKGAAGPLPSEAVQWLCHQAFLL 1080
Qy 1081 KLTRHRVTYVPLGSLRTAQQLSRKLPCTTLTALEAAANPALPSDFKTILD 1132
Db 1081 KLTRHRVTYVPLGSLRTAQQLSRKLPCTTLTALEAAANPALPSDFKTILD 1132

RESULT 4

US-09-953-052-2
; Sequence 2, Application US/09953052
; Patent No. US20020173476A1
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; Lingner, Joachim
; Nakamura, Toru
; Chapman, Karen B.
; Morin, Gregg B.
; Harley, Calvin B.
; Andrews, William H.
; TITLE OF INVENTION: Antisense Compositions for Detecting and
; Inhibiting Telomerase Reverse Transcriptase
; NUMBER OF SEQUENCES: 72
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/953,052
; FILING DATE: 14-Sep-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/052,919
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; APPLICATION NUMBER: US 08/851,843
; FILING DATE: 06-MAY-1997
; APPLICATION NUMBER: US 08/854,050
; FILING DATE: 09-MAY-1997
; APPLICATION NUMBER: US 08/911,312
; FILING DATE: 14-AUG-1997
; APPLICATION NUMBER: US 08/912,951
; FILING DATE: 14-AUG-1997
; APPLICATION NUMBER: US 08/915,503
; FILING DATE: 14-AUG-1997
; APPLICATION NUMBER: US 08/974,549
; FILING DATE: 19-NOV-1997

; APPLICATION NUMBER: US 08/974,584
; FILING DATE: 19-NOV-1997
; APPLICATION NUMBER: WO PCT/US97/17618
; FILING DATE: 01-OCT-1997
; APPLICATION NUMBER: WO PCT/US97/17885
; FILING DATE: 01-OCT-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Parent, Annette S.
; REGISTRATION NUMBER: 42,058
; REFERENCE/DOCKET NUMBER: 015389-00360005
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1132 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-953-052-2

Query Match 100.0%; Score 5961; DB 9; Length 1132;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MPRAPRCRAVRSLLRSHYREVLPPLATEFVRLGPGQWMLVQRGDPAAPRALVAQCLVCVPW 60
Db 1 MPRAPRCRAVRSLLRSHYREVLPPLATEFVRLGPGQWMLVQRGDPAAPRALVAQCLVCVPW 60

Qy 61 DARPPPAAPSFQVSCCLKELVARVLQRLCERGAKNVLAFGFALLDGGAGGPEAFTTSVR 120
Db 61 DARPPPAAPSFQVSCCLKELVARVLQRLCERGAKNVLAFGFALLDGGAGGPEAFTTSVR 120

Qy 121 SYLPNTVTDALRGSGAWGLLLRRVGGDVLVHLLARCALFVLVAPSCAYQVCGPPLYOLGA 180
Db 121 SYLPNTVTDALRGSGAWGLLLRRVGGDVLVHLLARCALFVLVAPSCAYQVCGPPLYOLGA 180

Qy 181 ATQARPPPHASGPRRRRLGCERAMNHSVREAGVPLGLPAPGARRRRGGASRSLSLPKRP 240
Db 181 ATQARPPPHASGPRRRRLGCERAMNHSVREAGVPLGLPAPGARRRRGGASRSLSLPKRP 240

Qy 241 GAAPEPERTVPGQSWAHPCGTRGSDRGFCVSPARPAEATSEALSTRHSHPSVG 300
Db 241 GAAPEPERTVPGQSWAHPCGTRGSDRGFCVSPARPAEATSEALSTRHSHPSVG 300

Qy 301 ROHHAGPSTSRPPRPWDTPCPPVYATKHFLYSSGDKQLRPSFLLSSLRPSLTGARRL 360
Db 301 ROHHAGPSTSRPPRPWDTPCPPVYATKHFLYSSGDKQLRPSFLLSSLRPSLTGARRL 360

Qy 361 VETIFLGSRPWMPGTTPRRLPRLPQRYWQMRPLFLELLGNHAQCYPYVLLKTHCPLRAAVT 420
Db 361 VETIFLGSRPWMPGTTPRRLPRLPQRYWQMRPLFLELLGNHAQCYPYVLLKTHCPLRAAVT 420

Qy 421 PAAGVCAREKPGQSVAAPEEEDTPRLVOLLROHSSFPWQYGVFRACLRLRLVPPGLWGS 480
Db 421 PAAGVCAREKPGQSVAAPEEEDTPRLVOLLROHSSFPWQYGVFRACLRLRLVPPGLWGS 480

Qy 481 RHNERRFLRNTKFPISLGKHAQLSLOELTWKMSVRDCAWLRRSPGVGCVPAAEHRLREI 540
Db 481 RHNERRFLRNTKFPISLGKHAQLSLOELTWKMSVRDCAWLRRSPGVGCVPAAEHRLREI 540

Qy 541 LAKFLHLMMSVYVVELLSRFFYVTTTTFQKNRLFFYRKSVMKLSQSIGIRQHLKRVQURE 600
Db 541 LAKFLHLMMSVYVVELLSRFFYVTTTTFQKNRLFFYRKSVMKLSQSIGIRQHLKRVQURE 600

Qy 601 LSEAEVQHREARPAALLTSRLRFPKPDGLRPIVNDYVVGARTFRREKRAERLTSRKA 660
Db 601 LSEAEVQHREARPAALLTSRLRFPKPDGLRPIVNDYVVGARTFRREKRAERLTSRKA 660

Qy 661 LFSVLNYERARRPGLLGASVLGLDDIHRWRTFVLVRQAQDPPPELYFVKVDVTGAYDTI 720
Db 661 LFSVLNYERARRPGLLGASVLGLDDIHRWRTFVLVRQAQDPPPELYFVKVDVTGAYDTI 720


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QY 721 PODRLTEVIASIIKPNQTYCVRRYAVVQKAAHGHVRKAFKSHVSTLTDLPYMRQFVAHL 780
DB 721 PODRLTEVIASIIKPNQTYCVRRYAVVQKAAHGHVRKAFKSHVSTLTDLPYMRQFVAHL 780
QY 781 QETSPLRDAVTEQSSSINEASSGLFDVFLRPMCHHVRIRGKSVVQCGIPIQGSILSTL 840
DB 781 QETSPLRDAVTEQSSSINEASSGLFDVFLRPMCHHVRIRGKSVVQCGIPIQGSILSTL 840
QY 841 LCSLCYGMENKLFAGIRRDGLLLRVDVDFLLVTPHLLTHAKTFLTLVRGPEYGCNVNL 900
DB 841 LCSLCYGMENKLFAGIRRDGLLLRVDVDFLLVTPHLLTHAKTFLTLVRGPEYGCNVNL 900
QY 901 RKTVVNPFVEDEALGGTAFVQMPAHGLFPWCGLLDDTRTLEVSQSYSSYARTSIRASLTF 960
DB 901 RKTVVNPFVEDEALGGTAFVQMPAHGLFPWCGLLDDTRTLEVSQSYSSYARTSIRASLTF 960
QY 961 NRGFKAGNMRKLFGLVRLKCHSLFDLDQVNSLQTVCTNIYKILLQAYRPHACVLOLP 1020
DB 961 NRGFKAGNMRKLFGLVRLKCHSLFDLDQVNSLQTVCTNIYKILLQAYRPHACVLOLP 1020
QY 1021 FHOQWKNTPTFLRVIISDTASLCYILKAKNAGMSLGAKGAGPLPSEAVQWLCHQAFLL 1080
DB 1021 FHOQWKNTPTFLRVIISDTASLCYILKAKNAGMSLGAKGAGPLPSEAVQWLCHQAFLL 1080
QY 1081 KLTHRVTVVPLGLSLRTAQTSLSRKLPGTTLTALAAAAANPALPSDFKTILD 1132
DB 1081 KLTHRVTVVPLGLSLRTAQTSLSRKLPGTTLTALAAAAANPALPSDFKTILD 1132

RESULT 5
US-09-788-110A-23
; Sequence 23, Application US/09788110A
; Publication No. US20040086518A1
; GENERAL INFORMATION:
; APPLICANT: Zanetti, Maurizio
; TITLE OF INVENTION: A Universal Vaccine and Method for Treating Cancer Employing
; FILE REFERENCE: UCSD-07017
; CURRENT APPLICATION NUMBER: US/09/788,110A
; CURRENT FILING DATE: 2001-02-15
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 23
; LENGTH: 1132
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-788-110A-23

Query Match 100.0%; Score 5961; DB 11; Length 1132;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 MPRAPRCRAVRSLSRSHYREVLPATFVRRLGPOGWRLVQRGDPAAFRALVAQCLVCPW 60
QY 61 DARPPPAAPSFRQVSKLKVRLQRLCERCAKVLAFGFALLDAGRGPEAFTTSVR 120
DB 61 DARPPPAAPSFRQVSKLKVRLQRLCERCAKVLAFGFALLDAGRGPEAFTTSVR 120
QY 121 SYLPNTVTDALRGSGAWGLLRVGDVLLVLLARCALFVLVAPSCVQCGPPYQLGA 180
DB 121 SYLPNTVTDALRGSGAWGLLRVGDVLLVLLARCALFVLVAPSCVQCGPPYQLGA 180
QY 181 ATQARPPPHASGPRRLGGERAWNHSVREAGVPLGLPAGPARRRGSGASRSLPLKPRR 240
DB 181 ATQARPPPHASGPRRLGGERAWNHSVREAGVPLGLPAGPARRRGSGASRSLPLKPRR 240
QY 241 GAAPPERTPVQCGSWAHPGRTGSDRGFCVVSAPABEATSLEGALSGTRHSHPSVG 300
DB 241 GAAPPERTPVQCGSWAHPGRTGSDRGFCVVSAPABEATSLEGALSGTRHSHPSVG 300
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QY 301 RQHIAGPSTSRPRPMDTPCPVYAEATKHFLYSSGDKQELRPSFLLSSLRPSLTGARRL 360
DB 301 RQHIAGPSTSRPRPMDTPCPVYAEATKHFLYSSGDKQELRPSFLLSSLRPSLTGARRL 360
QY 361 VETIFLGSRRPMPGTPRRLPRLPORYWQMRPLFLELLGNHQAQCPYGVLLKTHCPLRAAVT 420
DB 361 VETIFLGSRRPMPGTPRRLPRLPORYWQMRPLFLELLGNHQAQCPYGVLLKTHCPLRAAVT 420
QY 421 PAAGYCAREKPGQGSVAAPPEEDTDPRLVLQRLRHSSPWQVYGVFVRACLRRLRVPGLMGS 480
DB 421 PAAGYCAREKPGQGSVAAPPEEDTDPRLVLQRLRHSSPWQVYGVFVRACLRRLRVPGLMGS 480
QY 481 RHNERRFLNRTKFTISLGKHAQLSLOELTWKMSVRDCAWLRRSPGVGCPVAAEHLRBEI 540
DB 481 RHNERRFLNRTKFTISLGKHAQLSLOELTWKMSVRDCAWLRRSPGVGCPVAAEHLRBEI 540
QY 541 LAKFLHLMWSVYVVELLRSFFVTETTFQKNRLFFYKSVMSKLSQSIGIROHLKRVQJRE 600
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QY 601 LSEAEVROHREARPAALLTSRLRFIPKPDGLRPIVNMVYVVGARTFRREKRAERLTSRVKA 660
DB 601 LSEAEVROHREARPAALLTSRLRFIPKPDGLRPIVNMVYVVGARTFRREKRAERLTSRVKA 660
QY 661 LFSVLNTERARRPGLLGASVLGLDDIHRAMTFVLRVRAQDPPPELYFVKVDVTGAYDTI 720
DB 661 LFSVLNTERARRPGLLGASVLGLDDIHRAMTFVLRVRAQDPPPELYFVKVDVTGAYDTI 720
QY 721 PODRLTEVIASIIKPNQTYCVRRYAVVQKAAHGHVRKAFKSHVSTLTDLPYMRQFVAHL 780
DB 721 PODRLTEVIASIIKPNQTYCVRRYAVVQKAAHGHVRKAFKSHVSTLTDLPYMRQFVAHL 780
QY 781 QETSPLRDAVTEQSSSINEASSGLFDVFLRPMCHHVRIRGKSVVQCGIPIQGSILSTL 840
DB 781 QETSPLRDAVTEQSSSINEASSGLFDVFLRPMCHHVRIRGKSVVQCGIPIQGSILSTL 840
QY 841 LCSLCYGMENKLFAGIRRDGLLLRVDVDFLLVTPHLLTHAKTFLTLVRGPEYGCNVNL 900
DB 841 LCSLCYGMENKLFAGIRRDGLLLRVDVDFLLVTPHLLTHAKTFLTLVRGPEYGCNVNL 900
QY 901 RKTVVNPFVEDEALGGTAFVQMPAHGLFPWCGLLDDTRTLEVSQSYSSYARTSIRASLTF 960
DB 901 RKTVVNPFVEDEALGGTAFVQMPAHGLFPWCGLLDDTRTLEVSQSYSSYARTSIRASLTF 960
QY 961 NRGFKAGNMRKLFGLVRLKCHSLFDLDQVNSLQTVCTNIYKILLQAYRPHACVLOLP 1020
DB 961 NRGFKAGNMRKLFGLVRLKCHSLFDLDQVNSLQTVCTNIYKILLQAYRPHACVLOLP 1020
QY 1021 FHOQWKNTPTFLRVIISDTASLCYILKAKNAGMSLGAKGAGPLPSEAVQWLCHQAFLL 1080
DB 1021 FHOQWKNTPTFLRVIISDTASLCYILKAKNAGMSLGAKGAGPLPSEAVQWLCHQAFLL 1080
QY 1081 KLTHRVTVVPLGLSLRTAQTSLSRKLPGTTLTALAAAAANPALPSDFKTILD 1132
DB 1081 KLTHRVTVVPLGLSLRTAQTSLSRKLPGTTLTALAAAAANPALPSDFKTILD 1132

RESULT 6
US-10-053-758-225
; Sequence 225, Application US/10053758
; Publication No. US20030032075A1
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; Lingner, Joachim
; Nakamura, Toru
; Chapman, Karen B.
; Morin, Gregg B.
; Harley, Calvin
; Andrews, William H.
; TITLE OF INVENTION: No. US20030032075A1el Telomerase
; NUMBER OF SEQUENCES: 225
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
```

STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: United States of America
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/053,758
FILING DATE: 18-Jan-2002
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/854,050
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002930US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 225:
SEQUENCE CHARACTERISTICS:
LENGTH: 1132 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 225:
US-10-053-758-225

Query Match 100.0%; Score 5961; DB 14; Length 1132;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MPAPRCRAVRSLLRSHYREVLPATFVRRLLGPGQWRVLRQDPAAFRALVAQCLVCPW 60
DB 1 MPAPRCRAVRSLLRSHYREVLPATFVRRLLGPGQWRVLRQDPAAFRALVAQCLVCPW 60
QY 61 DARPPAAPSPROVSCLELVARVLQRLCERGAKNVLAFGFALLDGGAGGPPPEAFTTSVR 120
DB 61 DARPPAAPSPROVSCLELVARVLQRLCERGAKNVLAFGFALLDGGAGGPPPEAFTTSVR 120
QY 121 SYLPTNTVDALRGSGAWGLLRVGGDVLVHLARFALFVLVAPSCAYQVCGPPLYQIGA 180
DB 121 SYLPTNTVDALRGSGAWGLLRVGGDVLVHLARFALFVLVAPSCAYQVCGPPLYQIGA 180
QY 181 ATQARPPPHAGPRRRRLCERAWNHSVREAGVPLGAPGARRRGGSASRLPLPKRRR 240
DB 181 ATQARPPPHAGPRRRRLCERAWNHSVREAGVPLGAPGARRRGGSASRLPLPKRRR 240
QY 241 GAAPPEPTPVQGSWAHPGTRGSDRGFCVVSAPAEATSLGALSGTRHSPSVG 300
DB 241 GAAPPEPTPVQGSWAHPGTRGSDRGFCVVSAPAEATSLGALSGTRHSPSVG 300
QY 301 RQHHAGPSTSRPPRPMTTPCPVVAETKHFYSSGDKQLRPSPLSSRLPSLTGARRL 360
DB 301 RQHHAGPSTSRPPRPMTTPCPVVAETKHFYSSGDKQLRPSPLSSRLPSLTGARRL 360
QY 361 VETIFLGRPNWPGTPRRLPRLPQRYWQMRPLFLELLGNHACQPYGVLLKTHCPLRAAVT 420
DB 361 VETIFLGRPNWPGTPRRLPRLPQRYWQMRPLFLELLGNHACQPYGVLLKTHCPLRAAVT 420

QY 421 PAAGVCAREKPGQSVAAPEEEDTPRLVQLLRHSSPQVYGFVACLRRLVPPGLWGS 480
DB 421 PAAGVCAREKPGQSVAAPEEEDTPRLVQLLRHSSPQVYGFVACLRRLVPPGLWGS 480
QY 481 RHNERFRNTKTFISLGKIAKLSQBLTWKMSVRDCAWLRRSPGVGCVPAAEHRLREI 540
DB 481 RHNERFRNTKTFISLGKIAKLSQBLTWKMSVRDCAWLRRSPGVGCVPAAEHRLREI 540
QY 541 LAKFLHLMMSVYVVELLRSFFYVTTFTFQKNRLFYRKSVMKLSQSIGIRHKLKVQURE 600
DB 541 LAKFLHLMMSVYVVELLRSFFYVTTFTFQKNRLFYRKSVMKLSQSIGIRHKLKVQURE 600
QY 601 LSEAEVQHREARPAALLTSRLRFPKPDGLRPIVNDYVVGARTFRREKRAERLTSRKA 660
DB 601 LSEAEVQHREARPAALLTSRLRFPKPDGLRPIVNDYVVGARTFRREKRAERLTSRKA 660
QY 661 LFSVLYNERARRPGLLGASVLGLDDIHRWRTFVLVRADQPPPELVFKVDVVTGAYDTI 720
DB 661 LFSVLYNERARRPGLLGASVLGLDDIHRWRTFVLVRADQPPPELVFKVDVVTGAYDTI 720
QY 721 PQDLTEVIASIIKPONTYCVRRYAVVQKAAHGHVRKAFKSHVSTLTDLQPYMRQFVAHL 780
DB 721 PQDLTEVIASIIKPONTYCVRRYAVVQKAAHGHVRKAFKSHVSTLTDLQPYMRQFVAHL 780
QY 781 QETSPLRDAVVIEQSSSINEASSGLFDVFLRPMCHHAVIRGKSYVQCQGIPOGSIILSTL 840
DB 781 QETSPLRDAVVIEQSSSINEASSGLFDVFLRPMCHHAVIRGKSYVQCQGIPOGSIILSTL 840
QY 841 LCSLCYGDMEKLPAGIRRDGLLRLVDDFLVTPHLLTHAKTFLRTRVLRGPEYGCVVNL 900
DB 841 LCSLCYGDMEKLPAGIRRDGLLRLVDDFLVTPHLLTHAKTFLRTRVLRGPEYGCVVNL 900
QY 901 RKTVVNPFVEDEALGGTAFVQMPAHGLFPMCGLLDTRTLEVSQSDYSYARTSIRASLTF 960
DB 901 RKTVVNPFVEDEALGGTAFVQMPAHGLFPMCGLLDTRTLEVSQSDYSYARTSIRASLTF 960
QY 961 NRGEKAGNRMRKLFVGLRLKCHSLFDLQVNSLQTVCTNIYKILLLOAVERPHACVLQLP 1020
DB 961 NRGEKAGNRMRKLFVGLRLKCHSLFDLQVNSLQTVCTNIYKILLLOAVERPHACVLQLP 1020
QY 1021 FHQOVKNPTFFLRVISTASLCYSILKAKNAGSLGAKGAGPLPSEAVQWLCHOAFLL 1080
DB 1021 FHQOVKNPTFFLRVISTASLCYSILKAKNAGSLGAKGAGPLPSEAVQWLCHOAFLL 1080
QY 1081 KLTRHRVTVYVPLLGSLTAQTQLSRKLPGTTLTALAANAANPALPSDFKTILD 1132
DB 1081 KLTRHRVTVYVPLLGSLTAQTQLSRKLPGTTLTALAANAANPALPSDFKTILD 1132

RESULT 7

US-10-208-243-2
; Sequence 2, Application US/10208243
; Publication No. US20030044394A1
; GENERAL INFORMATION:
; APPLICANT: Gaeta, Federico C.A.
; APPLICANT: Geron Corporation
; TITLE OF INVENTION: Methods and Compositions for Eliciting an Immune
; TITLE OF INVENTION: Response to a Telomerase Antigen
; FILE REFERENCE: 015389-003500PC
; CURRENT APPLICATION NUMBER: US/10/208,243
; CURRENT FILING DATE: 2002-07-30
; PRIOR APPLICATION NUMBER: US/09/675,321
; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: US 60/112,006
; PRIOR FILING DATE: 1998-03-31
; PRIOR APPLICATION NUMBER: WO PCT/US99/06898
; PRIOR FILING DATE: 1999-03-30
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 2
; LENGTH: 1132
; TYPE: PRT
; ORGANISM: Homo sapiens

US-10-208-243-2

Query Match 100.0%; Score 5961; DB 14; Length 1132;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPRAPRCRAVRSLLSHYREVLPATFVRRLPQGWRLVQRGDPAAFRALVAQCLVCPW 60
DB 1 MPRAPRCRAVRSLLSHYREVLPATFVRRLPQGWRLVQRGDPAAFRALVAQCLVCPW 60

QY 61 DARPPAPSPFOVSLKELVARVLOLRCERKAKVLAFFGALLDARGGPPPEATTTSVR 120
DB 61 DARPPAPSPFOVSLKELVARVLOLRCERKAKVLAFFGALLDARGGPPPEATTTSVR 120

QY 121 SYLPTNTVDALRGSGAWGLLLRRVGDVLLHLLARCALFVLVAPSCAYQVCGPPPLYQLGA 180
DB 121 SYLPTNTVDALRGSGAWGLLLRRVGDVLLHLLARCALFVLVAPSCAYQVCGPPPLYQLGA 180

QY 181 ATQARPPPHASGPRRLGRCERAWNHSVREAGVPLGLPAPGARRRGGASRSLLPKRPRR 240
DB 181 ATQARPPPHASGPRRLGRCERAWNHSVREAGVPLGLPAPGARRRGGASRSLLPKRPRR 240

QY 241 GAAPERTPVQCGSWAHPGRTGSDRGFCVVSARPABEATSLEGALSGRHSHPSVG 300
DB 241 GAAPERTPVQCGSWAHPGRTGSDRGFCVVSARPABEATSLEGALSGRHSHPSVG 300

QY 301 RQHAGAPSTSPRPPMDTPCPVVAETKHFLYSSGDKQLRPSFLSSLRPSLTGARRL 360
DB 301 RQHAGAPSTSPRPPMDTPCPVVAETKHFLYSSGDKQLRPSFLSSLRPSLTGARRL 360

QY 361 VETIFLGSRPMPGTPRRLPLRPQRYQWRPFLFELLLGNHACQPYGVLLKTHCPLRAAVT 420
DB 361 VETIFLGSRPMPGTPRRLPLRPQRYQWRPFLFELLLGNHACQPYGVLLKTHCPLRAAVT 420

QY 421 PAAGCAREKPGSVAAPEEBTDPRRLVOLLRQHSSPWQVYGFVRACLRRLVPPGLWGS 480
DB 421 PAAGCAREKPGSVAAPEEBTDPRRLVOLLRQHSSPWQVYGFVRACLRRLVPPGLWGS 480

QY 481 RHNERFLRNTKFTSLGHAKLSLQELTWKMSVRDCAWLRS PGVGVCPAAEHLRREI 540
DB 481 RHNERFLRNTKFTSLGHAKLSLQELTWKMSVRDCAWLRS PGVGVCPAAEHLRREI 540

QY 541 LAKFLHMLSVVVELLSFFVYTTTFOKNRLFYRKSVMKLSQSIGIRQLKRVQLE 600
DB 541 LAKFLHMLSVVVELLSFFVYTTTFOKNRLFYRKSVMKLSQSIGIRQLKRVQLE 600

QY 601 LSEAVRQHREARPAALLTSRLRFIPKPDGLRPIVNDYVVGARTFRREKABRLTSRVKA 660
DB 601 LSEAVRQHREARPAALLTSRLRFIPKPDGLRPIVNDYVVGARTFRREKABRLTSRVKA 660

QY 661 LFSVLNYSRARPGLLGASVLGLDDIHRARWTFVLVRADQPPPELYFKVDVTCAYDTI 720
DB 661 LFSVLNYSRARPGLLGASVLGLDDIHRARWTFVLVRADQPPPELYFKVDVTCAYDTI 720

QY 721 PDRLTEVIASIIKQNTYCVRYAVVQKAAGHVRKAFKSHVSTLTLDQPMRQFVAHL 780
DB 721 PDRLTEVIASIIKQNTYCVRYAVVQKAAGHVRKAFKSHVSTLTLDQPMRQFVAHL 780

QY 781 QETSLRDAVWIEQSSSNEASSGLFDVFLRFMCHAVIRKGSYVQCGIPQGSILSTL 840
DB 781 QETSLRDAVWIEQSSSNEASSGLFDVFLRFMCHAVIRKGSYVQCGIPQGSILSTL 840

QY 841 LCSLCYGMENKLFAGIRDDGLLRLVDDFLVTHPLTHAKTFLRLVRGVEYCVNVL 900
DB 841 LCSLCYGMENKLFAGIRDDGLLRLVDDFLVTHPLTHAKTFLRLVRGVEYCVNVL 900

QY 901 RKTVMNFPVEDEALGATFQVMPAHGLFPWCGLLDTRTLEVQSDYSSVARTSIRASLTF 960
DB 901 RKTVMNFPVEDEALGATFQVMPAHGLFPWCGLLDTRTLEVQSDYSSVARTSIRASLTF 960

QY 961 NRGFKAGNRNRKLFVGLRLKCHSLFLDLQVNSLQTVCTNIYKILLQAYRFHACVLQLP 1020
DB 961 NRGFKAGNRNRKLFVGLRLKCHSLFLDLQVNSLQTVCTNIYKILLQAYRFHACVLQLP 1020

RESULT 8

US-10-054-295-225
; Sequence 225, Application US/10054295
; Publication No. US20030044953A1
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; ; Lingner, Joachim
; ; Nakamura, Toru
; ; Chapman, Karen B.
; ; Morin, Gregg B.
; ; Harley, Calvin
; ; Andrews, William H.
; TITLE OF INVENTION: NO. US20030044953A1el Telomerase
; NUMBER OF SEQUENCES: 225
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/054,295
; FILING DATE: 18-Jan-2002
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/854,050
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph T.
; REGISTRATION NUMBER: 36,429
; REFERENCE/POCKET NUMBER: 015389-002930US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 225:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1132 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 225:
US-10-054-295-225

Query Match 100.0%; Score 5961; DB 14; Length 1132;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPRAPRCRAVRSLLSHYREVLPATFVRRLPQGWRLVQRGDPAAFRALVAQCLVCPW 60
DB 1 MPRAPRCRAVRSLLSHYREVLPATFVRRLPQGWRLVQRGDPAAFRALVAQCLVCPW 60

QY 61 DARPPAAPSPROVSCLELVARVLQRLCERCAKNVLAFGFALLDARGGPEAFTTSVR 120
DB 61 DARPPAAPSPROVSCLELVARVLQRLCERCAKNVLAFGFALLDARGGPEAFTTSVR 120
QY 121 SYLNTVNTDALRGSGAWGLLRVGGDDVLVHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180
DB 121 SYLNTVNTDALRGSGAWGLLRVGGDDVLVHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180
QY 181 ATQARPPPHAGSPRRRLCERAWNHSVREAGVPLGLPAPGARRRGGSSASRLPLPKRPRR 240
DB 181 ATQARPPPHAGSPRRRLCERAWNHSVREAGVPLGLPAPGARRRGGSSASRLPLPKRPRR 240
QY 241 GAAPPEPTPGQSWAHPGTRGSDRGFCVSPARPAEATSLLEGALSCTRSHSPSVG 300
DB 241 GAAPPEPTPGQSWAHPGTRGSDRGFCVSPARPAEATSLLEGALSCTRSHSPSVG 300
QY 301 RQHAGPSTSRPPRPMDTPCPVVAETKHFLYSSGDEQLRPSFLSSLRPSLTGARRL 360
DB 301 RQHAGPSTSRPPRPMDTPCPVVAETKHFLYSSGDEQLRPSFLSSLRPSLTGARRL 360
QY 361 VETIFLGRPMWPGTRPLRLPORYWQMRPLFLELLGNHQAQCPYGVLLKTHCPLRAAVT 420
DB 361 VETIFLGRPMWPGTRPLRLPORYWQMRPLFLELLGNHQAQCPYGVLLKTHCPLRAAVT 420
QY 421 PAAGVCAREKPGQSVAAPEEDTDPRRLVOLLRHSSPWQYVGFVRACLRRLVPPGLWS 480
DB 421 PAAGVCAREKPGQSVAAPEEDTDPRRLVOLLRHSSPWQYVGFVRACLRRLVPPGLWS 480
QY 481 RHNERFLRNTKFTSLGKHAKLSQELTWKMSVRDCAWLRRSPGVGCPVAAEHLRREI 540
DB 481 RHNERFLRNTKFTSLGKHAKLSQELTWKMSVRDCAWLRRSPGVGCPVAAEHLRREI 540
QY 541 LAKFLHMLSVVVBELLRSFFVYTTTFQKNRLFYRKSVMSKLSQIGIRQLKRVOLRE 600
DB 541 LAKFLHMLSVVVBELLRSFFVYTTTFQKNRLFYRKSVMSKLSQIGIRQLKRVOLRE 600
QY 601 LSEAEVROHREARPAALLTSRLRFIPKPGCLAPINVMDYVVGARTFRREKRAERLTSRVKA 660
DB 601 LSEAEVROHREARPAALLTSRLRFIPKPGCLAPINVMDYVVGARTFRREKRAERLTSRVKA 660
QY 661 LFSVLNYERARRPGLLGASVLGLDDIHRARTFVLVRQAQDPPPLYPVKVDVTCAYDTI 720
DB 661 LFSVLNYERARRPGLLGASVLGLDDIHRARTFVLVRQAQDPPPLYPVKVDVTCAYDTI 720
QY 721 PODRLTEVIASIIKPNQTYCVRRYAVQKAAHGHVRKAFKSHVSTLTDLQPMRQFVAHL 780
DB 721 PODRLTEVIASIIKPNQTYCVRRYAVQKAAHGHVRKAFKSHVSTLTDLQPMRQFVAHL 780
QY 781 QETSLRDVAVTEQSSSLNEASSGLFDVFLRFMCHHAVRIKGSYVOCQIPQGSILSTL 840
DB 781 QETSLRDVAVTEQSSSLNEASSGLFDVFLRFMCHHAVRIKGSYVOCQIPQGSILSTL 840
QY 841 LCSLCYGMENKLFAGIRRDGLLLRLVDDFLVTPHLTHAKTFLRTLVRGVPYGCVVNL 900
DB 841 LCSLCYGMENKLFAGIRRDGLLLRLVDDFLVTPHLTHAKTFLRTLVRGVPYGCVVNL 900
QY 901 RKTVNPFVEDBALGCTAFVQMPAHGLFPWCGLLDDTLTEVQSYSSYARTSIRASLTF 960
DB 901 RKTVNPFVEDBALGCTAFVQMPAHGLFPWCGLLDDTLTEVQSYSSYARTSIRASLTF 960
QY 961 NRGFKAGNMRKLFGLRLKCHSLFLDLQVNSLQTVCTNIYKILLQAYRPHACVLQLP 1020
DB 961 NRGFKAGNMRKLFGLRLKCHSLFLDLQVNSLQTVCTNIYKILLQAYRPHACVLQLP 1020
QY 1021 FHOQWKNPTFFLRVISTASLCYSLKAKNAGMSLGKAGAGPLPSEAVOWLCHOAFL 1080
DB 1021 FHOQWKNPTFFLRVISTASLCYSLKAKNAGMSLGKAGAGPLPSEAVOWLCHOAFL 1080
QY 1081 KLTHRVTVVPLLGSLRTAQTSRLPGTTLTALAEAAANPALPSDFKLTLD 1132
DB 1081 KLTHRVTVVPLLGSLRTAQTSRLPGTTLTALAEAAANPALPSDFKLTLD 1132

RESULT 9
US-10-054-611-225
; Sequence 225, Application US/10054611
; Publication No. US20030059787A1
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; Lingner, Joachim
; Nakamura, Toru
; Chapman, Karen B.
; Morin, Gregg B.
; Harley, Calvin
; Andrews, William H.
; TITLE OF INVENTION: No. US20030059787A1el Telomerase
; NUMBER OF SEQUENCES: 225
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/054,611
; FILING DATE: 18-Jan-2002
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/854,050
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph T.
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-002930US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 225:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1132 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 225:
US-10-054-611-225

Query Match 100.0%; Score 5961; DB 14; Length 1132;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MPRAPRCRAVRSLRSHYREVLPVPLATFVRRIGPQGRWLRVQGRDPAAPRALVAQCLVCPW 60
DB 1 MPRAPRCRAVRSLRSHYREVLPVPLATFVRRIGPQGRWLRVQGRDPAAPRALVAQCLVCPW 60
QY 61 DARPPAAPSPROVSCLELVARVLQRLCERCAKNVLAFGFALLDARGGPEAFTTSVR 120
DB 61 DARPPAAPSPROVSCLELVARVLQRLCERCAKNVLAFGFALLDARGGPEAFTTSVR 120
QY 121 SYLNTVNTDALRGSGAWGLLRVGGDDVLVHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180
DB 121 SYLNTVNTDALRGSGAWGLLRVGGDDVLVHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180
QY 181 ATQARPPPHAGSPRRRLCERAWNHSVREAGVPLGLPAPGARRRGGSSASRLPLPKRPRR 240
DB 181 ATQARPPPHAGSPRRRLCERAWNHSVREAGVPLGLPAPGARRRGGSSASRLPLPKRPRR 240

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Db 181 ATQARPPPHASGRRRLGGERAWNHSVREAGVPLGLPAPGARRRGGASRSPLPKRPRR 240
Qy 241 GAAPERTPVQGGSWAHPCRTGSDRGFCVVSPPARPAEATSLGALSGLTSHSPSVG 300
Db 241 GAAPERTPVQGGSWAHPCRTGSDRGFCVVSPPARPAEATSLGALSGLTSHSPSVG 300
Qy 301 ROHAGPPTSPRPPWDTPCPVYATKHFYSSGDKQLRPSFLLSLRSLTGAARL 360
Db 301 ROHAGPPTSPRPPWDTPCPVYATKHFYSSGDKQLRPSFLLSLRSLTGAARL 360
Qy 361 VETIFLGSPPMWTGTPRRLPRLPQRYWQMRPLFLELLGNHQAQCPYGVLLKTHCPLRAAVT 420
Db 361 VETIFLGSPPMWTGTPRRLPRLPQRYWQMRPLFLELLGNHQAQCPYGVLLKTHCPLRAAVT 420
Qy 421 PAAGVCAREKPGQSVAAPEEEDTPRRLVQLLRQHSPPMQVYGFVRACLRLRLLVPPGLWGS 480
Db 421 PAAGVCAREKPGQSVAAPEEEDTPRRLVQLLRQHSPPMQVYGFVRACLRLRLLVPPGLWGS 480
Qy 481 RHNERFLRNTKFFISLGHAKLSLOELTWKMSVRDCAWLRSPGVGCVPAAEHRLREI 540
Db 481 RHNERFLRNTKFFISLGHAKLSLOELTWKMSVRDCAWLRSPGVGCVPAAEHRLREI 540
Qy 541 LAKFLHMLSVVYVVELLRFFVYTTTFOKNRLFYRKSVWSKLSQSIGIRQHLKRVOLRE 600
Db 541 LAKFLHMLSVVYVVELLRFFVYTTTFOKNRLFYRKSVWSKLSQSIGIRQHLKRVOLRE 600
Qy 601 LSEAEVRQREARPAALLTSRLRFPKPDGLRPIVNMVYVVGARTFRREKRAERLTSRVKA 660
Db 601 LSEAEVRQREARPAALLTSRLRFPKPDGLRPIVNMVYVVGARTFRREKRAERLTSRVKA 660
Qy 661 LFSVLNERARPPGLLGASVLGLDDIHRARWTFVLRVRAQDPPPELYFVKVDVTGAYDTI 720
Db 661 LFSVLNERARPPGLLGASVLGLDDIHRARWTFVLRVRAQDPPPELYFVKVDVTGAYDTI 720
Qy 721 PODRLTEVIASIIKPNQTYCVRRYAVVQKAAHGHVKAFKSHVSTLTDLOPYMRQFVAHL 780
Db 721 PODRLTEVIASIIKPNQTYCVRRYAVVQKAAHGHVKAFKSHVSTLTDLOPYMRQFVAHL 780
Qy 781 QETSPLRDAVIEQSSSLEASGLFDVFLRPMCHHAVIRGKSVYQCOGIPQGSILSTL 840
Db 781 QETSPLRDAVIEQSSSLEASGLFDVFLRPMCHHAVIRGKSVYQCOGIPQGSILSTL 840
Qy 841 LCSLCYGDMEKLFAGIRDGILLRLVDLFTPLTHAKTFLRLTVRGVPEYGCNVNL 900
Db 841 LCSLCYGDMEKLFAGIRDGILLRLVDLFTPLTHAKTFLRLTVRGVPEYGCNVNL 900
Qy 901 RKTVNFVEDEALGCTAFVQMPAHGLFPWCGLLDDTRILEVQSDYSSYARTSIRASLTF 960
Db 901 RKTVNFVEDEALGCTAFVQMPAHGLFPWCGLLDDTRILEVQSDYSSYARTSIRASLTF 960
Qy 961 NRGFKAGRNMRKLFGLRLKCHSLFDLDQVNSLQTVCTNIYKILLLOAYRFHACVLQLP 1020
Db 961 NRGFKAGRNMRKLFGLRLKCHSLFDLDQVNSLQTVCTNIYKILLLOAYRFHACVLQLP 1020
Qy 1021 FHOQVWKNPTFFLRVISTASLCYSLKAKNAGMSLGAKGAAGPLPSEAVQMLCHQAFLL 1080
Db 1021 FHOQVWKNPTFFLRVISTASLCYSLKAKNAGMSLGAKGAAGPLPSEAVQMLCHQAFLL 1080
Qy 1081 KLTHRVTVVPLLSRLTAQTOLSRKLPCTTTLTALEAANPALPSDFKTILD 1132
Db 1081 KLTHRVTVVPLLSRLTAQTOLSRKLPCTTTLTALEAANPALPSDFKTILD 1132

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RESULT 10
US-10-105-963-2
; Sequence 2, Application US/10105963
; Publication No. US20030068818A1
; GENERAL INFORMATION:
; APPLICANT: Genon Corporation
; APPLICANT: Denning, Chris
; APPLICANT: Clark, A. John
; APPLICANT: Schiff, J. Michael
; TITLE OF INVENTION: Animal Tissue with Carbohydrate Antigens Compatible for Human

```

; TITLE OF INVENTION: Transplantation and a Carbohydrate Determinant Selection System
; FILE OF INVENTION: Recombination
; FILE REFERENCE: 731/002
; CURRENT APPLICATION NUMBER: US/10/105,963
; CURRENT FILING DATE: 2002-03-21
; PRIOR APPLICATION NUMBER: US 60/277,811
; PRIOR FILING DATE: 2001-03-21
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 1132
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-105-963-2

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Query Match 100.0%; Score 5961; DB 14; Length 1132;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MPRAPRCRAVRSLLRSHYREVLPATFVRRLGPFQGWRLVQRGDPAAAFRALVAQCLVCVPW 60
Db 1 MPRAPRCRAVRSLLRSHYREVLPATFVRRLGPFQGWRLVQRGDPAAAFRALVAQCLVCVPW 60
Qy 61 DARPPAAPSPFQVSCLEKELVARVQLRCERGAKNVLAFGFALLDGAAGPPPEAFTTSVR 120
Db 61 DARPPAAPSPFQVSCLEKELVARVQLRCERGAKNVLAFGFALLDGAAGPPPEAFTTSVR 120
Qy 121 SYLPTNTVDALRSGAWGLLRVDDVLLHLLARCALFVLVAPSCAYVCGPPPLYOLGA 180
Db 121 SYLPTNTVDALRSGAWGLLRVDDVLLHLLARCALFVLVAPSCAYVCGPPPLYOLGA 180
Qy 181 ATQARPPPHASGRRRLGGERAWNHSVREAGVPLGLPAPGARRRGGASRSPLPKRPRR 240
Db 181 ATQARPPPHASGRRRLGGERAWNHSVREAGVPLGLPAPGARRRGGASRSPLPKRPRR 240
Qy 241 GAAPERTPVQGGSWAHPCRTGSDRGFCVVSPPARPAEATSLGALSGLTSHSPSVG 300
Db 241 GAAPERTPVQGGSWAHPCRTGSDRGFCVVSPPARPAEATSLGALSGLTSHSPSVG 300
Qy 301 ROHAGPPTSPRPPWDTPCPVYATKHFYSSGDKQLRPSFLLSLRSLTGAARL 360
Db 301 ROHAGPPTSPRPPWDTPCPVYATKHFYSSGDKQLRPSFLLSLRSLTGAARL 360
Qy 361 VETIFLGSPPMWTGTPRRLPRLPQRYWQMRPLFLELLGNHQAQCPYGVLLKTHCPLRAAVT 420
Db 361 VETIFLGSPPMWTGTPRRLPRLPQRYWQMRPLFLELLGNHQAQCPYGVLLKTHCPLRAAVT 420
Qy 421 PAAGVCAREKPGQSVAAPEEEDTPRRLVQLLRQHSPPMQVYGFVRACLRLRLLVPPGLWGS 480
Db 421 PAAGVCAREKPGQSVAAPEEEDTPRRLVQLLRQHSPPMQVYGFVRACLRLRLLVPPGLWGS 480
Qy 481 RHNERFLRNTKFFISLGHAKLSLOELTWKMSVRDCAWLRSPGVGCVPAAEHRLREI 540
Db 481 RHNERFLRNTKFFISLGHAKLSLOELTWKMSVRDCAWLRSPGVGCVPAAEHRLREI 540
Qy 541 LAKFLHMLSVVYVVELLRFFVYTTTFOKNRLFYRKSVWSKLSQSIGIRQHLKRVOLRE 600
Db 541 LAKFLHMLSVVYVVELLRFFVYTTTFOKNRLFYRKSVWSKLSQSIGIRQHLKRVOLRE 600
Qy 601 LSEAEVRQREARPAALLTSRLRFPKPDGLRPIVNMVYVVGARTFRREKRAERLTSRVKA 660
Db 601 LSEAEVRQREARPAALLTSRLRFPKPDGLRPIVNMVYVVGARTFRREKRAERLTSRVKA 660
Qy 661 LFSVLNERARPPGLLGASVLGLDDIHRARWTFVLRVRAQDPPPELYFVKVDVTGAYDTI 720
Db 661 LFSVLNERARPPGLLGASVLGLDDIHRARWTFVLRVRAQDPPPELYFVKVDVTGAYDTI 720
Qy 721 PODRLTEVIASIIKPNQTYCVRRYAVVQKAAHGHVKAFKSHVSTLTDLOPYMRQFVAHL 780
Db 721 PODRLTEVIASIIKPNQTYCVRRYAVVQKAAHGHVKAFKSHVSTLTDLOPYMRQFVAHL 780
Qy 781 QETSPLRDAVIEQSSSLEASGLFDVFLRPMCHHAVIRGKSVYQCOGIPQGSILSTL 840

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Db 781 QETSPDRDAVVIQSSSLNEASSGLFDVFLRFMCHHVRIRGKSVVQCQIPQGSILSTL 840
Qy 841 LCSLCYGDWENKLFAGIRRDGLLLRLVDLFTLTHAKTFLTRVGRVPEYGCVVNL 900
Db 841 LCSLCYGDWENKLFAGIRRDGLLLRLVDLFTLTHAKTFLTRVGRVPEYGCVVNL 900
Qy 901 RKTUVNFEVEALGGTAFVQMPAHGLFPWCGLLDLDTLTVQSDYSSYARTSIRASLTF 960
Db 901 RKTUVNFEVEALGGTAFVQMPAHGLFPWCGLLDLDTLTVQSDYSSYARTSIRASLTF 960
Qy 961 NRGFKAGNMRKLFGLVRLKCHSLFDLQVNSLQTVCTNIVKILLQAYRPHACVLQLP 1020
Db 961 NRGFKAGNMRKLFGLVRLKCHSLFDLQVNSLQTVCTNIVKILLQAYRPHACVLQLP 1020
Qy 1021 FHQQWKNPTFFLRVISDTASLCYSILKAKNAGMSLGAKGAAGPLPSEAVQWLCHQAFLL 1080
Db 1021 FHQQWKNPTFFLRVISDTASLCYSILKAKNAGMSLGAKGAAGPLPSEAVQWLCHQAFLL 1080
Qy 1081 KLTRHRVTYVPLGLSLRTAQQLSRKLPGLTTLTALEAAANPALPSDFKTILD 1132
Db 1081 KLTRHRVTYVPLGLSLRTAQQLSRKLPGLTTLTALEAAANPALPSDFKTILD 1132

RESULT 11

US-10-044-692-2
; Sequence 2, Application US/10044692
; Publication No. US20030096344A1
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; Lingner, Joachim
; Nakamura, Toru
; Chapman, Karen B.
; Morin, Gregg B.
; Harley, Calvin
; Andrews, William H.
; TITLE OF INVENTION: HUMAN TELOMERASE CATALYTIC SUBUNIT: DIAGNOSTIC AND
; THERAPEUTIC METHODS
; NUMBER OF SEQUENCES: 335
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/044,692
; FILING DATE: 11-Jan-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/912,951
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US 08/854,050
; FILING DATE: 09-MAY-1997
; APPLICATION NUMBER: US 08/851,843
; FILING DATE: 06-MAY-1997
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph T.
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-002600US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200

; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1132 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-044-692-2

Query Match 100.0%; Score 5961; DB 14; Length 1132;
Beet Local Similarity 100.0%; Pred. No. 0;
Matches 1132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MPRAPRCRAVRSLLRSHYREVLPATFVRRIGPQGWRLVQRGDPAAFRALVAQCLVCVPW 60
Db 1 MPRAPRCRAVRSLLRSHYREVLPATFVRRIGPQGWRLVQRGDPAAFRALVAQCLVCVPW 60
Qy 61 DARPPPAAPSPRQVSCIKELVARVLQRLCERGAQNVLAFGFALLDARGGPEAFTTSVR 120
Db 61 DARPPPAAPSPRQVSCIKELVARVLQRLCERGAQNVLAFGFALLDARGGPEAFTTSVR 120
Qy 121 SYLENTVTDALRGSGAWGLLLRRVGDVVLVHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180
Db 121 SYLENTVTDALRGSGAWGLLLRRVGDVVLVHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180
Qy 181 ATQARPPPHASGPRRRRLGCERAMNHSVREAGVPLGLPAPGARRRGGSASRSLPLPKRPRR 240
Db 181 ATQARPPPHASGPRRRRLGCERAMNHSVREAGVPLGLPAPGARRRGGSASRSLPLPKRPRR 240
Qy 241 GAAPERTPTVGQGSWAHPGTRGSDRGFCVSPARPAEATSLGALSCTRHSHPVSG 300
Db 241 GAAPERTPTVGQGSWAHPGTRGSDRGFCVSPARPAEATSLGALSCTRHSHPVSG 300
Qy 301 RQHHAGPSPSRPRPMDTCPVYAEYTKHLYSSGDKQLRPSFLSSLSRPSLTGARRL 360
Db 301 RQHHAGPSPSRPRPMDTCPVYAEYTKHLYSSGDKQLRPSFLSSLSRPSLTGARRL 360
Qy 361 VETIFLGSRRPMPCTPRRLPRLPQRYQMRLPFLLELGNHAQCPYGVLLKTHCPRAAAT 420
Db 361 VETIFLGSRRPMPCTPRRLPRLPQRYQMRLPFLLELGNHAQCPYGVLLKTHCPRAAAT 420
Qy 421 PAAGVCAREKPOGSVAAPPEEDTDPRLVQLRHOSSPQVYGVFRACLRLLVPPLGWS 480
Db 421 PAAGVCAREKPOGSVAAPPEEDTDPRLVQLRHOSSPQVYGVFRACLRLLVPPLGWS 480
Qy 481 RHNERRFLRNTKFTISLGKIAKLSLQELTWKMSVRDCAWLRSPGVGCVPAAEHRLRBEI 540
Db 481 RHNERRFLRNTKFTISLGKIAKLSLQELTWKMSVRDCAWLRSPGVGCVPAAEHRLRBEI 540
Qy 541 LAKFLHLMMSVYVVELLRSFPYVTTTFOKNRLLPFYRKSVMSKLSQSIGIRHLKRVQURE 600
Db 541 LAKFLHLMMSVYVVELLRSFPYVTTTFOKNRLLPFYRKSVMSKLSQSIGIRHLKRVQURE 600
Qy 601 LSEAEVRQHRERAPALLTSRLRFTPKDGLRPIVNMDDYVVGARTFRERKRAERLTSRVKA 660
Db 601 LSEAEVRQHRERAPALLTSRLRFTPKDGLRPIVNMDDYVVGARTFRERKRAERLTSRVKA 660
Qy 661 LFSVLNVERARRPGLLGASVLGLDDIHRAWTFLVRVRAQDPPPELYFVKVDVTGAYDTI 720
Db 661 LFSVLNVERARRPGLLGASVLGLDDIHRAWTFLVRVRAQDPPPELYFVKVDVTGAYDTI 720
Qy 721 PQDLRTEVIASIIKPNQTYCVRRYAVQKAAHGVKAFKSHVSTLTDLQPMRQFVAHL 780
Db 721 PQDLRTEVIASIIKPNQTYCVRRYAVQKAAHGVKAFKSHVSTLTDLQPMRQFVAHL 780
Qy 781 QETSPDRDAVVIQSSSLNEASSGLFDVFLRFMCHHVRIRGKSVVQCQIPQGSILSTL 840
Db 781 QETSPDRDAVVIQSSSLNEASSGLFDVFLRFMCHHVRIRGKSVVQCQIPQGSILSTL 840
Qy 841 LCSLCYGDWENKLFAGIRRDGLLLRLVDLFTLTHAKTFLTRVGRVPEYGCVVNL 900
Db 841 LCSLCYGDWENKLFAGIRRDGLLLRLVDLFTLTHAKTFLTRVGRVPEYGCVVNL 900

901 RKTVMNPFVEDEALGCTAFVQMPAHGLFPWCGLLDTRTLEVSQSDYSYSSVARTSIRASLTF 960
901 RKTVMNPFVEDEALGCTAFVQMPAHGLFPWCGLLDTRTLEVSQSDYSYSSVARTSIRASLTF 960
961 NRGFKAGNMRKLFVRLKCHSLFDLDQVNSLQVCTNIIKILLQAYRFHACVQLQP 1020
961 NRGFKAGNMRKLFVRLKCHSLFDLDQVNSLQVCTNIIKILLQAYRFHACVQLQP 1020
1021 FHOQWKNPTFFLRVISDTASLCYSILKAKNAGMSLGAKGAGPLPSEAVOMLCHQAFLL 1080
1021 FHOQWKNPTFFLRVISDTASLCYSILKAKNAGMSLGAKGAGPLPSEAVOMLCHQAFLL 1080
1081 KLTRHRVTVPILGSLRTAQOLSRKLPCTTTTALAEAAANPALPSDFKTILD 1132
1081 KLTRHRVTVPILGSLRTAQOLSRKLPCTTTTALAEAAANPALPSDFKTILD 1132

RESULT 12
US-10-044-539-2
Sequence 2, Application US/10044539
Publication No. US20030100093A1
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin
Andrews, William H.

TITLE OF INVENTION: HUMAN TELOMERASE CATALYTIC SUBUNIT: DIAGNOSTIC AND
THERAPEUTIC METHODS

NUMBER OF SEQUENCES: 335
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
City: San Francisco
STATE: California
COUNTRY: United States of America
ZIP: 94111

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/044,539
FILING DATE: 11-Jan-2002
CLASSIFICATION: 435

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/912,951
FILING DATE: <Unknown>
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996

ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002600US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300

INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1132 amino acids
TYPE: amino acid

TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-044-539-2

Query Match 100.0%; Score 5961; DB 14; Length 1132;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPRAPRCRAVRSLSRSHYREVLPATFVRRLLGPGQWRVLVQRGDPAARALVAQCLVCPW 60
Db 1 MPRAPRCRAVRSLSRSHYREVLPATFVRRLLGPGQWRVLVQRGDPAARALVAQCLVCPW 60

QY 61 DARPPAAPSPRQVSCLELVARVLQRLCERGAKNVLAFGFALLDGAAGGPPPEAFTTSVR 120
Db 61 DARPPAAPSPRQVSCLELVARVLQRLCERGAKNVLAFGFALLDGAAGGPPPEAFTTSVR 120

QY 121 SYLPNTVTDALRGSGAWGLLRRVGDVVLVHLLARCALFVLVAPSCAVQVCGPPLVQLGA 180
Db 121 SYLPNTVTDALRGSGAWGLLRRVGDVVLVHLLARCALFVLVAPSCAVQVCGPPLVQLGA 180

QY 181 ATQARPPPHASGPRRLGGERAWNHSVREAGVPLGLPAPGARRRGGSSASRSLPLKPRPR 240
Db 181 ATQARPPPHASGPRRLGGERAWNHSVREAGVPLGLPAPGARRRGGSSASRSLPLKPRPR 240

QY 241 GAAPEPERTVQGGSWAHPGRTGSDRGFCVSPARPAEAEATSLEGALSGTRHSHPSVG 300
Db 241 GAAPEPERTVQGGSWAHPGRTGSDRGFCVSPARPAEAEATSLEGALSGTRHSHPSVG 300

QY 301 RQHAGPSTSRPRPMDTPCPVYAEATKHFYLSGSGDEQLRPPSLLSRLPSLTGARRL 360
Db 301 RQHAGPSTSRPRPMDTPCPVYAEATKHFYLSGSGDEQLRPPSLLSRLPSLTGARRL 360

QY 361 VETIFLGSRPWMPGTPLRLPRLPQYQWMPRLPLFLELLGNHACPYGVLLKTHCPRAAYT 420
Db 361 VETIFLGSRPWMPGTPLRLPRLPQYQWMPRLPLFLELLGNHACPYGVLLKTHCPRAAYT 420

QY 421 PAAGVCAREKPGQSVAAPEEEDTDPRRLVQLLRQHSHPWQVYGFVRACLRLVPPGLWGS 480
Db 421 PAAGVCAREKPGQSVAAPEEEDTDPRRLVQLLRQHSHPWQVYGFVRACLRLVPPGLWGS 480

QY 481 RHNERFLRNTKFTISLGHAKLSLOELTWKMSVRDCAWLRRSPGVCGVPAAEHLRREI 540
Db 481 RHNERFLRNTKFTISLGHAKLSLOELTWKMSVRDCAWLRRSPGVCGVPAAEHLRREI 540

QY 541 LAKFLHLMVSVVVELLSRFFVVTETTFQKRLFFYRSKSVMSKLOSIGIRQHLKRVQRE 600
Db 541 LAKFLHLMVSVVVELLSRFFVVTETTFQKRLFFYRSKSVMSKLOSIGIRQHLKRVQRE 600

QY 601 LSEAEVRQHREARPALTSRLRFIPKPDGLRPIVNMDDYVVGARTFRERKRAERLTSRVKA 660
Db 601 LSEAEVRQHREARPALTSRLRFIPKPDGLRPIVNMDDYVVGARTFRERKRAERLTSRVKA 660

QY 661 LFSVLNVERARRPGLLGASVLGLDDIHRARWTFVLVRQAQDPPPELYFVKVDVTGAYDTI 720
Db 661 LFSVLNVERARRPGLLGASVLGLDDIHRARWTFVLVRQAQDPPPELYFVKVDVTGAYDTI 720

QY 721 PQDLRLTEVIASIIKPQNTYCVRRYAVQKAAHGHVKAFKSHVSTLTDLPQYMRQFVAHL 780
Db 721 PQDLRLTEVIASIIKPQNTYCVRRYAVQKAAHGHVKAFKSHVSTLTDLPQYMRQFVAHL 780

QY 781 QETSPLRDAVVIQSSSLNEASSGLFDVFLRFMCHHVRIRGKSVYVQCGIPOQSILSTL 840
Db 781 QETSPLRDAVVIQSSSLNEASSGLFDVFLRFMCHHVRIRGKSVYVQCGIPOQSILSTL 840

QY 841 LCSLCYGDMEKNLFAGTRRDGLLLRLVDDFLVTPHLLTHAKTFLRTLVRGVPEYCVVNL 900
Db 841 LCSLCYGDMEKNLFAGTRRDGLLLRLVDDFLVTPHLLTHAKTFLRTLVRGVPEYCVVNL 900

QY 901 RKTVMNPFVEDEALGCTAFVQMPAHGLFPWCGLLDTRTLEVSQSDYSYSSVARTSIRASLTF 960
Db 901 RKTVMNPFVEDEALGCTAFVQMPAHGLFPWCGLLDTRTLEVSQSDYSYSSVARTSIRASLTF 960

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QY 961 NRGFAGRNMRKLFGLVRLKCHSLFDLQVNSLQTVCTNIYKILLQAYRHFACVLQLP 1020
DB 961 NRGFAGRNMRKLFGLVRLKCHSLFDLQVNSLQTVCTNIYKILLQAYRHFACVLQLP 1020
QY 1021 FHQOVKNPTFFLRVISTASLCYSILKAKNAGSLGAKGAGPLPSEAVOMLCHOAFLL 1080
DB 1021 FHQOVKNPTFFLRVISTASLCYSILKAKNAGSLGAKGAGPLPSEAVOMLCHOAFLL 1080
QY 1081 KLTHRVTVYVPLGSLRTAQOLSKLPGTTLTALAAAAANPALPSDFKTILD 1132
DB 1081 KLTHRVTVYVPLGSLRTAQOLSKLPGTTLTALAAAAANPALPSDFKTILD 1132

RESULT 13
US-10-295-681-57
; Sequence 57, Application US/10295681
; Publication No. US20030166270A1
; GENERAL INFORMATION:
; APPLICANT: E. Premkumar Reddy
; APPLICANT: Sushil G. Kane
; APPLICANT: Richard V. Mettus
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR REVERSIBLY
; TITLE OF INVENTION: INDUCING CONTINUAL GROWTH IN NORMAL CELLS
; FILE REFERENCE: 6056-307
; CURRENT APPLICATION NUMBER: US/10/295,681
; PRIORITY FILING DATE: 2002-11-15
; PRIOR FILING DATE: 2001-11-15
; NUMBER OF SEQ ID NOS: 69
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 57
; LENGTH: 1132
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-295-681-57

Query Match 100.0%; Score 5961; DB 14; Length 1132;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPRAPRCRAVRLSLRSHREVLPATFVRRLGPOQWRVLVQRGDPAAFRALVAQCILVCVPM 60
DB 1 MPRAPRCRAVRLSLRSHREVLPATFVRRLGPOQWRVLVQRGDPAAFRALVAQCILVCVPM 60

QY 61 DARPPAAPSPROVSCLEKELVARVLQRLCERGAKNVLAFGFALLDARGGPPPEAFTTSVR 120
DB 61 DARPPAAPSPROVSCLEKELVARVLQRLCERGAKNVLAFGFALLDARGGPPPEAFTTSVR 120

QY 121 SYLPNTVTDALRGSGAWGLLRRVGDVLLVHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180
DB 121 SYLPNTVTDALRGSGAWGLLRRVGDVLLVHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180

QY 181 ATQARPPPHASPRRLGRCERAWNHSVREAGVPLGLPAPGARRRGCSASRSLPLPKRPRR 240
DB 181 ATQARPPPHASPRRLGRCERAWNHSVREAGVPLGLPAPGARRRGCSASRSLPLPKRPRR 240

QY 241 GAAPPERTPVQGSWAHPGRTGSDRGFCVVSAPAEATSLEGALSGTRHSHPSVG 300
DB 241 GAAPPERTPVQGSWAHPGRTGSDRGFCVVSAPAEATSLEGALSGTRHSHPSVG 300

QY 301 RQHAGAPSTSRPPRPWDTPCPVVAETHKFLYSSGDKQLRPSFLLSLRPSLTGARRL 360
DB 301 RQHAGAPSTSRPPRPWDTPCPVVAETHKFLYSSGDKQLRPSFLLSLRPSLTGARRL 360

QY 361 VETIFLGSRPWMPGTPRRLPLRQYQWOMRPLFELLGNHACQPYGVLLKTHCPLRAAVT 420
DB 361 VETIFLGSRPWMPGTPRRLPLRQYQWOMRPLFELLGNHACQPYGVLLKTHCPLRAAVT 420

QY 421 PAAGYCAKEKPGSVAAPPEEDTPRRLVQLLRQHSPPQVYGFVRACLRRLVPPGLWGS 480
DB 421 PAAGYCAKEKPGSVAAPPEEDTPRRLVQLLRQHSPPQVYGFVRACLRRLVPPGLWGS 480

QY 481 RHNERFLRNTKFTISLGKHAQLSLQELTWKMSVRDCAWLRRSPGVGCVPAEHLRREI 540

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DB 481 RHNERFLRNTKFTISLGKHAQLSLQELTWKMSVRDCAWLRRSPGVGCVPAEHLRREI 540
QY 541 LAKELHLMMSVYVVELLRSFFYVTTTFQKNRLEFFYKSVMSKLQSIGIRQHLKRVQLRE 600
DB 541 LAKELHLMMSVYVVELLRSFFYVTTTFQKNRLEFFYKSVMSKLQSIGIRQHLKRVQLRE 600
QY 601 LSEAEVQHRREARALLTSRLRPIPKPDGLRPIVNDYVVGARTFRREKRAERLTSRVA 660
DB 601 LSEAEVQHRREARALLTSRLRPIPKPDGLRPIVNDYVVGARTFRREKRAERLTSRVA 660
QY 661 LFSVLNTERARRPGLLGASVLGLDDIHRAMTFVLRVRAQDPPPELVEFKVVDVTGAYDTI 720
DB 661 LFSVLNTERARRPGLLGASVLGLDDIHRAMTFVLRVRAQDPPPELVEFKVVDVTGAYDTI 720
QY 721 PQDLTEVIASIIKPQNTYCVRRYAVVQKAAHGHVRKAFKSHVSTLTDLQPMRQFVAHL 780
DB 721 PQDLTEVIASIIKPQNTYCVRRYAVVQKAAHGHVRKAFKSHVSTLTDLQPMRQFVAHL 780
QY 781 QETSPLRDVAVIEOSSSINEASSGLFDVFLRFMCHHAVIRGKSVYVQCGIPQGSILSTL 840
DB 781 QETSPLRDVAVIEOSSSINEASSGLFDVFLRFMCHHAVIRGKSVYVQCGIPQGSILSTL 840
QY 841 LCSLCYGDMEKLFAGIRRDGLLRLVDDFLVTPHLLTHAKTFLRTLVRGVEYGCVVNL 900
DB 841 LCSLCYGDMEKLFAGIRRDGLLRLVDDFLVTPHLLTHAKTFLRTLVRGVEYGCVVNL 900
QY 901 RKTVNFPEDEALGGTAFVQMPAHGLFPWCGLLDDTTLTLEVDQSDYSSYARTSIRASLTF 960
DB 901 RKTVNFPEDEALGGTAFVQMPAHGLFPWCGLLDDTTLTLEVDQSDYSSYARTSIRASLTF 960
QY 961 NRGFAGRNMRKLFGLVRLKCHSLFDLQVNSLQTVCTNIYKILLQAYRHFACVLQLP 1020
DB 961 NRGFAGRNMRKLFGLVRLKCHSLFDLQVNSLQTVCTNIYKILLQAYRHFACVLQLP 1020
QY 1021 FHQOVKNPTFFLRVISTASLCYSILKAKNAGSLGAKGAGPLPSEAVOMLCHOAFLL 1080
DB 1021 FHQOVKNPTFFLRVISTASLCYSILKAKNAGSLGAKGAGPLPSEAVOMLCHOAFLL 1080
QY 1081 KLTHRVTVYVPLGSLRTAQOLSKLPGTTLTALAAAAANPALPSDFKTILD 1132
DB 1081 KLTHRVTVYVPLGSLRTAQOLSKLPGTTLTALAAAAANPALPSDFKTILD 1132

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RESULT 14
US-10-325-810-2
; Sequence 2, Application US/10325810
; Publication No. US20030204069A1
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; Lingner, Joachim
; Nakamura, Toru
; Chapman, Karen B.
; Morin, Gregg B.
; Harley, Calvin B.
; Andrews, William H.

```

```

; TITLE OF INVENTION: Human Telomerase Catalytic Subunit
; NUMBER OF SEQUENCES: 633
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/325,810
; FILING DATE: 20-Dec-2002

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;
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: US/09/402,181
;   FILING DATE: 29-Sep-1997
;   APPLICATION NUMBER: US 08/724,643
;   FILING DATE: 01-OCT-1996
;   APPLICATION NUMBER: US 08/844,419
;   FILING DATE: 18-APR-1997
;   APPLICATION NUMBER: US 08/846,017
;   FILING DATE: 25-APR-1997
;   APPLICATION NUMBER: US 08/851,843
;   FILING DATE: 06-MAY-1997
;   APPLICATION NUMBER: US 08/854,050
;   FILING DATE: 09-MAY-1997
;   APPLICATION NUMBER: US 08/911,312
;   FILING DATE: 14-AUG-1997
;   APPLICATION NUMBER: US 08/912,951
;   FILING DATE: 14-AUG-1997
;   APPLICATION NUMBER: US 08/915,503
;   FILING DATE: 14-AUG-1997
;   APPLICATION NUMBER: WO PCT/US97/17885
;
; ATTORNEY/AGENT INFORMATION:
;   NAME: Ausenhus, Scott L.
;   REGISTRATION NUMBER: 42,271
;   REFERENCE/DOCKET NUMBER: 015389-002620US
;
; TELECOMMUNICATION INFORMATION:
;   TELEPHONE: (415) 576-0200
;   TELEFAX: (415) 576-0300
;
; INFORMATION FOR SEQ ID NO: 2:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH: 1132 amino acids
;     TYPE: amino acid
;     TOPOLOGY: linear
;   MOLECULE TYPE: protein
;   SEQUENCE DESCRIPTION: SEQ ID NO: 2:
;
US-10-325-810-2
;
; Query Match 100.0%; Score 5961; DB 15; Length 1132;
; Best Local Similarity 100.0%; Pred. No. 0;
; Matches 1132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
QY 1 MPAPRCRAVRSLLRSHYREVLPATFVRRLLGPGQWRLVQRGDPAAFRALVAQCLVCPW 60
DB 1 MPAPRCRAVRSLLRSHYREVLPATFVRRLLGPGQWRLVQRGDPAAFRALVAQCLVCPW 60
;
QY 61 DARPPAPSPFQVSCLEKELVARVLQRLCERGAKNVLAFGPALLDGAAGGPPPEAFTTSVR 120
DB 61 DARPPAPSPFQVSCLEKELVARVLQRLCERGAKNVLAFGPALLDGAAGGPPPEAFTTSVR 120
;
QY 121 SYLPNTVTDALRGSGAWGLLRVGDVLLHLLARCALFVLVAPSCAYOVCGPPLYQLGA 180
DB 121 SYLPNTVTDALRGSGAWGLLRVGDVLLHLLARCALFVLVAPSCAYOVCGPPLYQLGA 180
;
QY 181 ATQARPPPHASGPRRLRCERAWNHSVREAGVPLGLPAGARRRGSGASRSLPLPKRPRR 240
DB 181 ATQARPPPHASGPRRLRCERAWNHSVREAGVPLGLPAGARRRGSGASRSLPLPKRPRR 240
;
QY 241 GAAPSPERTPVQGGWAHPGRTGRGSDRGFCVVSPPAPAEATSLEGALSGTRHSHPSVG 300
DB 241 GAAPSPERTPVQGGWAHPGRTGRGSDRGFCVVSPPAPAEATSLEGALSGTRHSHPSVG 300
;
QY 301 ROHAGPPTSPRPPRMDTPCPVVAETHKFLYSSGDKQLRPSFLSLRSLTGARRL 360
DB 301 ROHAGPPTSPRPPRMDTPCPVVAETHKFLYSSGDKQLRPSFLSLRSLTGARRL 360
;
QY 361 VETIFLGSPPMPGTPRRPLPQRYQWMPRLFLELLGNHACPYGVLLKTHCPLRAAVT 420
DB 361 VETIFLGSPPMPGTPRRPLPQRYQWMPRLFLELLGNHACPYGVLLKTHCPLRAAVT 420
;
QY 421 PAAGVCAREKPGQSVAAPEEDTDPRRLVQLLRQHSSPMQVYGFVRACLRRLVPPGLMGS 480
DB 421 PAAGVCAREKPGQSVAAPEEDTDPRRLVQLLRQHSSPMQVYGFVRACLRRLVPPGLMGS 480

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QY 481 RHNERFLRNTKFTSLGKHAKLSLQELTWKMSVRDCAWLRBSPGVGCVPAAEHLRREI 540
DB 481 RHNERFLRNTKFTSLGKHAKLSLQELTWKMSVRDCAWLRSPGVGCVPAAEHLRREI 540
;
QY 541 LAKFLHLMWSVYVVELLSRFFVYVTTTQKNRLFYRKSVMSKLSQSIGIRQHLKRVQLRE 600
DB 541 LAKFLHLMWSVYVVELLSRFFVYVTTTQKNRLFYRKSVMSKLSQSIGIRQHLKRVQLRE 600
;
QY 601 LSEAEVROHREARPAALLTSRLRFIPKPDGLRPIVMDYVVGARTPRREKRAERLSRVKA 660
DB 601 LSEAEVROHREARPAALLTSRLRFIPKPDGLRPIVMDYVVGARTPRREKRAERLSRVKA 660
;
QY 661 LFSVLNYERARRPGLLGASVLGLDDIHRARWTFVLVRQAQDPPPPYFYKVDVDTGAYDTI 720
DB 661 LFSVLNYERARRPGLLGASVLGLDDIHRARWTFVLVRQAQDPPPPYFYKVDVDTGAYDTI 720
;
QY 721 PODRLTEVIASIIKPQNTYCVRRYAVVQKAAHGHVRKAFKSHVSTLTDLPQNMRFVAHL 780
DB 721 PODRLTEVIASIIKPQNTYCVRRYAVVQKAAHGHVRKAFKSHVSTLTDLPQNMRFVAHL 780
;
QY 781 QETSLRDVAVIEQSSSLNEASSGLFDVFLRPMCHHVRIRGKSVVOCOGIPQGSILSTL 840
DB 781 QETSLRDVAVIEQSSSLNEASSGLFDVFLRPMCHHVRIRGKSVVOCOGIPQGSILSTL 840
;
QY 841 LCSLCYGDMEKLPAGIRRDGLLLRLVDDFLVLTPLTHAKTFFLRTLVGRVPEYGCNVNL 900
DB 841 LCSLCYGDMEKLPAGIRRDGLLLRLVDDFLVLTPLTHAKTFFLRTLVGRVPEYGCNVNL 900
;
QY 901 RKTVVNPFVEDEALGGTAFVQMPAHGLFPWCGLLDTRTLEVSQSYSSYARTSIRASLTF 960
DB 901 RKTVVNPFVEDEALGGTAFVQMPAHGLFPWCGLLDTRTLEVSQSYSSYARTSIRASLTF 960
;
QY 961 NRGFKAGNMRRKLPGLVRLKCHSLFDLQVNSLQTVCTNYKILLQAYRHACVQLQP 1020
DB 961 NRGFKAGNMRRKLPGLVRLKCHSLFDLQVNSLQTVCTNYKILLQAYRHACVQLQP 1020
;
QY 1021 FHQVWKNTFTFLRVISDTASLCYSILKAKAGMSLGAKGAGPLPSEAVOMLCHQAFLL 1080
DB 1021 FHQVWKNTFTFLRVISDTASLCYSILKAKAGMSLGAKGAGPLPSEAVOMLCHQAFLL 1080
;
QY 1081 KLTRHRTVYVPLGSLRTAQTLRSKLPCTTTLTALEAAANPALPSDFKTILD 1132
DB 1081 KLTRHRTVYVPLGSLRTAQTLRSKLPCTTTLTALEAAANPALPSDFKTILD 1132

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RESULT 15

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US-10-388-578-2
; Sequence 2, Application US/10388578
; Publication No. US20030224411A1
; GENERAL INFORMATION:
;   APPLICANT: Geron Corporation
;   APPLICANT: Stanton, Lawrence
;   APPLICANT: Ralph, Brandenberger
;   APPLICANT: Joseph, Gold D.
;   APPLICANT: John, Irving
;   APPLICANT: Mandalam, Ramkumar
;   APPLICANT: Mok, Michael
;   APPLICANT: Shelton, Dawne
;   TITLE OF INVENTION: Genes that are Up- or Down-Regulated During Differentiation of H
;   TITLE OF INVENTION: Embryonic Stem Cells
;   FILE REFERENCE: 135/001
;   CURRENT APPLICATION NUMBER: US/10/388,578
;   CURRENT FILING DATE: 2003-03-13
;   NUMBER OF SEQ ID NOS: 139
;   SOFTWARE: Custom
;   SEQ ID NO 2
;   LENGTH: 1132
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-388-578-2
; Query Match 100.0%; Score 5961; DB 15; Length 1132;

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Best Local Similarity 100.0%; Pred. No. 0;		Matches 1132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
Qy	1	MPRAPRCRAVRSLLRSHYREVLP	1	MPRAPRCRAVRSLLRSHYREVLP
Db	1	MPRAPRCRAVRSLLRSHYREVLP	1	MPRAPRCRAVRSLLRSHYREVLP
Qy	61	DARPPAAPSPROVSKLKLVARVLQ	61	DARPPAAPSPROVSKLKLVARVLQ
Db	61	DARPPAAPSPROVSKLKLVARVLQ	61	DARPPAAPSPROVSKLKLVARVLQ
Qy	121	SYLNTVTDALRGSGAWGLLRVGGD	121	SYLNTVTDALRGSGAWGLLRVGGD
Db	121	SYLNTVTDALRGSGAWGLLRVGGD	121	SYLNTVTDALRGSGAWGLLRVGGD
Qy	181	ATQARPPPHASGPRRLGGERAWNS	181	ATQARPPPHASGPRRLGGERAWNS
Db	181	ATQARPPPHASGPRRLGGERAWNS	181	ATQARPPPHASGPRRLGGERAWNS
Qy	241	GAAPERTPVQGSWAHPGTRGSDRG	241	GAAPERTPVQGSWAHPGTRGSDRG
Db	241	GAAPERTPVQGSWAHPGTRGSDRG	241	GAAPERTPVQGSWAHPGTRGSDRG
Qy	301	RQHAGPSTSRPPRPMWDTCPVVAE	301	RQHAGPSTSRPPRPMWDTCPVVAE
Db	301	RQHAGPSTSRPPRPMWDTCPVVAE	301	RQHAGPSTSRPPRPMWDTCPVVAE
Qy	361	VETIFLGSRPMPGTPRRLPQRYQW	361	VETIFLGSRPMPGTPRRLPQRYQW
Db	361	VETIFLGSRPMPGTPRRLPQRYQW	361	VETIFLGSRPMPGTPRRLPQRYQW
Qy	421	PAAGVCAREKPGQSVAAPEEEDT	421	PAAGVCAREKPGQSVAAPEEEDT
Db	421	PAAGVCAREKPGQSVAAPEEEDT	421	PAAGVCAREKPGQSVAAPEEEDT
Qy	481	RHNERFLRNTKFTISLGHAKLSIQ	481	RHNERFLRNTKFTISLGHAKLSIQ
Db	481	RHNERFLRNTKFTISLGHAKLSIQ	481	RHNERFLRNTKFTISLGHAKLSIQ
Qy	541	LAKFLHMLMSVYVVELLRSFFVT	541	LAKFLHMLMSVYVVELLRSFFVT
Db	541	LAKFLHMLMSVYVVELLRSFFVT	541	LAKFLHMLMSVYVVELLRSFFVT
Qy	601	LSEAEVRQHREARPAALLSRFLPK	601	LSEAEVRQHREARPAALLSRFLPK
Db	601	LSEAEVRQHREARPAALLSRFLPK	601	LSEAEVRQHREARPAALLSRFLPK
Qy	661	LFSVLNVERARRPGLLGASVLG	661	LFSVLNVERARRPGLLGASVLG
Db	661	LFSVLNVERARRPGLLGASVLG	661	LFSVLNVERARRPGLLGASVLG
Qy	721	PODRLTEVIASIIKPNQYCVRRY	721	PODRLTEVIASIIKPNQYCVRRY
Db	721	PODRLTEVIASIIKPNQYCVRRY	721	PODRLTEVIASIIKPNQYCVRRY
Qy	781	QETSPLRDAVITEQSSSNEASSGL	781	QETSPLRDAVITEQSSSNEASSGL
Db	781	QETSPLRDAVITEQSSSNEASSGL	781	QETSPLRDAVITEQSSSNEASSGL
Qy	841	LCSLCYGDMENKLFAGIRDDGL	841	LCSLCYGDMENKLFAGIRDDGL
Db	841	LCSLCYGDMENKLFAGIRDDGL	841	LCSLCYGDMENKLFAGIRDDGL
Qy	901	RKTVNVFVEDEALGCTAFVQMP	901	RKTVNVFVEDEALGCTAFVQMP
Db	901	RKTVNVFVEDEALGCTAFVQMP	901	RKTVNVFVEDEALGCTAFVQMP
Qy	961	NRGFAGRNMRKLFVRLKCHSLF	961	NRGFAGRNMRKLFVRLKCHSLF
Db	961	NRGFAGRNMRKLFVRLKCHSLF	961	NRGFAGRNMRKLFVRLKCHSLF
Qy	1021	FHQQWKNPTFFLRVSDTASLCYS	1021	FHQQWKNPTFFLRVSDTASLCYS

Db	1021	FHQQVWKNPTFFLRVSDTASLCYSILKAKVAGWSLGA	1021	FHQQVWKNPTFFLRVSDTASLCYSILKAKVAGWSLGA
Qy	1081	KLTRHRVTYVPLIGSLRRTAQTLQSRKLPGTTLTALEA	1081	KLTRHRVTYVPLIGSLRRTAQTLQSRKLPGTTLTALEA
Db	1081	KLTRHRVTYVPLIGSLRRTAQTLQSRKLPGTTLTALEA	1081	KLTRHRVTYVPLIGSLRRTAQTLQSRKLPGTTLTALEA
RESULT 16				
US-10-602-441-2				
; Sequence 2, Application US/10602441				
; Publication No. US20040106128A1				
GENERAL INFORMATION:				
; APPLICANT: Geron Corporation				
; APPLICANT: Majumdar, Anish Sen				
; APPLICANT: Ferber, Iris				
; APPLICANT: Frolkis, Maria				
; APPLICANT: Wang, Zhuo				
; TITLE OF INVENTION: Cancer Vaccines Containing Xenogeneic Epitopes of Telomerase Re				
; FILE REFERENCE: 086/002				
; CURRENT APPLICATION NUMBER: US/10/602,441				
; CURRENT FILING DATE: 2003-06-24				
; PRIOR APPLICATION NUMBER: 60/393,295				
; PRIOR FILING DATE: 2002-06-27				
; NUMBER OF SEQ ID NOS: 12				
; SOFTWARE: PatentIn version 3.1				
; SEQ ID NO 2				
; LENGTH: 1132				
; TYPE: PRT				
; ORGANISM: Homo sapiens				
US-10-602-441-2				
Query Match 100.0%; Score 5961; DB 16; Length 1132;				
Best Local Similarity 100.0%; Pred. No. 0;				
Matches 1132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;				
Qy	1	MPRAPRCRAVRSLLRSHYREVLP	1	MPRAPRCRAVRSLLRSHYREVLP
Db	1	MPRAPRCRAVRSLLRSHYREVLP	1	MPRAPRCRAVRSLLRSHYREVLP
Qy	61	DARPPAAPSPROVSKLKLVARVLQ	61	DARPPAAPSPROVSKLKLVARVLQ
Db	61	DARPPAAPSPROVSKLKLVARVLQ	61	DARPPAAPSPROVSKLKLVARVLQ
Qy	121	SYLNTVTDALRGSGAWGLLRVGGD	121	SYLNTVTDALRGSGAWGLLRVGGD
Db	121	SYLNTVTDALRGSGAWGLLRVGGD	121	SYLNTVTDALRGSGAWGLLRVGGD
Qy	181	ATQARPPPHASGPRRLGGERAWNS	181	ATQARPPPHASGPRRLGGERAWNS
Db	181	ATQARPPPHASGPRRLGGERAWNS	181	ATQARPPPHASGPRRLGGERAWNS
Qy	241	GAAPERTPVQGSWAHPGTRGSDRG	241	GAAPERTPVQGSWAHPGTRGSDRG
Db	241	GAAPERTPVQGSWAHPGTRGSDRG	241	GAAPERTPVQGSWAHPGTRGSDRG
Qy	301	RQHAGPSTSRPPRPMWDTCPVVAE	301	RQHAGPSTSRPPRPMWDTCPVVAE
Db	301	RQHAGPSTSRPPRPMWDTCPVVAE	301	RQHAGPSTSRPPRPMWDTCPVVAE
Qy	361	VETIFLGSRPMPGTPRRLPQRYQW	361	VETIFLGSRPMPGTPRRLPQRYQW
Db	361	VETIFLGSRPMPGTPRRLPQRYQW	361	VETIFLGSRPMPGTPRRLPQRYQW
Qy	421	PAAGVCAREKPGQSVAAPEEEDT	421	PAAGVCAREKPGQSVAAPEEEDT
Db	421	PAAGVCAREKPGQSVAAPEEEDT	421	PAAGVCAREKPGQSVAAPEEEDT
Qy	481	RHNERFLRNTKFTISLGHAKLSIQ	481	RHNERFLRNTKFTISLGHAKLSIQ
Db	481	RHNERFLRNTKFTISLGHAKLSIQ	481	RHNERFLRNTKFTISLGHAKLSIQ
Qy	541	LAKFLHMLMSVYVVELLRSFFVT	541	LAKFLHMLMSVYVVELLRSFFVT

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541 LAKFLHLMVSVVVELESLRFFYVTTTFQKRLFFYKSVMSKIQIGIROHLKRVQLRE 600
601 LSEAEVRQREARPAALLTSRLREIPKPDGLRPVNMNDYVVGARTFRREKRAERLTISRVA 660
601 LSEAEVRQREARPAALLTSRLREIPKPDGLRPVNMNDYVVGARTFRREKRAERLTISRVA 660
661 LFSVLNYSERARRPGLLGASVLGDDIHRARWTFVLRVRAQDPPPELYFVKVDVDTGAYDTI 720
661 LFSVLNYSERARRPGLLGASVLGDDIHRARWTFVLRVRAQDPPPELYFVKVDVDTGAYDTI 720
721 PODRLTEVIASIIKPONTYCVRRYAVVQKAAHGHVRKAFKSHVSTLTDLPYMRQFVAHL 780
721 PODRLTEVIASIIKPONTYCVRRYAVVQKAAHGHVRKAFKSHVSTLTDLPYMRQFVAHL 780
781 QETSPLRDAVITEQSSSLNEASSGLFDVFLRFMCHHAVIRGKSVYQCOGIPGSGILSTL 840
781 QETSPLRDAVITEQSSSLNEASSGLFDVFLRFMCHHAVIRGKSVYQCOGIPGSGILSTL 840
841 LCSLCYGMENKLFAGIRRDGLLLRLVDDFLVTPHLLTHAKTFLRLTVRGVPEYGCVVNL 900
841 LCSLCYGMENKLFAGIRRDGLLLRLVDDFLVTPHLLTHAKTFLRLTVRGVPEYGCVVNL 900
901 RKTVMNFPVEDEALGCTAFVQMPAHGLFPWCGLLLDTRTLEVSQDYSSYARTSIRASLTF 960
901 RKTVMNFPVEDEALGCTAFVQMPAHGLFPWCGLLLDTRTLEVSQDYSSYARTSIRASLTF 960
961 NRGFKAGRNMRKLFVGLRLKCHSLFLLDQVNSLQVCTNIIKILLQAYRHACVQLP 1020
961 NRGFKAGRNMRKLFVGLRLKCHSLFLLDQVNSLQVCTNIIKILLQAYRHACVQLP 1020
1021 FHOQVWKNPTFFLRVSDTASLCYSILKAKNAGMSLGAKGAGPLPSEAVQMLCHQAFLL 1080
1021 FHOQVWKNPTFFLRVSDTASLCYSILKAKNAGMSLGAKGAGPLPSEAVQMLCHQAFLL 1080
1081 KLTRHRVTYVPLGLSLRTAQOLSRKLPCTTTLTALAAAANPALPSDFKTILD 1132
1081 KLTRHRVTYVPLGLSLRTAQOLSRKLPCTTTLTALAAAANPALPSDFKTILD 1132

RESULT 17
US-10-389-431-2
; Sequence 2, Application US/10389431
; Publication NO. US20040180347A1
; GENERAL INFORMATION:
; APPLICANT: Stanton, Lawrence
; APPLICANT: Ralph, Brandenberger
; APPLICANT: Joseph, Gold D.
; APPLICANT: John, Irving
; APPLICANT: Mandalam, Ramkumar
; APPLICANT: Mok, Michael
; TITLE OF INVENTION: A Marker System for Preparing and Characterizing High-Quality Hum
; TITLE OF INVENTION: Embryonic Stem Cells
; FILE REFERENCE: 135/002
; CURRENT APPLICATION NUMBER: US/10/389,431
; CURRENT FILING DATE: 2003-03-13
; NUMBER OF SEQ ID NOS: 100
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 1132
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-389-431-2

Query Match 100.0%; Score 5961; DB 16; Length 1132;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPAPRCRAVRSLLSHYREVLPATFVRRLGQWRLVQRGDPAAFRALVAQCLVCPW 60
DB 1 MPAPRCRAVRSLLSHYREVLPATFVRRLGQWRLVQRGDPAAFRALVAQCLVCPW 60
```

RESULT 18
 US-10-877-124-2
 ; Sequence 2, Application US/10877124
 ; Publication No. US20040242529A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Cech, Thomas R.
 ; Lingner, Joachim
 ; Nakamura, Toru
 ; Chapman, Karen B.
 ; Morin, Gregg B.
 ; Harley, Calvin B.
 ; Andrews, William H.
 ; TITLE OF INVENTION: Human Telomerase Catalytic Subunit
 ; NUMBER OF SEQUENCES: 727
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Townsend and Townsend and Crew LLP
 ; STREET: Two Embarcadero Center, Eighth Floor
 ; CITY: San Francisco
 ; STATE: California
 ; COUNTRY: USA
 ; ZIP: 94111-3834
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/10/877,124
 ; FILING DATE: 24-Jun-2004
 ; CLASSIFICATION: <Unknown>
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/432,503
 ; FILING DATE: 02-Nov-1999
 ; APPLICATION NUMBER: 08/974,549
 ; FILING DATE: <Unknown>
 ; APPLICATION NUMBER: US 08/844,419
 ; FILING DATE: 18-Apr-1997
 ; APPLICATION NUMBER: US 08/846,017
 ; FILING DATE: 25-Apr-1997
 ; APPLICATION NUMBER: US 08/851,843
 ; FILING DATE: 06-May-1997
 ; APPLICATION NUMBER: US 08/854,050
 ; FILING DATE: 09-May-1997
 ; APPLICATION NUMBER: US 08/911,312
 ; FILING DATE: 14-Aug-1997
 ; APPLICATION NUMBER: US 08/912,951
 ; FILING DATE: 14-Aug-1997
 ; APPLICATION NUMBER: US 08/915,503
 ; FILING DATE: 14-Aug-1997
 ; APPLICATION NUMBER: WO PCT/US97/17618
 ; FILING DATE: 01-Oct-1997
 ; APPLICATION NUMBER: WO PCT/US97/17885
 ; FILING DATE: 01-Oct-1997
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Apple, Randolph Ted
 ; REGISTRATION NUMBER: 36,429
 ; REFERENCE/DOCKET NUMBER: 015389-002610US
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (415) 576-0200
 ; TELEFAX: (415) 576-0300
 ; INFORMATION FOR SEQ ID NO: 2:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 1132 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 2:

Query Match 100.0%; Score 5961; DB 16; Length 1132;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MPRAPRCRAVRSLLRSHYREVLPLATFVRRLLGPOGWRLVQRGDPAAFPALVAOCLVCVPW	60
DB	1	MPRAPRCRAVRSLLRSHYREVLPLATFVRRLLGPOGWRLVQRGDPAAFPALVAOCLVCVPW	60
QY	61	DARPPPAAPSPROVSKLKLVARVLQRLCERGAKNVLAFFGALLDGGAGGPEAFTTSVR	120
DB	61	DARPPPAAPSPROVSKLKLVARVLQRLCERGAKNVLAFFGALLDGGAGGPEAFTTSVR	120
QY	121	SYLENTVTDALRGSGAWGLLLRRVGDVLLVHLARCALFVLVAPSCAYQVCGPPLYQLGA	180
DB	121	SYLENTVTDALRGSGAWGLLLRRVGDVLLVHLARCALFVLVAPSCAYQVCGPPLYQLGA	180
QY	181	ATQARPPPHASGPRRRRLGCERAWNHSYREAGVPLGLPAPGARRRGGSSASRSILPUPKRPR	240
DB	181	ATQARPPPHASGPRRRRLGCERAWNHSYREAGVPLGLPAPGARRRGGSSASRSILPUPKRPR	240
QY	241	GAAPERTPVGQGSWAHPGTRGPDSDRGFCVSPARPABEATSLGALSSTRHSPSVG	300
DB	241	GAAPERTPVGQGSWAHPGTRGPDSDRGFCVSPARPABEATSLGALSSTRHSPSVG	300
QY	301	RQHHAGPPSTSRPPMDTPCPPVYAEKTFELYSYGDKQLRPSFLSSLPSTGARRL	360
DB	301	RQHHAGPPSTSRPPMDTPCPPVYAEKTFELYSYGDKQLRPSFLSSLPSTGARRL	360
QY	361	VETIFLGSRRPMPGTPRRLPRLPORYQWMLPFLLELGNHAOCYPYGVLLKTHCPLRAAVT	420
DB	361	VETIFLGSRRPMPGTPRRLPRLPORYQWMLPFLLELGNHAOCYPYGVLLKTHCPLRAAVT	420
QY	421	PAAGVCAREKPGQSVAAPEBEDTPRRLVOLLROHSSSPWVYGFVRACLRLLVPGLWGS	480
DB	421	PAAGVCAREKPGQSVAAPEBEDTPRRLVOLLROHSSSPWVYGFVRACLRLLVPGLWGS	480
QY	481	RHNERFLRNTKTFISLGKHAKLISLQELTWQMSVRDCAWLRSPGVGCVPAAEHRLREI	540
DB	481	RHNERFLRNTKTFISLGKHAKLISLQELTWQMSVRDCAWLRSPGVGCVPAAEHRLREI	540
QY	541	LAKFLHMLMSYVVVLELRSFFYVTTTFQKNRLFYRKSVMSKLOSIGIROHLKRVQURE	600
DB	541	LAKFLHMLMSYVVVLELRSFFYVTTTFQKNRLFYRKSVMSKLOSIGIROHLKRVQURE	600
QY	601	LSEAEVRQHREARPAALLTSRLRFPKPDGLRPIVNMDYVVGARTPRRKRERLTLSRKA	660
DB	601	LSEAEVRQHREARPAALLTSRLRFPKPDGLRPIVNMDYVVGARTPRRKRERLTLSRKA	660
QY	661	LFSVLNYERARRPGLLGASVLGLDDIHRAWTFVLRVRAQDPPPELYFVKVDVTGAYDTI	720
DB	661	LFSVLNYERARRPGLLGASVLGLDDIHRAWTFVLRVRAQDPPPELYFVKVDVTGAYDTI	720
QY	721	PDRLTEVIASIIKPNQTYCVRRYAVVQAAHGHVRKAFKSHVSTLTDLQPMRQFVAHL	780
DB	721	PDRLTEVIASIIKPNQTYCVRRYAVVQAAHGHVRKAFKSHVSTLTDLQPMRQFVAHL	780
QY	781	QETSPLRDADVIEOSSSLNEASSGLFDVFLRFMCHAVRIRGKSVYVQCGIPQGSILSTL	840
DB	781	QETSPLRDADVIEOSSSLNEASSGLFDVFLRFMCHAVRIRGKSVYVQCGIPQGSILSTL	840
QY	841	LCSLCYGDMENKLPAGIRRDGLLLRLVDDFLLVTPHLTHAKTFLRTLVRGPEYGCNVNL	900
DB	841	LCSLCYGDMENKLPAGIRRDGLLLRLVDDFLLVTPHLTHAKTFLRTLVRGPEYGCNVNL	900
QY	901	RKTVNPFEVEALGGTAFVQMPAHLFPWCGLLDITLTTLEVSQSDSYASRTSTRASLTF	960
DB	901	RKTVNPFEVEALGGTAFVQMPAHLFPWCGLLDITLTTLEVSQSDSYASRTSTRASLTF	960
QY	961	NRGFKAGNMRKLFVGLRLKCHSLFDLQVNSLQTVCTNIIYKILLQAYRPHACVLQLP	1020
DB	961	NRGFKAGNMRKLFVGLRLKCHSLFDLQVNSLQTVCTNIIYKILLQAYRPHACVLQLP	1020
QY	1021	FHQQWKNPTFFLRVSDTASLCYSILKAKNAGMSLGAKGAGLPSPSAVOMLCHOAFLL	1080
DB	1021	FHQQWKNPTFFLRVSDTASLCYSILKAKNAGMSLGAKGAGLPSPSAVOMLCHOAFLL	1080
QY	1081	KLTRHRTVYVPLGLSLRTAQTQLSRKLPGTTLTALAAANPALPSDFKTLTD 1132	

1081 KLTRHRTVYVPLGLSLRTAQOLSRKLPCTTLTALEAANPALPSDFKTILD 1132

RESULT 19

US-10-877-022-2

Sequence 2, Application US/10877022

Publication NO. US20040247613A1

GENERAL INFORMATION:

APPLICANT: Cech, Thomas R.

Lingner, Joachim

Nakamura, Toru

Chapman, Karen B.

Morin, Gregg B.

Harley, Calvin B.

Andrews, William H.

TITLE OF INVENTION: Human Telomerase Catalytic Subunit

NUMBER OF SEQUENCES: 727

CORRESPONDENCE ADDRESS:

ADDRESSEE: Townsend and Townsend and Crew LLP

STREET: Two Embarcadero Center, Eighth Floor

CITY: San Francisco

STATE: California

COUNTRY: USA

ZIP: 94111-3834

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/877,022

FILING DATE: 24-Jun-2004

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/432,503

FILING DATE: 02-Nov-1999

APPLICATION NUMBER: 08/974,549

FILING DATE: <Unknown>

APPLICATION NUMBER: US 08/844,419

FILING DATE: 18-Apr-1997

APPLICATION NUMBER: US 08/846,017

FILING DATE: 25-Apr-1997

APPLICATION NUMBER: US 08/851,843

FILING DATE: 06-May-1997

APPLICATION NUMBER: US 08/854,050

FILING DATE: 09-May-1997

APPLICATION NUMBER: US 08/911,312

FILING DATE: 14-Aug-1997

APPLICATION NUMBER: US 08/912,951

FILING DATE: 14-Aug-1997

APPLICATION NUMBER: US 08/915,503

FILING DATE: 14-Aug-1997

APPLICATION NUMBER: WO PCT/US97/17618

FILING DATE: 01-Oct-1997

APPLICATION NUMBER: WO PCT/US97/17885

FILING DATE: 01-Oct-1997

ATTORNEY/AGENT INFORMATION:

NAME: Apple, Randolph Ted

REGISTRATION NUMBER: 36,429

REFERENCE/DOCKET NUMBER: 015389-002610US

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 576-0200

TELEFAX: (415) 576-0300

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 1132 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 2:

US-10-877-022-2

Query Match	100.0%	Score 5961	DB 16	Length 1132
Best Local Similarity	100.0%	Pred. No. 0		
Matches 1132	Conservative 0	Mismatches 0	Indels 0	Gaps 0
QY	1	MPRAPRCRAVRSLLRSHYREVLP	PLATFVRRLQPOCWRLLVORGD	PAAFRALVAQCLVCVPM 60
DB	1	MPRAPRCRAVRSLLRSHYREVLP	PLATFVRRLQPOCWRLLVORGD	PAAFRALVAQCLVCVPM 60
QY	61	DARPPPAAPSPROVSKLVELVAR	LQRLCERAKNVLAFGFALLDGA	RGPPEAFTTSVR 120
DB	61	DARPPPAAPSPROVSKLVELVAR	LQRLCERAKNVLAFGFALLDGA	RGPPEAFTTSVR 120
QY	121	SYLPNTVTDALRGSGAWGLLRV	GDVVLHLLARCALFVLVAPSCA	YVCGPPPLYQLGA 180
DB	121	SYLPNTVTDALRGSGAWGLLRV	GDVVLHLLARCALFVLVAPSCA	YVCGPPPLYQLGA 180
QY	181	ATOARPPPHASGPRRLGCERAW	HSVREAGVPLGLPAPGARRRGS	ASRSILPKRPRR 240
DB	181	ATOARPPPHASGPRRLGCERAW	HSVREAGVPLGLPAPGARRRGS	ASRSILPKRPRR 240
QY	241	GAAPEPERTVQOGSWAHPGRTR	GPSDRGFCVSPARPAEATSLEG	ALSGTRHSHPSVG 300
DB	241	GAAPEPERTVQOGSWAHPGRTR	GPSDRGFCVSPARPAEATSLEG	ALSGTRHSHPSVG 300
QY	301	RQHAGPPSTSRPRPMDTPCPPV	YAAETKHFLYSSGDKQLRPSFL	LLSLRPSLTGARL 360
DB	301	RQHAGPPSTSRPRPMDTPCPPV	YAAETKHFLYSSGDKQLRPSFL	LLSLRPSLTGARL 360
QY	361	VETIFLGSRPWMPGTPRLPLR	LQRYQWMRPLFLELLGNHAOC	PYGVLLKTHCPIRAAVT 420
DB	361	VETIFLGSRPWMPGTPRLPLR	LQRYQWMRPLFLELLGNHAOC	PYGVLLKTHCPIRAAVT 420
QY	421	PAAVCAREKPOGSAVAAPEED	TDPRRLVOLLROHSSPWQVY	GFVRACLRLLVPCLWGS 480
DB	421	PAAVCAREKPOGSAVAAPEED	TDPRRLVOLLROHSSPWQVY	GFVRACLRLLVPCLWGS 480
QY	481	RHNERRFLRNTKCFISLKGAK	LSLQELTWKMSVRDCAWLRSP	GVCGVPAAEHLRREI 540
DB	481	RHNERRFLRNTKCFISLKGAK	LSLQELTWKMSVRDCAWLRSP	GVCGVPAAEHLRREI 540
QY	541	LAKFLHLMMSVYVVELLSRFF	YVTTTQKNRLLFFYRKSVMS	KLOSIGIRQHLKRVOLRE 600
DB	541	LAKFLHLMMSVYVVELLSRFF	YVTTTQKNRLLFFYRKSVMS	KLOSIGIRQHLKRVOLRE 600
QY	601	LSEAEVROHREARPAALLTS	RLRFPKPDGLRPIVNMVDYV	VGARTPRRKRABRLSRVKA 660
DB	601	LSEAEVROHREARPAALLTS	RLRFPKPDGLRPIVNMVDYV	VGARTPRRKRABRLSRVKA 660
QY	661	LFSVLNYERARRPGLLGASV	LGDDIHRARWTFVLRVRAQD	PPPELYFVKVDVTGAYDTI 720
DB	661	LFSVLNYERARRPGLLGASV	LGDDIHRARWTFVLRVRAQD	PPPELYFVKVDVTGAYDTI 720
QY	721	PODLRTEVIASIIKPQNTY	CVRRYAVVQKAHGHVRKAFK	SHVSTLTDLQPMRQFVAHL 780
DB	721	PODLRTEVIASIIKPQNTY	CVRRYAVVQKAHGHVRKAFK	SHVSTLTDLQPMRQFVAHL 780
QY	781	QETSPLRDVAVTEQSSSINE	ASSGLFDVFLRPMCHHAVRI	RKSVVQCGIPOGSIISLTL 840
DB	781	QETSPLRDVAVTEQSSSINE	ASSGLFDVFLRPMCHHAVRI	RKSVVQCGIPOGSIISLTL 840
QY	841	LCSLCYGDMEKNLPAFIRRD	GLLRLVDDFLLVTPHLTHAK	TFTLRTLVRGVPEYCVVNL 900
DB	841	LCSLCYGDMEKNLPAFIRRD	GLLRLVDDFLLVTPHLTHAK	TFTLRTLVRGVPEYCVVNL 900
QY	901	RKTVMNPFVEDEALGGTAF	VQMPAHLFPWCGLLDTRTLE	VQSDYSYASRTSIRASLTF 960
DB	901	RKTVMNPFVEDEALGGTAF	VQMPAHLFPWCGLLDTRTLE	VQSDYSYASRTSIRASLTF 960
QY	961	NRGFKAGNMRKLPGLVLRK	CHSLFLDLQVNSLOTCTNIY	KILLLOAYRFHACVLQLP 1020
DB	961	NRGFKAGNMRKLPGLVLRK	CHSLFLDLQVNSLOTCTNIY	KILLLOAYRFHACVLQLP 1020
QY	1021	FHQQVWKNPFTFLRVISDT	ASILKAKNAGMSLGAGALP	SEAVQWLCHQAFLL 1080

Db 1021 FHQQWKNPTFLRVLSTASLCYSILKAKAGWSLGAAGPPLPSAVQWLCHQAPLL 1080
Qy 1081 KLTRHRTVTVPLGLSLRTAQQLSKLPGLTTLTALEAAANPALPSDFKTIILD 1132
Db 1081 KLTRHRTVTVPLGLSLRTAQQLSKLPGLTTLTALEAAANPALPSDFKTIILD 1132

RESULT 20

US-10-862-698-3

Sequence 3, Application US/10862698

Publication No. US20040253701A1

GENERAL INFORMATION:

APPLICANT: Morin, Gregg B.

Allsopp, Richard

Definho, Ronald

Greenberg, Roger

TITLE OF INVENTION: Mouse Telomerase Reverse Transcriptase

NUMBER OF SEQUENCES: 101

CORRESPONDENCE ADDRESS:

ADDRESSEE: Townsend and Townsend and Crew LLP

STREET: Two Embarcadero Center, Eighth Floor

CITY: San Francisco

STATE: California

COUNTRY: USA

ZIP: 94111-3834

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: IBM PC compatible

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/862,698

FILING DATE: 07-Jun-2004

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/042,460

FILING DATE: 16-MAR-1998

APPLICATION NUMBER: US 08/724,643

FILING DATE: 01-OCT-1996

APPLICATION NUMBER: US 08/844,419

FILING DATE: 18-APR-1997

APPLICATION NUMBER: US 08/846,017

FILING DATE: 25-APR-1997

APPLICATION NUMBER: US 08/851,843

FILING DATE: 06-MAY-1997

APPLICATION NUMBER: US 08/854,050

FILING DATE: 09-MAY-1997

APPLICATION NUMBER: US 08/911,312

FILING DATE: 14-AUG-1997

APPLICATION NUMBER: US 08/912,951

FILING DATE: 14-AUG-1997

APPLICATION NUMBER: US 08/915,503

FILING DATE: 14-AUG-1997

APPLICATION NUMBER: WO PCT/US97/17618

FILING DATE: 01-OCT-1997

APPLICATION NUMBER: WO PCT/US97/17885

FILING DATE: 01-OCT-1997

APPLICATION NUMBER: US 08/974,549

FILING DATE: 19-NOV-1997

APPLICATION NUMBER: US 08/974,584

FILING DATE: 19-NOV-1997

APPLICATION NUMBER: US 08/979,742

FILING DATE: 26-NOV-1997

ATTORNEY/AGENT INFORMATION:

NAME: Einhorn, Gregory P.

REGISTRATION NUMBER: 38,440

REFERENCE/DOCKET NUMBER: 015389-00311005

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 576-0200

TELEFAX: (415) 576-0300

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:

LENGTH: 1132 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
NAME/KEY: Protein
LOCATION: 1..1132
OTHER INFORMATION: /note= "human telomerase reverse
transcriptase (hTERT)"
SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-10-862-698-3

Query Match 100.0%; Score 5961; DB 16; Length 1132;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MPRAPRCRAVRSLLRSHYREVLPATFVRLGPGWRLVORGDPAAAFALVAQCILVCVPM 60

Db 1 MPRAPRCRAVRSLLRSHYREVLPATFVRLGPGWRLVORGDPAAAFALVAQCILVCVPM 60

Qy 61 DARPPPAAPSFQVSCCLKELVARVLQRLCERGAKNVLAFGFALLDGARGGPEAFTTSVR 120

Db 61 DARPPPAAPSFQVSCCLKELVARVLQRLCERGAKNVLAFGFALLDGARGGPEAFTTSVR 120

Qy 121 SYLPTNTVDALRGSGAWGLLLRRVGGDVLVHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180

Db 121 SYLPTNTVDALRGSGAWGLLLRRVGGDVLVHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180

Qy 181 ATQARPPPHASGPPRRRLGRCERAMNHSVREAGVPLGLPAGARRRGGSASRSLPLPKRRR 240

Db 181 ATQARPPPHASGPPRRRLGRCERAMNHSVREAGVPLGLPAGARRRGGSASRSLPLPKRRR 240

Qy 241 GAAPPERTPVQGSWAHPGRTGRGSDRGFCVSPARPABEATSLEGALSCTRHSHPVG 300

Db 241 GAAPPERTPVQGSWAHPGRTGRGSDRGFCVSPARPABEATSLEGALSCTRHSHPVG 300

Qy 301 RQHHAGPSTSRPPRPMDTTPCPVYAEKHLFYSYGDKQLRPSFLSSLPSLTGAARL 360

Db 301 RQHHAGPSTSRPPRPMDTTPCPVYAEKHLFYSYGDKQLRPSFLSSLPSLTGAARL 360

Qy 361 VETIFLGSRPWMPGTPRRLPRLPORYWQMRPLFLELGNHAQCYPVGLLTKHCPRAAVT 420

Db 361 VETIFLGSRPWMPGTPRRLPRLPORYWQMRPLFLELGNHAQCYPVGLLTKHCPRAAVT 420

Qy 421 PAAGVCAREKPPQGSVAAPAEEDTDPRLVQLLRQHSPPWQVYGVFVRACLRLVPPGLWGS 480

Db 421 PAAGVCAREKPPQGSVAAPAEEDTDPRLVQLLRQHSPPWQVYGVFVRACLRLVPPGLWGS 480

Qy 481 RHNERFLRNTKTFISLGKHAQLSLOBLTWQMSVRDCAWLRSPGVGCVPAAEHRLREI 540

Db 481 RHNERFLRNTKTFISLGKHAQLSLOBLTWQMSVRDCAWLRSPGVGCVPAAEHRLREI 540

Qy 541 LAKFLHLMMSVYVVELLRSFPYVTTTFQKURLFFYKRSVWSKLQSIGIROHLKRVQURE 600

Db 541 LAKFLHLMMSVYVVELLRSFPYVTTTFQKURLFFYKRSVWSKLQSIGIROHLKRVQURE 600

Qy 601 LSEAEVRQHREARPAALLTSRLRFIPKPDGLRPIVNMMDYVVGARTFRREKRAERLTSRKA 660

Db 601 LSEAEVRQHREARPAALLTSRLRFIPKPDGLRPIVNMMDYVVGARTFRREKRAERLTSRKA 660

Qy 661 LFSVLYNERARRPGLLGASVLGLDDIHRAMRTFVLVRAQDPPPELYFVKVDVTGAYDTI 720

Db 661 LFSVLYNERARRPGLLGASVLGLDDIHRAMRTFVLVRAQDPPPELYFVKVDVTGAYDTI 720

Qy 721 PQDLRLTEVIASIIKPONTYCVRRYAVVQKAAHGHVRKAFKSHVSTLTDLQPYMQFVAHL 780

Db 721 PQDLRLTEVIASIIKPONTYCVRRYAVVQKAAHGHVRKAFKSHVSTLTDLQPYMQFVAHL 780

Qy 781 QETSPLRDAVVIEQSSSINEASSGLFDVFLRFMCHHAVIRKGSYVQCGIPOQSILSTL 840

Db 781 QETSPLRDAVVIEQSSSINEASSGLFDVFLRFMCHHAVIRKGSYVQCGIPOQSILSTL 840

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QY 841 LCSLCYGDMMENKLFAGIRRDGLLLRLVDDFLVTPHLTHAKTFLRTLVRGVPYGCVMNL 900
DB 841 LCSLCYGDMMENKLFAGIRRDGLLLRLVDDFLVTPHLTHAKTFLRTLVRGVPYGCVMNL 900
QY 901 RKTIVNFPVEDEALGCTAFVQMPAHGLFPWCGLLLDTRILEVQSDYSSVARTSIRASLTF 960
DB 901 RKTIVNFPVEDEALGCTAFVQMPAHGLFPWCGLLLDTRILEVQSDYSSVARTSIRASLTF 960
QY 961 NRGFKAGNRMRKLFGLVRLKCHSLFELDLQVNSLQVCTNIIYKILLQAYRHACVQLQP 1020
DB 961 NRGFKAGNRMRKLFGLVRLKCHSLFELDLQVNSLQVCTNIIYKILLQAYRHACVQLQP 1020
QY 1021 FHOQVWKNPTFFLRVISTASLCYSILKAKNAGMSLGAKGAGPLPSEAVQMLCHOAFLL 1080
DB 1021 FHOQVWKNPTFFLRVISTASLCYSILKAKNAGMSLGAKGAGPLPSEAVQMLCHOAFLL 1080
QY 1081 KLTRHRVTYVPLGLSLRTAQOLSRKLPCTTLTAAEAANPALPSDFKTILD 1132
DB 1081 KLTRHRVTYVPLGLSLRTAQOLSRKLPCTTLTAAEAANPALPSDFKTILD 1132

RESULT 21
US-10-831-266-4
; Sequence 4, Application US/10831266
; Publication No. US20050003404A1
; GENERAL INFORMATION:
; APPLICANT: Rowley, Peter T.
; TITLE OF INVENTION: TELOMERASE INTERFERENCE
; FILE REFERENCE: A-71506-1/RFT/THR
; CURRENT APPLICATION NUMBER: US/10/831,266
; CURRENT FILING DATE: 2004-04-22
; PRIOR APPLICATION NUMBER: PCT/US 02/33065
; PRIOR FILING DATE: 2002-10-16
; PRIOR APPLICATION NUMBER: US 60/345,326
; PRIOR FILING DATE: 2001-10-22
; PRIOR APPLICATION NUMBER: US 60/359,196
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/383,195
; PRIOR FILING DATE: 2002-05-22
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4
; LENGTH: 1132
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-831-266-4

Query Match 100.0%; Score 5961; DB 17; Length 1132;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPRAPRCRAVRSLLRSHYEVLPATFVRRLGQGHVLRGDPAAFRALVAQCLVCVPM 60
DB 1 MPRAPRCRAVRSLLRSHYEVLPATFVRRLGQGHVLRGDPAAFRALVAQCLVCVPM 60

QY 61 DARPPAAPSFQVSCLEKELVARVLQRLCERGAKNVLAFCFALLDGCARGPPEAFTTSVR 120
DB 61 DARPPAAPSFQVSCLEKELVARVLQRLCERGAKNVLAFCFALLDGCARGPPEAFTTSVR 120

QY 121 SYLPTNTVDALRGSGAWGLLLRRVGDVLLHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180
DB 121 SYLPTNTVDALRGSGAWGLLLRRVGDVLLHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180

QY 181 ATQARPPPHASGPRRLRCERAWNSVREAGVPLGLPAPGARRGGSASRSPLPKRPRR 240
DB 181 ATQARPPPHASGPRRLRCERAWNSVREAGVPLGLPAPGARRGGSASRSPLPKRPRR 240

QY 241 GAAPERTPVGGSWAHGPRTRGSDRGFCVVSPPARPAEATSLGALSGRHSHPSVG 300
DB 241 GAAPERTPVGGSWAHGPRTRGSDRGFCVVSPPARPAEATSLGALSGRHSHPSVG 300

QY 301 ROHAGPPSTSRPPPDWTPCPVVAETHKFLYSSGDKQLRPSFLLSLRPSLTGARLL 360
DB 301 ROHAGPPSTSRPPPDWTPCPVVAETHKFLYSSGDKQLRPSFLLSLRPSLTGARLL 360
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DB 301 ROHAGPPSTSRPPPDWTPCPVVAETHKFLYSSGDKQLRPSFLLSLRPSLTGARLL 360
QY 361 VETIFLGSPWMPGTPRRLPRLPQRYWQMRPLFLELLGNHQAOCPCYGVLLKTHCPLRAAAT 420
DB 361 VETIFLGSPWMPGTPRRLPRLPQRYWQMRPLFLELLGNHQAOCPCYGVLLKTHCPLRAAAT 420
QY 421 PAAGVCAREKPGSGVAAPBEEDTDPRRLVQLLRQHSHPQVYGFVRACLRLRLLVPPGLWGS 480
DB 421 PAAGVCAREKPGSGVAAPBEEDTDPRRLVQLLRQHSHPQVYGFVRACLRLRLLVPPGLWGS 480
QY 481 RNEERFLRNTKCFISLGHAKLSLOELTKMSVRDCAMLRSPGVCVCPAAEHRUREEI 540
DB 481 RNEERFLRNTKCFISLGHAKLSLOELTKMSVRDCAMLRSPGVCVCPAAEHRUREEI 540
QY 541 LAKFLHMLMSVVVVELLSRFFVYVTTTFOKRLFFYRKSVWSKLSQSIGIRQHLKRVLRE 600
DB 541 LAKFLHMLMSVVVVELLSRFFVYVTTTFOKRLFFYRKSVWSKLSQSIGIRQHLKRVLRE 600
QY 601 LSEAEVRQHREARPAALLTSRLRFIPKPDGLRPIVNMDDYVVGARTFRREKRAERLTSRVKA 660
DB 601 LSEAEVRQHREARPAALLTSRLRFIPKPDGLRPIVNMDDYVVGARTFRREKRAERLTSRVKA 660
QY 661 LFSVLNYERARRPGLIGASVLGDDIHRARWTFVLRAQDDPPPELYFVKVDVTGAYDTI 720
DB 661 LFSVLNYERARRPGLIGASVLGDDIHRARWTFVLRAQDDPPPELYFVKVDVTGAYDTI 720
QY 721 PODRLTEVIASIIKPQNTYCVRRYAVVQAAHGHVKAFKSHVSTLTDLPYMRQFVAHL 780
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QY 781 QETSPLRDAVIEQSSSLNEASSGLFVFLRPFMCHAVRIRKSVYQCGIPQGSILSTL 840
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QY 841 LCSLCYGDMMENKLFAGIRRDGLLLRLVDDFLVTPHLTHAKTFLRTLVRGVPYGCVMNL 900
DB 841 LCSLCYGDMMENKLFAGIRRDGLLLRLVDDFLVTPHLTHAKTFLRTLVRGVPYGCVMNL 900
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QY 1021 FHOQVWKNPTFFLRVISTASLCYSILKAKNAGMSLGAKGAGPLPSEAVQMLCHOAFLL 1080
DB 1021 FHOQVWKNPTFFLRVISTASLCYSILKAKNAGMSLGAKGAGPLPSEAVQMLCHOAFLL 1080
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DB 1081 KLTRHRVTYVPLGLSLRTAQOLSRKLPCTTLTAAEAANPALPSDFKTILD 1132
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RESULT 22

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US-10-492-034-2
; Sequence 2, Application US/10492034
; Publication No. US20050008621A1
; GENERAL INFORMATION:
; APPLICANT: Kirkland, James
; APPLICANT: Tchkonla, Tamara
; TITLE OF INVENTION: PREADIPOCYTE CELL STRAINS AND USES THEREFORE
; FILE REFERENCE: BUI-011US
; CURRENT APPLICATION NUMBER: US/10/492,034
; CURRENT FILING DATE: 2004-04-06
; PRIOR APPLICATION NUMBER: PCT/US02/31635
; PRIOR FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: 60/327650
; PRIOR FILING DATE: 2001-10-06
; PRIOR APPLICATION NUMBER: 60/327651
; PRIOR FILING DATE: 2001-10-06
; NUMBER OF SEQ ID NOS: 12
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; SOFTWARE: FastSeq for Windows Version 4.0															
; SEQ ID NO 2															
; LENGTH: 1132															
; TYPE: PRT															
; ORGANISM: Homo sapiens															
US-10-492-034-2															
Query Match 100.0%; Score 5961; DB 17; Length 1132;															
Best Local Similarity 100.0%; Pred. No. 0;															
Matches 1132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;															
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Db	1	MPRAPRCRAVRSLLRSHYREVLP	PLATFVRR	LGPOGWR	LVRQ	GDPAA	FRALVAQ	CLVCVPW	60						
QY	61	DARPPPAAPSRQVSC	LKELVAR	VLQRC	ERGA	KNVLA	FGFALL	DGARGG	PEAFTTSVR 120						
Db	61	DARPPPAAPSRQVSC	LKELVAR	VLQRC	ERGA	KNVLA	FGFALL	DGARGG	PEAFTTSVR 120						
QY	121	SYLNTVTDALRGSGA	WGLLRV	GGDVL	VHLL	ARCAL	FVLV	APSCAY	QVCGPPIYLGA 180						
Db	121	SYLNTVTDALRGSGA	WGLLRV	GGDVL	VHLL	ARCAL	FVLV	APSCAY	QVCGPPIYLGA 180						
QY	181	ATQARPPPHASGPRRL	GCERAWNHS	VREAG	VPGL	PAGARR	RGSGAS	RSIPLPKRRR	240						
Db	181	ATQARPPPHASGPRRL	GCERAWNHS	VREAG	VPGL	PAGARR	RGSGAS	RSIPLPKRRR	240						
QY	241	GAAPPERTPVQGS	WAHPGTR	GRPSDR	GCFC	VVSPAR	PAEATS	LEGALS	GTRHSHPSVG 300						
Db	241	GAAPPERTPVQGS	WAHPGTR	GRPSDR	GCFC	VVSPAR	PAEATS	LEGALS	GTRHSHPSVG 300						
QY	301	RQHAGPPSTSRPR	PMDT	PCPV	YAE	TKHFL	YSSG	DEQ	LRSPLSSLTGARRL 360						
Db	301	RQHAGPPSTSRPR	PMDT	PCPV	YAE	TKHFL	YSSG	DEQ	LRSPLSSLTGARRL 360						
QY	361	VETIFLGS	RPMWPGT	PRRL	PLPQ	RYWQ	MRFL	FLELL	GNHAQCPYGVLLKTHCPLRAAVT 420						
Db	361	VETIFLGS	RPMWPGT	PRRL	PLPQ	RYWQ	MRFL	FLELL	GNHAQCPYGVLLKTHCPLRAAVT 420						
QY	421	PAAGVCAREK	POGSA	VAPEE	DDT	PRRL	VQLLR	QHSSP	QVYGFVRACLRRLVPPGLWGS 480						
Db	421	PAAGVCAREK	POGSA	VAPEE	DDT	PRRL	VQLLR	QHSSP	QVYGFVRACLRRLVPPGLWGS 480						
QY	481	RHNERFL	NTKFT	ISLGH	AKLS	LOEL	TWKMS	VRDC	AWLRSPGVGCPVAAEHLRBEI 540						
Db	481	RHNERFL	NTKFT	ISLGH	AKLS	LOEL	TWKMS	VRDC	AWLRSPGVGCPVAAEHLRBEI 540						
QY	541	LAKFLH	WLSV	VVVEL	LSR	FFV	YTTT	FOKN	ELFFYRKSVM	SKLOSIGIROHLKRVQRE 600					
Db	541	LAKFLH	WLSV	VVVEL	LSR	FFV	YTTT	FOKN	ELFFYRKSVM	SKLOSIGIROHLKRVQRE 600					
QY	601	LSEAEVRQ	HREAR	PALL	TSRL	FI	PKP	DGLR	I	VNM	DYVVGARTFRREKRAERLT	SRVKA 660			
Db	601	LSEAEVRQ	HREAR	PALL	TSRL	FI	PKP	DGLR	I	VNM	DYVVGARTFRREKRAERLT	SRVKA 660			
QY	661	LFSVLNER	ARRP	GLLG	ASV	GLDD	I	HRA	WRT	FVL	RAQDPPPELYFKVDVTGAYDTI 720				
Db	661	LFSVLNER	ARRP	GLLG	ASV	GLDD	I	HRA	WRT	FVL	RAQDPPPELYFKVDVTGAYDTI 720				
QY	721	PODLTE	VIASII	KPQ	NTY	CVRR	YAV	VQAA	HGHV	KAFKSHVSTLTDLPQYMRQFVAHL 780					
Db	721	PODLTE	VIASII	KPQ	NTY	CVRR	YAV	VQAA	HGHV	KAFKSHVSTLTDLPQYMRQFVAHL 780					
QY	781	QETSLR	DAV	WIEQ	SSS	NEA	SSGL	FDV	FLRF	PMCH	HAVRIRGKSVYVQCGIPQGSILSTL 840				
Db	781	QETSLR	DAV	WIEQ	SSS	NEA	SSGL	FDV	FLRF	PMCH	HAVRIRGKSVYVQCGIPQGSILSTL 840				
QY	841	LCSLC	YGD	MEN	KL	PAG	IR	DDG	LLRL	VDD	FLVTPHLTHAKTFLRTLVRGPEYCCVNL 900				
Db	841	LCSLC	YGD	MEN	KL	PAG	IR	DDG	LLRL	VDD	FLVTPHLTHAKTFLRTLVRGPEYCCVNL 900				
QY	901	RKT	VNFP	VE	DE	AL	GGT	AF	VQ	MPA	HGLFPW	CGLLDTRTLE	VQSDYS	SSVARTS	IRASLTFF 960

QY 421 PAAGVAREKPKQSGVAAPBEEDTDPRLVOLLRQHSHPQVYFVRACLRLRVPGLWGS 480
Db 421 PAAGVAREKPKQSGVAAPBEEDTDPRLVOLLRQHSHPQVYFVRACLRLRVPGLWGS 480
QY 481 RHNERFLRNTKFIISLGHAKLSLOBLTWKMSVRDCAMLRSPGVGCVPAAEHRLREI 540
Db 481 RHNERFLRNTKFIISLGHAKLSLOBLTWKMSVRDCAMLRSPGVGCVPAAEHRLREI 540
QY 541 LAKFLHMLSVYVVELLRSPFFVYTTETTFQKNRFFYRKSVWSKLSQIGIRQHLKRVQRE 600
Db 541 LAKFLHMLSVYVVELLRSPFFVYTTETTFQKNRFFYRKSVWSKLSQIGIRQHLKRVQRE 600
QY 601 LSAEVRQREARPAALLTSRLRPIPKPDGLRPIVNMDDYVVGARTFRREKRAELTSRVKA 660
Db 601 LSAEVRQREARPAALLTSRLRPIPKPDGLRPIVNMDDYVVGARTFRREKRAELTSRVKA 660
QY 661 LFSVLNVERARRPGLGASVIGLDDIHRARWRTFLVRAQDPPPELYFVKVDVTGAYDTI 720
Db 661 LFSVLNVERARRPGLGASVIGLDDIHRARWRTFLVRAQDPPPELYFVKVDVTGAYDTI 720
QY 721 PODRLTEVIASIIKPNQTYCVRYAVVQKAAHGHVKAFAKSHVSTLTDLQPYMRQFVAHL 780
Db 721 PODRLTEVIASIIKPNQTYCVRYAVVQKAAHGHVKAFAKSHVSTLTDLQPYMRQFVAHL 780
QY 781 QETSPLRDVAVIEQSSSLNEASGLFDVFLRFMCHHAVIRGKSVYVQCQGIPOQSILSTL 840
Db 781 QETSPLRDVAVIEQSSSLNEASGLFDVFLRFMCHHAVIRGKSVYVQCQGIPOQSILSTL 840
QY 841 LCSLCYGDENKLFAGIRDDGLLLRLVDDFLVTPHLTHAKTFLRLTVRGVPEYGCVNL 900
Db 841 LCSLCYGDENKLFAGIRDDGLLLRLVDDFLVTPHLTHAKTFLRLTVRGVPEYGCVNL 900
QY 901 RKTVMNFPVEDEALGTAFAVQMPAHGLFPWCGLLDTRILEVQSDYSSVARTSIRASLTF 960
Db 901 RKTVMNFPVEDEALGTAFAVQMPAHGLFPWCGLLDTRILEVQSDYSSVARTSIRASLTF 960
QY 961 NRGFKAGRNMRKLFVGLRLKCHSLFDLDQVNSLQTVCTNIYKILLQAYRFHACVQLP 1020
Db 961 NRGFKAGRNMRKLFVGLRLKCHSLFDLDQVNSLQTVCTNIYKILLQAYRFHACVQLP 1020
QY 1021 FHOQVWKNPTFLRVISDTASLCYSILKAKNAGMSLGAKGAGPLPSEAVQMLCHQAFLL 1080
Db 1021 FHOQVWKNPTFLRVISDTASLCYSILKAKNAGMSLGAKGAGPLPSEAVQMLCHQAFLL 1080
QY 1081 KLTRHRVTYVPLGLSLRTAQTLQSLKPLGTTITALEAANPALPSDFKTILD 1132
Db 1081 KLTRHRVTYVPLGLSLRTAQTLQSLKPLGTTITALEAANPALPSDFKTILD 1132

RESULT 24
US-10-877-146-2
; Sequence 2, Application US/10877146
; Publication No. US20050013825A1
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; ; Linsinger, Joachim
; ; Nakamura, Toru
; ; Chapman, Karen B.
; ; Morin, Gregg B.
; ; Harley, Calvin B.
; ; Andrews, William H.
; TITLE OF INVENTION: Human Telomerase Catalytic Subunit
; NUMBER OF SEQUENCES: 727
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; City: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/877,146
FILING DATE: 24-Jun-2004
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/432,503
FILING DATE: 02-Nov-1999
APPLICATION NUMBER: 08/974,549
FILING DATE: <Unknown>
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-Apr-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-Apr-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-May-1997
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-May-1997
APPLICATION NUMBER: US 08/911,312
FILING DATE: 14-Aug-1997
APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-Aug-1997
APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-Aug-1997
APPLICATION NUMBER: WO PCT/US97/17618
FILING DATE: 01-Oct-1997
APPLICATION NUMBER: WO PCT/US97/17885
FILING DATE: 01-Oct-1997
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph Ted
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002610US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1132 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-877-146-2
Query Match 100.0%; Score 5961; DB 17; Length 1132;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MPAPRCRAVRSLRSHYREVLPATFVRLPGQWRLVORGDPAAFRALVAQCLVCVPW 60
Db 1 MPAPRCRAVRSLRSHYREVLPATFVRLPGQWRLVORGDPAAFRALVAQCLVCVPW 60
QY 61 DARPPPAAPSFQVSCSLKELVARVLQRLCERCAKVNLAFFGALLDGAAGPPEAFTTSVR 120
Db 61 DARPPPAAPSFQVSCSLKELVARVLQRLCERCAKVNLAFFGALLDGAAGPPEAFTTSVR 120
QY 121 SYLPTNTVDALRGSGAWGLLLRVGDDVLLHLLARCALFVLVAPSCAYVCGPPLYQLGA 180
Db 121 SYLPTNTVDALRGSGAWGLLLRVGDDVLLHLLARCALFVLVAPSCAYVCGPPLYQLGA 180
QY 181 ATQARPPPHASGPRRLRCERAWNHSVREAGVPLGLPAPGARRRGSASRSLPLKPRPR 240
Db 181 ATQARPPPHASGPRRLRCERAWNHSVREAGVPLGLPAPGARRRGSASRSLPLKPRPR 240
QY 241 GAAPEPPTVQGSWAHPGTRGSDRGFCVWSPARPAEEATSLEGALSGTRHSHPSVG 300
Db 241 GAAPEPPTVQGSWAHPGTRGSDRGFCVWSPARPAEEATSLEGALSGTRHSHPSVG 300
QY 301 RQHAGPPTSRPPRPWDTPCPVVAETKHFYSSGDKQLRPPSFLLSLRSLTGARRL 360
Db 301 RQHAGPPTSRPPRPWDTPCPVVAETKHFYSSGDKQLRPPSFLLSLRSLTGARRL 360

Db 961 NRGFKAGNRMRKLFVLRKCHSLFLDLQVNSLQTVCTNYIKILLQAYRFHACVQLQP 1020
Qy 1021 FHQQVWKNPTFFLRVSDTASLCYSILKAKNAGMSLGAKGAGPLPSEAVQMLCHQAFLL 1080
Db 1021 FHQQVWKNPTFFLRVSDTASLCYSILKAKNAGMSLGAKGAGPLPSEAVQMLCHQAFLL 1080
Qy 1081 KLTRHRTVTVPLGLSLRTHAQOLSRKLPOTTTTALAEAAANPALPSDFKTILD 1132
Db 1081 KLTRHRTVTVPLGLSLRTHAQOLSRKLPOTTTTALAEAAANPALPSDFKTILD 1132

RESULT 26
US-10-918-739-2
; Sequence 2, Application US/10918739
; Publication No. US20050054093A1
; GENERAL INFORMATION:
; APPLICANT: Haas, Martin
; TITLE OF INVENTION: MULTIPOTENT AMNIOTIC FETAL STEM CELLS
; FILE REFERENCE: HAAS.004A
; CURRENT APPLICATION NUMBER: US/10/918,739
; CURRENT FILING DATE: 2004-08-13
; PRIOR APPLICATION NUMBER: 60/495,437
; PRIOR FILING DATE: 2003-08-14
; PRIOR APPLICATION NUMBER: 60/495,513
; PRIOR FILING DATE: 2003-08-14
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 1132
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-918-739-2

Query Match 100.0%; Score 5961; DB 17; Length 1132;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MPRAPCRRAVRSLRSHRYEVLPATFVRRLGPGQWRLVQRGDPAAFRALVAQCLVCPW 60
Db 1 MPRAPCRRAVRSLRSHRYEVLPATFVRRLGPGQWRLVQRGDPAAFRALVAQCLVCPW 60

Qy 61 DARPPAPAPSPQVSCLEKELVARVLCRCERGAKNVLPAGFALLDGAAGGPPPEATTSVR 120
Db 61 DARPPAPAPSPQVSCLEKELVARVLCRCERGAKNVLPAGFALLDGAAGGPPPEATTSVR 120

Qy 121 SYLPTNTVDALGSGANGLLRVRGDDVLVHLLARCALFVLVAPSCAYQVCGPPPLYQLGA 180
Db 121 SYLPTNTVDALGSGANGLLRVRGDDVLVHLLARCALFVLVAPSCAYQVCGPPPLYQLGA 180

Qy 181 ATQARPPPHASGPRRLGGERAWNHSVREAGVPLGLPAGARRRGSASRSLPLKPRR 240
Db 181 ATQARPPPHASGPRRLGGERAWNHSVREAGVPLGLPAGARRRGSASRSLPLKPRR 240

Qy 241 GAAPPERTPVQGSWAHPGRTGSDRGFCVVS PARPAEATSLEGALSGTRHSHPSVG 300
Db 241 GAAPPERTPVQGSWAHPGRTGSDRGFCVVS PARPAEATSLEGALSGTRHSHPSVG 300

Qy 301 ROHAGPSTSPRPRTDTPCPVVAETHKFLYSSGDKQLRPSFLSLRSLTGARRL 360
Db 301 ROHAGPSTSPRPRTDTPCPVVAETHKFLYSSGDKQLRPSFLSLRSLTGARRL 360

Qy 361 VETIFLGRPMWPGTPRRLPRLPQRYWQMRPLFELLGNHACOPYGVLLKTHCPRAAVT 420
Db 361 VETIFLGRPMWPGTPRRLPRLPQRYWQMRPLFELLGNHACOPYGVLLKTHCPRAAVT 420

Qy 421 PAAGVCAREKPGQSVAAPEEEDTPRRLVQLLRQHSSPMQVYGFVRACLRRLVPPGLMGS 480
Db 421 PAAGVCAREKPGQSVAAPEEEDTPRRLVQLLRQHSSPMQVYGFVRACLRRLVPPGLMGS 480

Qy 481 RHNERFLRNTKKFISLGHAKLSLOELTWKMSVRDCAWLRRSPGVCGVPAAEHLRBEI 540
Db 481 RHNERFLRNTKKFISLGHAKLSLOELTWKMSVRDCAWLRRSPGVCGVPAAEHLRBEI 540

Qy 541 LAKFLHLMSSVVVVELLSFFVYVTTTTFQKNLFFYRKSVMSKLSQSIGIROHLKRVQRE 600
Db 541 LAKFLHLMSSVVVVELLSFFVYVTTTTFQKNLFFYRKSVMSKLSQSIGIROHLKRVQRE 600

Qy 601 LSEAEVROHREARPAALLTSRLRFIPKPGRLPIVMDYVVGARTTFRKRAERLTSRVKA 660
Db 601 LSEAEVROHREARPAALLTSRLRFIPKPGRLPIVMDYVVGARTTFRKRAERLTSRVKA 660

Qy 661 LFSVLNYSERARRPGLLGASVLGLDDIHRARWTFVLRVAQDPPPELYFVKVDVTGAYDTI 720
Db 661 LFSVLNYSERARRPGLLGASVLGLDDIHRARWTFVLRVAQDPPPELYFVKVDVTGAYDTI 720

Qy 721 PODRLTEVIASIIKPONTYCVRRYAVVQAAHGHVRKAPKSHVSTLTDLPQYMRQFAHL 780
Db 721 PODRLTEVIASIIKPONTYCVRRYAVVQAAHGHVRKAPKSHVSTLTDLPQYMRQFAHL 780

Qy 781 QETSLRDAVVIQSSSLNEASSGLFDVFLRFMCHAVRIKSVYVOCQIPOGSILSTL 840
Db 781 QETSLRDAVVIQSSSLNEASSGLFDVFLRFMCHAVRIKSVYVOCQIPOGSILSTL 840

Qy 841 LCSLCYGDWENKLPAGIRRDGLLLRLVDDFLVTPHLTHAKTFLRTLVRGVEYGCVVNL 900
Db 841 LCSLCYGDWENKLPAGIRRDGLLLRLVDDFLVTPHLTHAKTFLRTLVRGVEYGCVVNL 900

Qy 901 RKTVVNPFVEDEALGGTAFVQMPAHGLFPWCGLLDTRTLLEVQSDYSSYARTSIRASLTF 960
Db 901 RKTVVNPFVEDEALGGTAFVQMPAHGLFPWCGLLDTRTLLEVQSDYSSYARTSIRASLTF 960

Qy 961 NRGFKAGNRMRKLPVLRKCHSLFLDLQVNSLQTVCTNYIKILLQAYRFHACVQLQP 1020
Db 961 NRGFKAGNRMRKLPVLRKCHSLFLDLQVNSLQTVCTNYIKILLQAYRFHACVQLQP 1020

Qy 1021 FHQQVWKNPTFFLRVSDTASLCYSILKAKNAGMSLGAKGAGPLPSEAVQMLCHQAFLL 1080
Db 1021 FHQQVWKNPTFFLRVSDTASLCYSILKAKNAGMSLGAKGAGPLPSEAVQMLCHQAFLL 1080

Qy 1081 KLTRHRTVTVPLGLSLRTHAQOLSRKLPOTTTTALAEAAANPALPSDFKTILD 1132
Db 1081 KLTRHRTVTVPLGLSLRTHAQOLSRKLPOTTTTALAEAAANPALPSDFKTILD 1132

RESULT 27
US-10-637-443-2
; Sequence 2, Application US/10637443
; Publication No. US20050070492A1
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; Lingner, Joachim
; Nakamura, Toru
; Chapman, Karen B.
; Morin, Gregg B.
; Harley, Calvin B.
; Andrews, William H.
; TITLE OF INVENTION: Antisense Compositions for Detecting and
; Inhibiting Telomerase Reverse Transcriptase
; NUMBER OF SEQUENCES: 72
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/637,443
; FILING DATE: 08-Aug-2003
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/953,052
FILING DATE: 14-Sep-2001
APPLICATION NUMBER: 09/052,919
FILING DATE: <Unknown>
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/911,312
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/974,549
FILING DATE: 19-NOV-1997
APPLICATION NUMBER: US 08/974,584
FILING DATE: 19-NOV-1997
APPLICATION NUMBER: WO PCT/US97/17618
FILING DATE: 01-OCT-1997
APPLICATION NUMBER: WO PCT/US97/17885
FILING DATE: 01-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Parent, Annette S.
REGISTRATION NUMBER: 42,058
REFERENCE/DOCKET NUMBER: 015389-00360005
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1132 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-637-443-2
Query Match 100.0%; Score 5963; DB 17; Length 1132;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MPAPRCRAVRSLLRSHYREVLPVPLATFVRRLLGPOGWRLVQRGDPAAPRALVAQCILVCVPW 60
DB 1 MPAPRCRAVRSLLRSHYREVLPVPLATFVRRLLGPOGWRLVQRGDPAAPRALVAQCILVCVPW 60
QY 61 DARPPAAPSPRQVSKLKVRLVQLRCERGAKNVLAFFGALLDGAAGGPPPEAFTTSVR 120
DB 61 DARPPAAPSPRQVSKLKVRLVQLRCERGAKNVLAFFGALLDGAAGGPPPEAFTTSVR 120
QY 121 SYLPTNTVDALRGSAWGLLRVDDVLLVHLLARCALFVLVAPSCAYQVCGPLYQLGA 180
DB 121 SYLPTNTVDALRGSAWGLLRVDDVLLVHLLARCALFVLVAPSCAYQVCGPLYQLGA 180
QY 181 ATQARPPHAGSPRRRLCERAWNHSVREAGVPLGLPAPGARRGGASRSLLPLPKRPRR 240
DB 181 ATQARPPHAGSPRRRLCERAWNHSVREAGVPLGLPAPGARRGGASRSLLPLPKRPRR 240
QY 241 GAAPEPERTVQGSWAHPGRTGSDRGFCVSPAPAEATSLGEGALSGTRHSHPSVG 300
DB 241 GAAPEPERTVQGSWAHPGRTGSDRGFCVSPAPAEATSLGEGALSGTRHSHPSVG 300
QY 301 RQHAGPSTSEPPRPWTPCPVVAETKHYLYSSGDKQLRPSFLLSLPSLTGARRL 360
DB 301 RQHAGPSTSEPPRPWTPCPVVAETKHYLYSSGDKQLRPSFLLSLPSLTGARRL 360
QY 361 VETIFLGRPWMPGTFRLLPRLPQRYQWMPRLFLELLGNHAQCPYGVLLKTHCPRAAVT 420
DB 361 VETIFLGRPWMPGTFRLLPRLPQRYQWMPRLFLELLGNHAQCPYGVLLKTHCPRAAVT 420

QY 421 PAAGVCAREXPQGSVAAPBEEDTDPRRLVQLLRHSSSPWQYGVFRACLRRLVPPGLMGS 480
DB 421 PAAGVCAREXPQGSVAAPBEEDTDPRRLVQLLRHSSSPWQYGVFRACLRRLVPPGLMGS 480
QY 481 RHNERREFLRNTKKFISLGGHAKLSLOELTWKMSVRDCAWLRSPGVCVPAAEHRLREEI 540
DB 481 RHNERREFLRNTKKFISLGGHAKLSLOELTWKMSVRDCAWLRSPGVCVPAAEHRLREEI 540
QY 541 LAKFLHLMMSVYVVELLRSFFYVTTTFFQKNRLFYFKSVMSKLSQICIRQHLKRVOLRE 600
DB 541 LAKFLHLMMSVYVVELLRSFFYVTTTFFQKNRLFYFKSVMSKLSQICIRQHLKRVOLRE 600
QY 601 LSEAEVRQHREARPAALITSLRFLPKDPGLRPIVNM DYVVGARTFRREKRAERLTSRVKA 660
DB 601 LSEAEVRQHREARPAALITSLRFLPKDPGLRPIVNM DYVVGARTFRREKRAERLTSRVKA 660
QY 661 LFSVLNYERARRPGLLGASVLGLDDIHRAMRTFVLVRAODPPPELYFVKVDVTGAYDTI 720
DB 661 LFSVLNYERARRPGLLGASVLGLDDIHRAMRTFVLVRAODPPPELYFVKVDVTGAYDTI 720
QY 721 PQDLTEVIASIIKPQNTYCVRRYAVVQKAAHGHVRKAFKSHVSTLTDLOPYMQFVAHL 780
DB 721 PQDLTEVIASIIKPQNTYCVRRYAVVQKAAHGHVRKAFKSHVSTLTDLOPYMQFVAHL 780
QY 781 QETSPLRDADVIEQSSSLNEASGLFDVFLRFMCHHVRIRGKSYVQCQGIPOQSILSTL 840
DB 781 QETSPLRDADVIEQSSSLNEASGLFDVFLRFMCHHVRIRGKSYVQCQGIPOQSILSTL 840
QY 841 LCSLCYGD MENKLPAGIRRDGLLRLVDDFLVTPHLLTHAKTFLRTLVRGVPEYGCVNVL 900
DB 841 LCSLCYGD MENKLPAGIRRDGLLRLVDDFLVTPHLLTHAKTFLRTLVRGVPEYGCVNVL 900
QY 901 RKTVVNFPVEDEALGGTAFVQMPAHGLFPWCGLLDTRTLEVVQSDYSYARTSIRASLTF 960
DB 901 RKTVVNFPVEDEALGGTAFVQMPAHGLFPWCGLLDTRTLEVVQSDYSYARTSIRASLTF 960
QY 961 NRGFKAGRNMRRLFGVLRKCHSLFLDLQVNSLQTVCTNIYKILLQAVRFHACVLOLP 1020
DB 961 NRGFKAGRNMRRLFGVLRKCHSLFLDLQVNSLQTVCTNIYKILLQAVRFHACVLOLP 1020
QY 1021 FHOQVKNPTFFLRVISDTASLCYSILKAKNAGSLGAKGAAGPLPSEAVOMLCHQAEFL 1080
DB 1021 FHOQVKNPTFFLRVISDTASLCYSILKAKNAGSLGAKGAAGPLPSEAVOMLCHQAEFL 1080
QY 1081 KLTFHRVTVYVPLLGSLRTAQTLRSKLPGLTTLTALEAAANPALPSDFKTILD 1132
DB 1081 KLTFHRVTVYVPLLGSLRTAQTLRSKLPGLTTLTALEAAANPALPSDFKTILD 1132

RESULT 28
US-10-490-143A-19
; Sequence 19, Application US/10490143A
; Publication No. US20050079606A1
; GENERAL INFORMATION:
; APPLICANT: TETSUO TAMAKI
; APPLICANT: KIYOSHI ANDO
; TITLE OF INVENTION: MULTIPOTENT STEM CELL IN THE INTERSTITIAL TISSUES OF SKELETAL MUS
; FILE REFERENCE: 766.108
; CURRENT APPLICATION NUMBER: US/10/490,143A
; PRIOR FILING DATE: 2004-03-19
; PRIOR APPLICATION NUMBER: JP2001-286332
; PRIOR FILING DATE: 2001-09-20
; PRIOR APPLICATION NUMBER: JP2002-133575
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 19
; LENGTH: 1132
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-490-143A-19

Query Match 100.0%; Score 5961; DB 17; Length 1132;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPAPRCRAVRSLLSHYREVLPATFVRRLLGPGQWRVLRQGDPAAFRALVAQCVCVPM 60
DB 1 MPAPRCRAVRSLLSHYREVLPATFVRRLLGPGQWRVLRQGDPAAFRALVAQCVCVPM 60

QY 61 DARPPPAAPSRQVSCLELVARVLQRLCERGAKNVLAFFGALLDGAAGGPPPEAFTTSVR 120
DB 61 DARPPPAAPSRQVSCLELVARVLQRLCERGAKNVLAFFGALLDGAAGGPPPEAFTTSVR 120

QY 121 SYLNTVTDALRGSGAWGLLLRRVGDVLLHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180
DB 121 SYLNTVTDALRGSGAWGLLLRRVGDVLLHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180

QY 181 ATQARPPPHASGPRRLGGERAWNHSVREAGVPLGLPAGARRRGGSSASRSLLPKRPRR 240
DB 181 ATQARPPPHASGPRRLGGERAWNHSVREAGVPLGLPAGARRRGGSSASRSLLPKRPRR 240

QY 241 GAAPPERTPVQGSWAHPGTRGSDRGFCVSPARPAEEATSLEGALSCTRHSHPVSG 300
DB 241 GAAPPERTPVQGSWAHPGTRGSDRGFCVSPARPAEEATSLEGALSCTRHSHPVSG 300

QY 301 ROHAGPSTSRPPRWDTPCPVVAETKHFYSSGDKQLRPSFLLSLRPSLTGARRL 360
DB 301 ROHAGPSTSRPPRWDTPCPVVAETKHFYSSGDKQLRPSFLLSLRPSLTGARRL 360

QY 361 VETIFLGSRRPMPGTPRRLPRLPQRYQWMLRFLLELGNHAQCYPVLLKTHCPLRAAVT 420
DB 361 VETIFLGSRRPMPGTPRRLPRLPQRYQWMLRFLLELGNHAQCYPVLLKTHCPLRAAVT 420

QY 421 PAAGVCAREKPGQSVAAPEEEDTPRRLVQLLRQHSPPQVYGFVRACLRLRVPGLWGS 480
DB 421 PAAGVCAREKPGQSVAAPEEEDTPRRLVQLLRQHSPPQVYGFVRACLRLRVPGLWGS 480

QY 481 RHNERRFLRNTKFTSLGKHAKLSLOELTWKMSVRDCAWLRSPGVCVPAEHLRREI 540
DB 481 RHNERRFLRNTKFTSLGKHAKLSLOELTWKMSVRDCAWLRSPGVCVPAEHLRREI 540

QY 541 LAKFLHLMMSVYVVELLRSFFVTETTFQKRLFPYKRSVMSKLSQSIGIROLKRVQLRE 600
DB 541 LAKFLHLMMSVYVVELLRSFFVTETTFQKRLFPYKRSVMSKLSQSIGIROLKRVQLRE 600

QY 601 LSEAVRQHRERARPAALLTSRLRFIPKPDGLRPIVNDYVVGARTFRERKRAERLTSRYKA 660
DB 601 LSEAVRQHRERARPAALLTSRLRFIPKPDGLRPIVNDYVVGARTFRERKRAERLTSRYKA 660

QY 661 LFSVLNYSERARRPGLLGASVLGLDDIHRARWTFVLRLVRAQDPPPELYFVKVDVTGAYDTI 720
DB 661 LFSVLNYSERARRPGLLGASVLGLDDIHRARWTFVLRLVRAQDPPPELYFVKVDVTGAYDTI 720

QY 721 PODRLTEVIASIIKQNTYCYRRYAVOKAAGHVRAKFSKHSVTLTDLQPMQFVAHL 780
DB 721 PODRLTEVIASIIKQNTYCYRRYAVOKAAGHVRAKFSKHSVTLTDLQPMQFVAHL 780

QY 781 QETSLRDAVITEQSSSINEASSGLFDVFLPMCHHVRIRGKSVVQCGIPQGSILSTL 840
DB 781 QETSLRDAVITEQSSSINEASSGLFDVFLPMCHHVRIRGKSVVQCGIPQGSILSTL 840

QY 841 LCSLCYGDMENKLFAGIRRDGLLLRLVDDFLVTPHLLTHAKTFLRTLVRGPEYGCNNL 900
DB 841 LCSLCYGDMENKLFAGIRRDGLLLRLVDDFLVTPHLLTHAKTFLRTLVRGPEYGCNNL 900

QY 901 RKTVNVFVEDEALGGTAFVQMPAHGLFPWCGLLDTRTLEVSQSYASRTSIRASLTF 960
DB 901 RKTVNVFVEDEALGGTAFVQMPAHGLFPWCGLLDTRTLEVSQSYASRTSIRASLTF 960

QY 961 NRGFKAGNMRRLKFGVRLKCHSLFLDLQVNSLQTVCTNIIKILLQAYRFHACVLOLP 1020
DB 961 NRGFKAGNMRRLKFGVRLKCHSLFLDLQVNSLQTVCTNIIKILLQAYRFHACVLOLP 1020

QY 1021 FHOQWKNPFTFLRVIDSTASLCYSILKAKNAGMSLGAKGAGPLPSEAVQWLCHQAFLL 1080

DB 1021 FHOQWKNPFTFLRVIDSTASLCYSILKAKNAGMSLGAKGAGPLPSEAVQWLCHQAFLL 1080

QY 1081 KLTRHRVTYVPLGSLRTAQTOLSKPLGTTTLTALEAANPALPSDFKTILD 1132
DB 1081 KLTRHRVTYVPLGSLRTAQTOLSKPLGTTTLTALEAANPALPSDFKTILD 1132

RESULT 29
US-10-794-514A-3
; Sequence 3, Application US/10794514A
; Publication No. US20050112134A1
; GENERAL INFORMATION:
; APPLICANT: Graddis, Thomas
; APPLICANT: Laus, Reiner
; APPLICANT: Diegel, Michael
; APPLICANT: Vidovic, Damir
; TITLE OF INVENTION: Compositions and Methods Employing Alternative
; TITLE OF INVENTION: Reading Frame Polypeptides for the Treatment of
; FILE REFERENCE: 11311.1003U
; CURRENT APPLICATION NUMBER: US/10/794,514A
; CURRENT FILING DATE: 2004-03-05
; NUMBER OF SEQ ID NOS: 733
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 1132
; TYPE: PRT
; ORGANISM: Human
US-10-794-514A-3

Query Match 100.0%; Score 5961; DB 17; Length 1132;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPAPRCRAVRSLLSHYREVLPATFVRRLLGPGQWRVLRQGDPAAFRALVAQCVCVPM 60
DB 1 MPAPRCRAVRSLLSHYREVLPATFVRRLLGPGQWRVLRQGDPAAFRALVAQCVCVPM 60

QY 61 DARPPPAAPSRQVSCLELVARVLQRLCERGAKNVLAFFGALLDGAAGGPPPEAFTTSVR 120
DB 61 DARPPPAAPSRQVSCLELVARVLQRLCERGAKNVLAFFGALLDGAAGGPPPEAFTTSVR 120

QY 121 SYLNTVTDALRGSGAWGLLLRRVGDVLLHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180
DB 121 SYLNTVTDALRGSGAWGLLLRRVGDVLLHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180

QY 181 ATQARPPPHASGPRRLGGERAWNHSVREAGVPLGLPAGARRRGGSSASRSLLPKRPRR 240
DB 181 ATQARPPPHASGPRRLGGERAWNHSVREAGVPLGLPAGARRRGGSSASRSLLPKRPRR 240

QY 241 GAAPPERTPVQGSWAHPGTRGSDRGFCVSPARPAEEATSLEGALSCTRHSHPVSG 300
DB 241 GAAPPERTPVQGSWAHPGTRGSDRGFCVSPARPAEEATSLEGALSCTRHSHPVSG 300

QY 301 ROHAGPSTSRPPRWDTPCPVVAETKHFYSSGDKQLRPSFLLSLRPSLTGARRL 360
DB 301 ROHAGPSTSRPPRWDTPCPVVAETKHFYSSGDKQLRPSFLLSLRPSLTGARRL 360

QY 361 VETIFLGSRRPMPGTPRRLPRLPQRYQWMLRFLLELGNHAQCYPVLLKTHCPLRAAVT 420
DB 361 VETIFLGSRRPMPGTPRRLPRLPQRYQWMLRFLLELGNHAQCYPVLLKTHCPLRAAVT 420

QY 421 PAAGVCAREKPGQSVAAPEEEDTPRRLVQLLRQHSPPQVYGFVRACLRLRVPGLWGS 480
DB 421 PAAGVCAREKPGQSVAAPEEEDTPRRLVQLLRQHSPPQVYGFVRACLRLRVPGLWGS 480

QY 481 RHNERRFLRNTKFTSLGKHAKLSLOELTWKMSVRDCAWLRSPGVCVPAEHLRREI 540
DB 481 RHNERRFLRNTKFTSLGKHAKLSLOELTWKMSVRDCAWLRSPGVCVPAEHLRREI 540

QY 541 LAKFLHLMMSVYVVELLRSFFVTETTFQKRLFPYKRSVMSKLSQSIGIROLKRVQLRE 600

Db 541 LAKFLHMLSVVVELLBSFPVVTETTFQKNRLFFYRKSVWSKLSQSIGRHLKRVQRE 600
Qy 601 LSEAFVROHREARPAALLTSRLRFPKPDGLRPVNMDDYVVGARTFRREKRAERLTSRYKA 660
Db 601 LSEAFVROHREARPAALLTSRLRFPKPDGLRPVNMDDYVVGARTFRREKRAERLTSRYKA 660
Qy 661 LFSVLNVERARRPGLIGASVGLDDIHRAMWTFVLRVAQDPPPELVKVDVVTGAYDTI 720
Db 661 LFSVLNVERARRPGLIGASVGLDDIHRAMWTFVLRVAQDPPPELVKVDVVTGAYDTI 720
Qy 721 PODRLTEVIASIIKPQNTYCVRRYAVVQKAAGHVRKAFKSHVSTLTDLOPYMQFVAHL 780
Db 721 PODRLTEVIASIIKPQNTYCVRRYAVVQKAAGHVRKAFKSHVSTLTDLOPYMQFVAHL 780
Qy 781 QETSPRLDAVVIQSSSLNEASSGLFDVFLRFMCHHAVIRKGSYVQCGIPQGSILSTL 840
Db 781 QETSPRLDAVVIQSSSLNEASSGLFDVFLRFMCHHAVIRKGSYVQCGIPQGSILSTL 840
Qy 841 LCSLCYGD MENKLFAGIRRDGLLLRLVDDFLVTPHLLTHAKTFLRTLVRGVPYGCVVNL 900
Db 841 LCSLCYGD MENKLFAGIRRDGLLLRLVDDFLVTPHLLTHAKTFLRTLVRGVPYGCVVNL 900
Qy 901 RKTVMNFPVEDEALGGTAFVQMPAHGLFPWCGLLLDTRTLEVSQDYSYARTSIRASLTF 960
Db 901 RKTVMNFPVEDEALGGTAFVQMPAHGLFPWCGLLLDTRTLEVSQDYSYARTSIRASLTF 960
Qy 961 NRGFKAGNNRRKLFVGLRLKCHSLFLLDLQVNSLQTVCTNIYKILLQAYRFHACVLQLP 1020
Db 961 NRGFKAGNNRRKLFVGLRLKCHSLFLLDLQVNSLQTVCTNIYKILLQAYRFHACVLQLP 1020
Qy 1021 FHQQWKNPTFFLRVISTASLCYSILKAKNAGSLGAKGAAGLPSEAVQWLCHQAPLL 1080
Db 1021 FHQQWKNPTFFLRVISTASLCYSILKAKNAGSLGAKGAAGLPSEAVQWLCHQAPLL 1080
Qy 1081 KLTRHRVTVYVPLGSLRTAQQLSRKLPQTTLTALEAAANPALPSDFKTILD 1132
Db 1081 KLTRHRVTVYVPLGSLRTAQQLSRKLPQTTLTALEAAANPALPSDFKTILD 1132
RESULT 30
US-10-143-536-2
; Sequence 2, Application US/10143536
; Publication No. US20040147465A1
; GENERAL INFORMATION:
; APPLICANT: Geron Corporation
; APPLICANT: Jiang, Xu-Rong
; APPLICANT: Chiu, Choy-Pik
; APPLICANT: Harley, Calvin B.
; TITLE OF INVENTION: Treatment for Wounds
; FILE REFERENCE: 120/200
; CURRENT APPLICATION NUMBER: US/10/143,536
; CURRENT FILING DATE: 2002-05-09
; PRIOR APPLICATION NUMBER: 60/289,903
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 1132
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-143-536-2

Query Match 100.0%; Score 5961; DB 18; Length 1132;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MPRAPCRCAVSSLRSHYREVLPATFVRRLLGPOGWRVQRPDPAAFALVAQCVCVPM 60
Db 1 MPRAPCRCAVSSLRSHYREVLPATFVRRLLGPOGWRVQRPDPAAFALVAQCVCVPM 60
Qy 61 DARPPPAAPSFRQVSCLELVARVLQRLCERGAKNVLAFGFALLDGAAGGPPPEAFTTSVR 120
Db 61 DARPPPAAPSFRQVSCLELVARVLQRLCERGAKNVLAFGFALLDGAAGGPPPEAFTTSVR 120

Qy 121 SYLPNTVTDALRGSGAWGLLLRRVDDVLVHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180
Db 121 SYLPNTVTDALRGSGAWGLLLRRVDDVLVHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180
Qy 181 ATQARPPPHASGRRRLGRCERAWNHSVREAGVPLGLPAPGARRRGGSASLSLPLPKPRR 240
Db 181 ATQARPPPHASGRRRLGRCERAWNHSVREAGVPLGLPAPGARRRGGSASLSLPLPKPRR 240
Qy 241 GAAPEPERTVPGQGSWAHPGRTGRGFCVVSPPARPAEBEATSEALSGSTRSHSPSVG 300
Db 241 GAAPEPERTVPGQGSWAHPGRTGRGFCVVSPPARPAEBEATSEALSGSTRSHSPSVG 300
Qy 301 RQHHAGPPTSRPRPMDTFCPPVYAEKTHFLYSSGDEKQRLRPSFLLSSRLPSLTGARRL 360
Db 301 RQHHAGPPTSRPRPMDTFCPPVYAEKTHFLYSSGDEKQRLRPSFLLSSRLPSLTGARRL 360
Qy 361 VETIFLGSRRPMBPCTPRRLPRLPQRYWQMRPLFLELLGNHAQCPYGVLLKTHCPLRAVT 420
Db 361 VETIFLGSRRPMBPCTPRRLPRLPQRYWQMRPLFLELLGNHAQCPYGVLLKTHCPLRAVT 420
Qy 421 PAAGVCAREKPOGSVAAPPEEDTPRRLVQLLRQHSSPMQVYGFVRACLRLVPPGLWGS 480
Db 421 PAAGVCAREKPOGSVAAPPEEDTPRRLVQLLRQHSSPMQVYGFVRACLRLVPPGLWGS 480
Qy 481 RHNERFLRNTKKPISLGKHAKLSLOBLTWKMSVRDCAWLRSPGVCVPAAEHRLREEI 540
Db 481 RHNERFLRNTKKPISLGKHAKLSLOBLTWKMSVRDCAWLRSPGVCVPAAEHRLREEI 540
Qy 541 LAKFLHMLSVVVELLBSFPVVTETTFQKNRLFFYRKSVWSKLSQSIGRHLKRVQRE 600
Db 541 LAKFLHMLSVVVELLBSFPVVTETTFQKNRLFFYRKSVWSKLSQSIGRHLKRVQRE 600
Qy 601 LSEAFVROHREARPAALLTSRLRFPKPDGLRPVNMDDYVVGARTFRREKRAERLTSRYKA 660
Db 601 LSEAFVROHREARPAALLTSRLRFPKPDGLRPVNMDDYVVGARTFRREKRAERLTSRYKA 660
Qy 661 LFSVLNVERARRPGLIGASVGLDDIHRAMWTFVLRVAQDPPPELVKVDVVTGAYDTI 720
Db 661 LFSVLNVERARRPGLIGASVGLDDIHRAMWTFVLRVAQDPPPELVKVDVVTGAYDTI 720
Qy 721 PODRLTEVIASIIKPQNTYCVRRYAVVQKAAGHVRKAFKSHVSTLTDLOPYMQFVAHL 780
Db 721 PODRLTEVIASIIKPQNTYCVRRYAVVQKAAGHVRKAFKSHVSTLTDLOPYMQFVAHL 780
Qy 781 QETSPRLDAVVIQSSSLNEASSGLFDVFLRFMCHHAVIRKGSYVQCGIPQGSILSTL 840
Db 781 QETSPRLDAVVIQSSSLNEASSGLFDVFLRFMCHHAVIRKGSYVQCGIPQGSILSTL 840
Qy 841 LCSLCYGD MENKLFAGIRRDGLLLRLVDDFLVTPHLLTHAKTFLRTLVRGVPYGCVVNL 900
Db 841 LCSLCYGD MENKLFAGIRRDGLLLRLVDDFLVTPHLLTHAKTFLRTLVRGVPYGCVVNL 900
Qy 901 RKTVMNFPVEDEALGGTAFVQMPAHGLFPWCGLLLDTRTLEVSQDYSYARTSIRASLTF 960
Db 901 RKTVMNFPVEDEALGGTAFVQMPAHGLFPWCGLLLDTRTLEVSQDYSYARTSIRASLTF 960
Qy 961 NRGFKAGNNRRKLFVGLRLKCHSLFLLDLQVNSLQTVCTNIYKILLQAYRFHACVLQLP 1020
Db 961 NRGFKAGNNRRKLFVGLRLKCHSLFLLDLQVNSLQTVCTNIYKILLQAYRFHACVLQLP 1020
Qy 1021 FHQQWKNPTFFLRVISTASLCYSILKAKNAGSLGAKGAAGLPSEAVQWLCHQAPLL 1080
Db 1021 FHQQWKNPTFFLRVISTASLCYSILKAKNAGSLGAKGAAGLPSEAVQWLCHQAPLL 1080
Qy 1081 KLTRHRVTVYVPLGSLRTAQQLSRKLPQTTLTALEAAANPALPSDFKTILD 1132
Db 1081 KLTRHRVTVYVPLGSLRTAQQLSRKLPQTTLTALEAAANPALPSDFKTILD 1132
RESULT 31
US-10-044-692-323
; Sequence 323, Application US/10044692

Publication No. US20030096344A1
 GENERAL INFORMATION:
 APPLICANT: Cech, Thomas R.
 Lingner, Joachim
 Nakamura, Toru
 Chapman, Karen B.
 Morin, Gregg B.
 Harley, Calvin
 Andrews, William H.
 TITLE OF INVENTION: HUMAN TELOMERASE CATALYTIC SUBUNIT: DIAGNOSTIC AND THERAPEUTIC METHODS
 NUMBER OF SEQUENCES: 335
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Townsend and Townsend and Crew LLP
 STREET: Two Embarcadero Center, 8th Floor
 CITY: San Francisco
 STATE: California
 COUNTRY: United States of America
 ZIP: 94111
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/10/044,692
 FILING DATE: 11-Jan-2002
 CLASSIFICATION: <Unknown>
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/912,951
 FILING DATE: <Unknown>
 APPLICATION NUMBER: US 08/854,050
 FILING DATE: 09-MAY-1997
 APPLICATION NUMBER: US 08/851,843
 FILING DATE: 06-MAY-1997
 APPLICATION NUMBER: US 08/846,017
 FILING DATE: 25-APR-1997
 APPLICATION NUMBER: US 08/844,419
 FILING DATE: 18-APR-1997
 APPLICATION NUMBER: US 08/724,643
 FILING DATE: 01-OCT-1996
 ATTORNEY/AGENT INFORMATION:
 NAME: Apple, Randolph T.
 REGISTRATION NUMBER: 36,429
 REFERENCE/DOCKET NUMBER: 015389-002600US
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 576-0200
 TELEFAX: (415) 576-0300
 INFORMATION FOR SEQ ID NO: 323:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1154 amino acids
 TYPE: amino acid
 STRANDEDNESS: <Unknown>
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 SEQUENCE DESCRIPTION: SEQ ID NO: 323:
 US-10-044-692-323

Query Match 100.0%; Score 5961; DB 14; Length 1154;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPRAPRCVRSLLSHREVLPATFVRRLLGPGQWRVLRVQGDPAAFALVAQCLVCVPM 60
 DB 1 MPRAPRCVRSLLSHREVLPATFVRRLLGPGQWRVLRVQGDPAAFALVAQCLVCVPM 60

QY 61 DARPPPAAPSFQVSLCKELVARVLQRCERGAKNVLAFGFALLDCARGGPEAFTTSVR 120
 DB 61 DARPPPAAPSFQVSLCKELVARVLQRCERGAKNVLAFGFALLDCARGGPEAFTTSVR 120

QY 121 SYLPNTVTDALRGSGAWGLLRRVGDVVLHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180
 DB 121 SYLPNTVTDALRGSGAWGLLRRVGDVVLHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180

QY 181 ATQARPPPHASGPRRRRLGGERAWNHSVREAGVPLGLPAPGARRRGGSASRSLLPKRRR 240
 DB 181 ATQARPPPHASGPRRRRLGGERAWNHSVREAGVPLGLPAPGARRRGGSASRSLLPKRRR 240

QY 241 GAPEPERTVPGQSWAHPTGRGSDRGFCVVSPPARPAEATSLEGALSCTRHHSPVSG 300
 DB 241 GAPEPERTVPGQSWAHPTGRGSDRGFCVVSPPARPAEATSLEGALSCTRHHSPVSG 300

QY 301 ROHAGAPSTSRPRPMDTPCPVVAETKHFYSSGDEQLRPSFLLSLRSLSLGGARL 360
 DB 301 ROHAGAPSTSRPRPMDTPCPVVAETKHFYSSGDEQLRPSFLLSLRSLSLGGARL 360

QY 361 VETIFLGSRRPMPGTPRRLPRLPQRYMQRPLFLELLGNHAQCPYGVLLKTHCPLRAAVT 420
 DB 361 VETIFLGSRRPMPGTPRRLPRLPQRYMQRPLFLELLGNHAQCPYGVLLKTHCPLRAAVT 420

QY 421 PAAGVCAREKPGQSVAAPEEDTDPRLVQLLRQHSPPWQVYGFVRACLRRLVPPGLWGS 480
 DB 421 PAAGVCAREKPGQSVAAPEEDTDPRLVQLLRQHSPPWQVYGFVRACLRRLVPPGLWGS 480

QY 481 RHNERRLNNTKFTISLGKHAKLSLOELTWKMSVRDCAWLRRSPGVCVPAEHLRBEI 540
 DB 481 RHNERRLNNTKFTISLGKHAKLSLOELTWKMSVRDCAWLRRSPGVCVPAEHLRBEI 540

QY 541 LAKFLHMLMSVYVVELLRSFFVTTETTPQKNRLFYRKSVMSKLSQSIGIRQHLKRVQLRE 600
 DB 541 LAKFLHMLMSVYVVELLRSFFVTTETTPQKNRLFYRKSVMSKLSQSIGIRQHLKRVQLRE 600

QY 601 LSEAEVQRHREARPAALLTSRLRFPKPDGLRPIVNMVYVVGARTFRREKRAERLTSRVKA 660
 DB 601 LSEAEVQRHREARPAALLTSRLRFPKPDGLRPIVNMVYVVGARTFRREKRAERLTSRVKA 660

QY 661 LFSVLNTERARRPGLLGASVLGLDDIHRAWETFLVRVAQDPPPELYFVKVDVTGAYDTI 720
 DB 661 LFSVLNTERARRPGLLGASVLGLDDIHRAWETFLVRVAQDPPPELYFVKVDVTGAYDTI 720

QY 721 PODRLTEVIASIIKPNQTYCVRRYAVVQKAHGHVRKAFKSHVSTLTDLQPMRQFVAHL 780
 DB 721 PODRLTEVIASIIKPNQTYCVRRYAVVQKAHGHVRKAFKSHVSTLTDLQPMRQFVAHL 780

QY 781 QETSPLRDAVVEQSSSLNEASSGLFDVFLRPMCHHVRIRGKSYVQCGIQQGSILSTL 840
 DB 781 QETSPLRDAVVEQSSSLNEASSGLFDVFLRPMCHHVRIRGKSYVQCGIQQGSILSTL 840

QY 841 LCSLCYGDMEKLFAGIRRDGLLLRLVDDFLVTPHLLTHAKTFLRTLVRGYPEYCVVNL 900
 DB 841 LCSLCYGDMEKLFAGIRRDGLLLRLVDDFLVTPHLLTHAKTFLRTLVRGYPEYCVVNL 900

QY 901 RKTVPNPFVEDEALGGTAFVQMPAHGLPPWCGLLDTRTLEVSQSDYSYARTSIRASLTF 960
 DB 901 RKTVPNPFVEDEALGGTAFVQMPAHGLPPWCGLLDTRTLEVSQSDYSYARTSIRASLTF 960

QY 961 NRGFKAGRNMRKLFVGLRLKCHSLFLDLQVNSLQTVCTNIYKILLQAYRFHACVQLQP 1020
 DB 961 NRGFKAGRNMRKLFVGLRLKCHSLFLDLQVNSLQTVCTNIYKILLQAYRFHACVQLQP 1020

QY 1021 FHOQWKNPTFFLRVSDTASLCYSILKAKVAGSLGAKGAGPLPSAVQWLCHOAFL 1080
 DB 1021 FHOQWKNPTFFLRVSDTASLCYSILKAKVAGSLGAKGAGPLPSAVQWLCHOAFL 1080

QY 1081 KLTRHRTVTVPLLGSLRTAQQLSRKLPGLTTLTALAAANPALPSDFKTILD 1132
 DB 1081 KLTRHRTVTVPLLGSLRTAQQLSRKLPGLTTLTALAAANPALPSDFKTILD 1132

RESULT 32
 US-10-044-539-323
 ; Sequence 323, Application US/10044539
 ; Publication No. US20030100093A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Cech, Thomas R.
 ; Lingner, Joachim

```

; Nakamura, Toru
; Chapman, Karen B.
; Morin, Gregg B.
; Harley, Calvin
; Andrews, William H.
; TITLE OF INVENTION: HUMAN TELOMERASE CATALYTIC SUBUNIT: DIAGNOSTIC AND
; THERAPEUTIC METHODS
; NUMBER OF SEQUENCES: 335
; CORRESPONDENCE ADDRESS:
; ADDRESS: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94111
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/044,539
; FILING DATE: 11-Jan-2002
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/912,951
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US 08/854,050
; FILING DATE: 09-MAY-1997
; APPLICATION NUMBER: US 08/851,843
; FILING DATE: 06-MAY-1997
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph T.
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-002600US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 323:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1154 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 323:
US-10-044-539-323

Query Match 100.0%; Score 5961; DB 14; Length 1154;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MPAPRCRAVSLRLSHRYEVLPLATFVRRLGPGQWRLVQRGDPAAFRALVAQCLVCVPW 60
Db 1 MPAPRCRAVSLRLSHRYEVLPLATFVRRLGPGQWRLVQRGDPAAFRALVAQCLVCVPW 60

Qy 61 DARPPPAAPSPQVSCLEKELVARVLQRLCERGAKNVLAFGPALLDGGAGGPEAFTTSVR 120
Db 61 DARPPPAAPSPQVSCLEKELVARVLQRLCERGAKNVLAFGPALLDGGAGGPEAFTTSVR 120

Qy 121 SYLPTNTVTDALRGSGAGCLLRRYGGDVLVHLLARCALFVLVAPSCAYQVCGPPLYOLGA 180
Db 121 SYLPTNTVTDALRGSGAGCLLRRYGGDVLVHLLARCALFVLVAPSCAYQVCGPPLYOLGA 180

Qy 181 ATOARPPPPHSGPRRLRGCEAMNHSVREAGVPLGLPAPGARRRGGSASRSPLPKPRR 240
Db 181 ATOARPPPPHSGPRRLRGCEAMNHSVREAGVPLGLPAPGARRRGGSASRSPLPKPRR 240

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Qy 241 GAAPEPERTVGGSGWAHPQRTGRGFCVSPARPABEATSLGALSSTRHSHPVSG 300
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Qy 301 ROHHAGPPSTRPRPMDTFCPPVYAEKHFVLYSSGDKQOLRPSFLSSRPSLTGARRL 360
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Qy 361 VETIFLGSRPWMPGTPRRLPRLPQRYWQMPLEFLLELGNHAQCYPYGVLLKTHCPLRAVT 420
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Qy 421 PAAGVCAREKPOGSAVAPEEEDTPRRLVOLLQHSPPWQYGVFVRACLRLRPVPGWGS 480
Db 421 PAAGVCAREKPOGSAVAPEEEDTPRRLVOLLQHSPPWQYGVFVRACLRLRPVPGWGS 480

Qy 481 RHNERRFLRNTKKFISLGHAKLSLOBLTWKMSVRDCAWLRRSPGVCVPAAEHRLREEI 540
Db 481 RHNERRFLRNTKKFISLGHAKLSLOBLTWKMSVRDCAWLRRSPGVCVPAAEHRLREEI 540

Qy 541 LAKFLHWMMSVYVVELLRSFFYVTTETTFQKNRFFFYKSVMSKLSQSIGIRQHLKRVQLRE 600
Db 541 LAKFLHWMMSVYVVELLRSFFYVTTETTFQKNRFFFYKSVMSKLSQSIGIRQHLKRVQLRE 600

Qy 601 LSAEVRQHRREARPALITSRLRFPKPDGLRPIVNDYVVGARTFRREKKAERLTSRVKA 660
Db 601 LSAEVRQHRREARPALITSRLRFPKPDGLRPIVNDYVVGARTFRREKKAERLTSRVKA 660

Qy 661 LFSVLNVERARRRGLIGASVLGLDDTHRAWRTFVLIRVRAODPPPELVFVKVDVTGADTI 720
Db 661 LFSVLNVERARRRGLIGASVLGLDDTHRAWRTFVLIRVRAODPPPELVFVKVDVTGADTI 720

Qy 721 PQDLTEVIASIIKPONTYCVRRYAVVQKAAGHVRKAFKSHVSTLTDLOPYMQFVAHL 780
Db 721 PQDLTEVIASIIKPONTYCVRRYAVVQKAAGHVRKAFKSHVSTLTDLOPYMQFVAHL 780

Qy 781 QETSPLRDAVVIQSSSLNEASSGLFDVFLRFMCHHAVIRGKSVYQCGIPOGSIILSTL 840
Db 781 QETSPLRDAVVIQSSSLNEASSGLFDVFLRFMCHHAVIRGKSVYQCGIPOGSIILSTL 840

Qy 841 LCSLCYGD MENKLPAGIRRDGLLRLVDDFLVTPHLLTHAKTFLRTLVRGVPEYGCVVNL 900
Db 841 LCSLCYGD MENKLPAGIRRDGLLRLVDDFLVTPHLLTHAKTFLRTLVRGVPEYGCVVNL 900

Qy 901 RKTVVNFPVEDEALGGTAFVQMPAHGLFPMCGLLDTRTLEVOQSDYSSYARTSIRASLTF 960
Db 901 RKTVVNFPVEDEALGGTAFVQMPAHGLFPMCGLLDTRTLEVOQSDYSSYARTSIRASLTF 960

Qy 961 NRGFKAGRNRRKLFVGLRLKCHSLFLDLQVNSLQTVCTNIYKILLQAVRFHACVQLPL 1020
Db 961 NRGFKAGRNRRKLFVGLRLKCHSLFLDLQVNSLQTVCTNIYKILLQAVRFHACVQLPL 1020

Qy 1021 FHQOVWKNPTFFELRVISDTSALCVSILKAKNAGMSLGAKGAAGPLPSEAOWMLCHQAPLL 1080
Db 1021 FHQOVWKNPTFFELRVISDTSALCVSILKAKNAGMSLGAKGAAGPLPSEAOWMLCHQAPLL 1080

Qy 1081 KLTRHRVTVYVPLGLSLRTAQTLQSLRKLPGTTLTALEAAANPALPSPDFKTIID 1132
Db 1081 KLTRHRVTVYVPLGLSLRTAQTLQSLRKLPGTTLTALEAAANPALPSPDFKTIID 1132

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RESULT 33
US-10-325-810-611
; Sequence 611, Application US/10325810
; Publication No. US20030204069A1
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
;             Lingner, Joachim
;             Nakamura, Toru
;             Chapman, Karen B.
;             Morin, Gregg B.
;             Harley, Calvin B.

```


Andrews, William H.
TITLE OF INVENTION: Human Telomerase Catalytic Subunit
NUMBER OF SEQUENCES: 633
CORRESPONDENCE ADDRESS:

ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/325,810

FILING DATE: 20-Dec-2002

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/402,181

FILING DATE: 29-Sep-1997

APPLICATION NUMBER: US 08/724,643

FILING DATE: 01-OCT-1996

APPLICATION NUMBER: US 08/844,419

FILING DATE: 18-APR-1997

APPLICATION NUMBER: US 08/846,017

FILING DATE: 25-APR-1997

APPLICATION NUMBER: US 08/851,843

FILING DATE: 06-MAY-1997

APPLICATION NUMBER: US 08/854,050

FILING DATE: 09-MAY-1997

APPLICATION NUMBER: US 08/911,312

FILING DATE: 14-AUG-1997

APPLICATION NUMBER: US 08/912,951

FILING DATE: 14-AUG-1997

APPLICATION NUMBER: US 08/915,503

FILING DATE: 14-AUG-1997

APPLICATION NUMBER: WO PCT/US97/17885

FILING DATE: 01-OCT-1997

ATTORNEY/AGENT INFORMATION:

NAME: Ausenhus, Scott L.

REGISTRATION NUMBER: 42,271

REFERENCE/DOCKET NUMBER: 015389-002620US

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 576-0200

TELEFAX: (415) 576-0300

INFORMATION FOR SEQ ID NO: 611:

SEQUENCE CHARACTERISTICS:

LENGTH: 1154 amino acids

TYPE: amino acid

STRANDEDNESS: <Unknown>

TOPOLOGY: linear

MOLECULE TYPE: protein

FEATURE:

NAME/KEY: protein

LOCATION: 1..1154

OTHER INFORMATION: /note= "fusion protein composed of hTERT

protein sequence, vector sequences, the

Myc epitope and His6 tag"

SEQUENCE DESCRIPTION: SEQ ID NO: 611:

US-10-325-810-611

Query Match 100.0%; Score 5961; DB 15; Length 1154;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPRAPCRAVRLSHRYEVLPLATFVRRILGPOGWRVQRCDPAAAFALVAQCILVCYPM 60
DB 1 MPRAPCRAVRLSHRYEVLPLATFVRRILGPOGWRVQRCDPAAAFALVAQCILVCYPM 60

QY 61 DARPPPAAPSPFQVSCLEKELVARLQRLCERGAKNVLAFGFALLDGAAGGPPPEAFTTSVR 120

Db 61 DARPPPAAPSPFQVSCLEKELVARLQRLCERGAKNVLAFGFALLDGAAGGPPPEAFTTSVR 120
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Db 121 SYLNTVTDALRGSGAWGLLLRRVGGDDVLVHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180
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Db 301 RQHAGPSTSRPPRPMDTPCPVYAEKHYLSGSGKEQLRPSFLLSLSPSLTGARRL 360
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Db 481 RHNERRFLRNTKFTISLGKHAQLSLQELTWKMSVRDCAWLRSPGVGCPAAEHLRREI 540
QY 541 LAKEFLHMLMSYVVELLRSFFVTETTFQKNRLFYRKSVMSKLSQSIGIRQHLKRVQLRE 600
Db 541 LAKEFLHMLMSYVVELLRSFFVTETTFQKNRLFYRKSVMSKLSQSIGIRQHLKRVQLRE 600
QY 601 LSEAEVROHREARPAALLTSRLRFPKPDGLRPIVNMMDYVVGARFRRKRAERLTSRYKA 660
Db 601 LSEAEVROHREARPAALLTSRLRFPKPDGLRPIVNMMDYVVGARFRRKRAERLTSRYKA 660
QY 661 LFSVLNTERARRPGLLGASVLGDDIHRAWTFVLVRAQDPPPELYFVKVDVTGAYDTI 720
Db 661 LFSVLNTERARRPGLLGASVLGDDIHRAWTFVLVRAQDPPPELYFVKVDVTGAYDTI 720
QY 721 PQDRLTEVIASIIKPQNTYCVRRYAVVQKAAHGHVKAFAKSHVSTLTLDQPMRQFVAHL 780
Db 721 PQDRLTEVIASIIKPQNTYCVRRYAVVQKAAHGHVKAFAKSHVSTLTLDQPMRQFVAHL 780
QY 781 QETSPLRDAVVIEQSSSLNEASSGLFDVFLRFMCHHAVIRGKSVYQCGIPQGSILSTL 840
Db 781 QETSPLRDAVVIEQSSSLNEASSGLFDVFLRFMCHHAVIRGKSVYQCGIPQGSILSTL 840
QY 841 LCSLCYGD MENKLPAGIRRDGLLRVDDFLLVTPHLTHAKTFLRTLVRGVPEYCVVNL 900
Db 841 LCSLCYGD MENKLPAGIRRDGLLRVDDFLLVTPHLTHAKTFLRTLVRGVPEYCVVNL 900
QY 901 RKTVMNPFVEDEALGGTAFVQMPAHGLFPWCGLLDTRTLEVQSDSYSSYARTSIRASLTF 960
Db 901 RKTVMNPFVEDEALGGTAFVQMPAHGLFPWCGLLDTRTLEVQSDSYSSYARTSIRASLTF 960
QY 961 NRGFKAGNMRKLFVGLRLKCHSLFDLQVNSLQTVCTNIYKILLQAYRHFACVLOLP 1020
Db 961 NRGFKAGNMRKLFVGLRLKCHSLFDLQVNSLQTVCTNIYKILLQAYRHFACVLOLP 1020
QY 1021 FHOQVKNPTFFLRVISTASLCYSILKAKNAGSLGAKGAGPLPSEAVOMLCHOAFLL 1080
Db 1021 FHOQVKNPTFFLRVISTASLCYSILKAKNAGSLGAKGAGPLPSEAVOMLCHOAFLL 1080
QY 1081 KLTRHRTYVPLIGSLRTAQOLSKRLPGTTLTALAAANPALPDSFKTILD 1132
Db 1081 KLTRHRTYVPLIGSLRTAQOLSKRLPGTTLTALAAANPALPDSFKTILD 1132

RESULT 34
US-10-877-124-611

; Sequence 611, Application US/10877124
; Publication No. US20040242529A1
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; Lingner, Joachim
; Nakamura, Toru
; Chapman, Karen B.
; Morin, Gregg B.
; Harley, Calvin B.
; Andrews, William H.
; TITLE OF INVENTION: Human Telomerase Catalytic Subunit
; NUMBER OF SEQUENCES: 727
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/877,124
; FILING DATE: 24-Jun-2004
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/432,503
; FILING DATE: 02-Nov-1999
; APPLICATION NUMBER: 08/974,549
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; APPLICATION NUMBER: US 08/851,843
; FILING DATE: 06-MAY-1997
; APPLICATION NUMBER: US 08/854,050
; FILING DATE: 09-MAY-1997
; APPLICATION NUMBER: US 08/911,312
; FILING DATE: 14-AUG-1997
; APPLICATION NUMBER: US 08/912,951
; FILING DATE: 14-AUG-1997
; APPLICATION NUMBER: US 08/915,503
; FILING DATE: 14-AUG-1997
; APPLICATION NUMBER: WO PCT/US97/17618
; FILING DATE: 01-OCT-1997
; APPLICATION NUMBER: WO PCT/US97/17885
; FILING DATE: 01-OCT-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph Ted
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-002610US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 611:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1154 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..1154
; OTHER INFORMATION: /note= "fusion protein composed of hTERT
; protein sequence, vector sequences, the
; Myc epitope and His6 tag"
; SEQUENCE DESCRIPTION: SEQ ID NO: 611:

Query Match 100.0%; Score 5961; DB 16; Length 1154;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MPRAPRCRAVRSLLRSHYREVLPPLATEFVRLPGQWELVORGDPAAAFRALVAQCLVCVPW 60
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 61 DARPPPAAPSFRQVSCCLKELVARVLQRLCERGANVLAFGFALIDGARGGPPPEAFTTSVR 120
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 61 DARPPPAAPSFRQVSCCLKELVARVLQRLCERGANVLAFGFALLDGARGGPPPEAFTTSVR 120
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 121 SYLPNTVTDALRGSGAWGLLLRRVGGDDVLAHLLARCALFVLVAPSCAYQVCGPPLYOLGA 180
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 121 SYLPNTVTDALRGSGAWGLLLRRVGGDDVLAHLLARCALFVLVAPSCAYQVCGPPLYOLGA 180
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 181 ATQARPPPHASGRRRLGRCERANNHVSREAGVPLGLPAGNRRRGGSASRLPLPKPRR 240
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 181 ATQARPPPHASGRRRLGRCERANNHVSREAGVPLGLPAGNRRRGGSASRLPLPKPRR 240
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 241 GAAPEPERTVPGQSWAHPCGTRGPDGFCVWSPARPABEATSLEGALSGTRSHPSVG 300
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 241 GAAPEPERTVPGQSWAHPCGTRGPDGFCVWSPARPABEATSLEGALSGTRSHPSVG 300
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 301 RQHHAGPPSTSRPPRMDTTPCPVYAEKTHPLSYSSGDKBOLEPFLSSLRPSLTGARRL 360
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 301 RQHHAGPPSTSRPPRMDTTPCPVYAEKTHPLSYSSGDKBOLEPFLSSLRPSLTGARRL 360
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 361 VETIFLGSRPMPGCTPRRLPRLPQRYWQMRPLFLELGNHAOCYPYGVLLKTHCPLRAVT 420
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 361 VETIFLGSRPMPGCTPRRLPRLPQRYWQMRPLFLELGNHAOCYPYGVLLKTHCPLRAVT 420
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 421 PAAGVCAREXPQGSVAAPPEEDTPRRLVQLLRQSSPWQYGVFVRACLRLVPPGLWGS 480
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 421 PAAGVCAREXPQGSVAAPPEEDTPRRLVQLLRQSSPWQYGVFVRACLRLVPPGLWGS 480
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 481 RHNRERPLNTKXKIFSLGKHAKLSLOBLTWKMSVRDCAWLRRSPGVGCVPAAEHRLREEI 540
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 481 RHNRERPLNTKXKIFSLGKHAKLSLOBLTWKMSVRDCAWLRRSPGVGCVPAAEHRLREEI 540
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 541 LAKFLHLMVSVYVVELLSRFYVTTETTFQKNRFFFYKRSVWSKLQSIGIQHKLKRVQURE 600
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 541 LAKFLHLMVSVYVVELLSRFYVTTETTFQKNRFFFYKRSVWSKLQSIGIQHKLKRVQURE 600
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 601 LSEAEVRQHEARPAALTSRLRFPKPDGLRPVNMDDYVVGARTFREKRAERLTSRVKA 660
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 601 LSEAEVRQHEARPAALTSRLRFPKPDGLRPVNMDDYVVGARTFREKRAERLTSRVKA 660
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 661 LFSVLNYERARRPGLLGASVGLDDIHRARWTFVLRVRAQDPPPELYFVKVDVTGAYDTI 720
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 661 LFSVLNYERARRPGLLGASVGLDDIHRARWTFVLRVRAQDPPPELYFVKVDVTGAYDTI 720
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 721 PQDLRTEVIASIIKPQNTYCVRRYAVVQKAHGHVKAFKSHVSTLTDLOPYMQFVAHL 780
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 721 PQDLRTEVIASIIKPQNTYCVRRYAVVQKAHGHVKAFKSHVSTLTDLOPYMQFVAHL 780
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 781 QETSPLRDAVVIQSSSLNEASSGLFDVFLRFMCHHAVRIRGSKSVQCGIPQGSILSTL 840
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 781 QETSPLRDAVVIQSSSLNEASSGLFDVFLRFMCHHAVRIRGSKSVQCGIPQGSILSTL 840
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 841 LCSLCYGD MENKLPAGIRRDGLLLRLVDDPFLVTPLTHAKTFLRTRTVRGVPEYGCVVNL 900
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 841 LCSLCYGD MENKLPAGIRRDGLLLRLVDDPFLVTPLTHAKTFLRTRTVRGVPEYGCVVNL 900
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 901 RKTVMNFPVEDEALGGTAFVQMPAHGLFPMCGLLDTRTLEVDQSDYSSYARTSIRASITP 960
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 901 RKTVMNFPVEDEALGGTAFVQMPAHGLFPMCGLLDTRTLEVDQSDYSSYARTSIRASITP 960
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 961 NRGFKAGRNMRRLFGVLRLLKCHSLFLLDLQVNSLQTVCTNIIYKILLQAYRFHACVLQLP 1020
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 961 NRGFKAGRNMRRLFGVLRLLKCHSLFLLDLQVNSLQTVCTNIIYKILLQAYRFHACVLQLP 1020
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

QY 1021 FHQVWKNPTFFLRLVISDTASLCYSLKAKNAGMSLGAKGAAGPLPSEAVOMLCHOAFLL 1080
Db 1021 FHQVWKNPTFFLRLVISDTASLCYSLKAKNAGMSLGAKGAAGPLPSEAVOMLCHOAFLL 1080
QY 1081 KLTRHRVTVPLGLSIRTAQTSLSKLPCTTTLTALEAANPALPSDFKTILD 1132
Db 1081 KLTRHRVTVPLGLSIRTAQTSLSKLPCTTTLTALEAANPALPSDFKTILD 1132

RESULT 35

US-10-877-022-611
; Sequence 611, Application US/10877022
; Publication No. US20040247613A1
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; Lingner, Joachim
; Nakamura, Toru
; Chapman, Karen B.
; Morin, Gregg B.
; Harley, Calvin B.
; Andrews, William H.
; TITLE OF INVENTION: Human Telomerase Catalytic Subunit
; NUMBER OF SEQUENCES: 727
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/877,022
; FILING DATE: 24-Jun-2004
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/432,503
; FILING DATE: 02-Nov-1999
; APPLICATION NUMBER: 08/974,549
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-Apr-1997
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-Apr-1997
; APPLICATION NUMBER: US 08/851,843
; FILING DATE: 06-May-1997
; APPLICATION NUMBER: US 08/854,050
; FILING DATE: 09-May-1997
; APPLICATION NUMBER: US 08/911,312
; FILING DATE: 14-Aug-1997
; APPLICATION NUMBER: US 08/912,951
; FILING DATE: 14-Aug-1997
; APPLICATION NUMBER: US 08/915,503
; FILING DATE: 14-Aug-1997
; APPLICATION NUMBER: WO PCT/US97/17618
; FILING DATE: 01-Oct-1997
; APPLICATION NUMBER: WO PCT/US97/17885
; FILING DATE: 01-Oct-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph Red
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-002610US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 611:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1154 amino acids
; TYPE: amino acid

; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..1154
; OTHER INFORMATION: /note= "fusion protein composed of. hTERT
; protein sequence, vector sequences, the
; Myc epitope and His6 tag"
; SEQUENCE DESCRIPTION: SEQ ID NO: 611:
US-10-877-022-611
Query Match 100.0%; Score 5961; DB 16; Length 1154;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MPRAPRCRAVRSLLRSHYREVLPLATFVRRLGPOGWRVLVORGDPAAFALVAQCILVCPWM 60
Db 1 MPRAPRCRAVRSLLRSHYREVLPLATFVRRLGPOGWRVLVORGDPAAFALVAQCILVCPWM 60
QY 61 DARPPAAPSPROVSKCLKELVARVLORLCERGAKNVLAFGFALLDGAAGGPPPEAFTTSVR 120
Db 61 DARPPAAPSPROVSKCLKELVARVLORLCERGAKNVLAFGFALLDGAAGGPPPEAFTTSVR 120
QY 121 SYLNTVTDALRGSGAWGLLLRRVDDVLLVHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180
Db 121 SYLNTVTDALRGSGAWGLLLRRVDDVLLVHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180
QY 181 ATQARPPPHASGPRRLGCRANWHSVREAGVPLGLPAGARRRGGSSASRLPLPKRPRR 240
Db 181 ATQARPPPHASGPRRLGCRANWHSVREAGVPLGLPAGARRRGGSSASRLPLPKRPRR 240
QY 241 GAAPEPERTVQGSWAHPGTRGSDRGFCVSPARPAEBATSLEGALSGRHSHPSVG 300
Db 241 GAAPEPERTVQGSWAHPGTRGSDRGFCVSPARPAEBATSLEGALSGRHSHPSVG 300
QY 301 RQHHAGPSTSRPPRMDTPCPVYAEKHYLYSSGDKQLRPSFLLSRLPSLTGARRL 360
Db 301 RQHHAGPSTSRPPRMDTPCPVYAEKHYLYSSGDKQLRPSFLLSRLPSLTGARRL 360
QY 361 VETIFLGSRPWMPGTTPRLPRLPQRYWQMRPLFLELLGNHAQCYPYGVLLKTHCPLRAAVT 420
Db 361 VETIFLGSRPWMPGTTPRLPRLPQRYWQMRPLFLELLGNHAQCYPYGVLLKTHCPLRAAVT 420
QY 421 PAAGVCAREKPGQSVAAPEEEDTPRRLVQLLRQHSWPQVYGFVRACLRLLVPPGLWGS 480
Db 421 PAAGVCAREKPGQSVAAPEEEDTPRRLVQLLRQHSWPQVYGFVRACLRLLVPPGLWGS 480
QY 481 RHNERRFLRNTKFTSLGKHAKLSLQELTWKMSVRDCAWLRRSPGVGCVPAAEHLRREI 540
Db 481 RHNERRFLRNTKFTSLGKHAKLSLQELTWKMSVRDCAWLRRSPGVGCVPAAEHLRREI 540
QY 541 LAKFLHLMMSVYVVELLSRFPYVTTETTPQKURLFPYRKSVMSKLOSIGIRQHLKRVQRE 600
Db 541 LAKFLHLMMSVYVVELLSRFPYVTTETTPQKURLFPYRKSVMSKLOSIGIRQHLKRVQRE 600
QY 601 LSEAEVROHREARPAALLTSRLRFTPKPDGLRPIVNMDDYVVGARTERRKRAERLTSRVKA 660
Db 601 LSEAEVROHREARPAALLTSRLRFTPKPDGLRPIVNMDDYVVGARTERRKRAERLTSRVKA 660
QY 661 LFSVLNTERARRPGLLGASVLGLDDIHRAWTFLVLRVRAQDPPPPPELYFVKVDVTGAYDTI 720
Db 661 LFSVLNTERARRPGLLGASVLGLDDIHRAWTFLVLRVRAQDPPPPPELYFVKVDVTGAYDTI 720
QY 721 PODRLTEVIASIIKPQNTYCVRRYAVVQAAHGHVRKAFKSHVSTLTDLQPMRFVLAHL 780
Db 721 PODRLTEVIASIIKPQNTYCVRRYAVVQAAHGHVRKAFKSHVSTLTDLQPMRFVLAHL 780
QY 781 QETSPLRDANVIEQSSSLNEASSGLFDVFLRFMCHAVRIEKSVMQCGIPQGSILSTL 840
Db 781 QETSPLRDANVIEQSSSLNEASSGLFDVFLRFMCHAVRIEKSVMQCGIPQGSILSTL 840
QY 841 LCSLCYGMENKLFAGIRRDGLLLRLVDDFLVTLPHLTHAKTFLRTLVRGVPYGCWNL 900

Db 841 LCSLCYGMENKLFAGIRROGLLRVLVDVFLVTPHLTHAKFTLTVRGVPETGCVNLL 900
Qy 901 RKTUVNPFVEALGGTAFAVQMPAHGLFPWCGLLLDTRTLEVQSDYSYARTSIRASLTF 960
Db 901 RKTUVNPFVEALGGTAFAVQMPAHGLFPWCGLLLDTRTLEVQSDYSYARTSIRASLTF 960
Qy 961 NRGFKAGNRMRKLFVGLRLKCHSLFLLDQVNSLQTVCTNLYKILLQAYRFHACVLQLP 1020
Db 961 NRGFKAGNRMRKLFVGLRLKCHSLFLLDQVNSLQTVCTNLYKILLQAYRFHACVLQLP 1020
Qy 1021 FHQQWKNPTFFLRVISTASLCYSILKAKNAGSLGAKGAAGPLPSEAVQWLCHQAFLL 1080
Db 1021 FHQQWKNPTFFLRVISTASLCYSILKAKNAGSLGAKGAAGPLPSEAVQWLCHQAFLL 1080
Qy 1081 KLTRHRVTYVPLGLSLRTAQQLSRKLPGLTTLTALAANAANPALPSDFKTILD 1132
Db 1081 KLTRHRVTYVPLGLSLRTAQQLSRKLPGLTTLTALAANAANPALPSDFKTILD 1132

RESULT 36

US-10-877-146-611
; Sequence 611, Application US/10877146
; Publication No. US20050013825A1
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; Lingner, Joachim
; Nakamura, Toru
; Chapman, Karen B.
; Morin, Gregg B.
; Harley, Calvin B.
; Andrews, William H.
; TITLE OF INVENTION: Human Telomerase Catalytic Subunit
; NUMBER OF SEQUENCES: 727
; CORRESPONDENCE ADDRESS:
; ADDRESS: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/877,146
; FILING DATE: 24-Jun-2004
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/432,503
; FILING DATE: 02-Nov-1999
; APPLICATION NUMBER: 08/974,549
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; APPLICATION NUMBER: US 08/851,843
; FILING DATE: 06-MAY-1997
; APPLICATION NUMBER: US 08/854,050
; FILING DATE: 09-MAY-1997
; APPLICATION NUMBER: US 08/911,312
; FILING DATE: 14-AUG-1997
; APPLICATION NUMBER: US 08/912,951
; FILING DATE: 14-AUG-1997
; APPLICATION NUMBER: US 08/915,503
; FILING DATE: 14-AUG-1997
; APPLICATION NUMBER: WO PCT/US97/17618
; FILING DATE: 01-OCT-1997
; APPLICATION NUMBER: WO PCT/US97/17885
; FILING DATE: 01-OCT-1997

; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph Ted
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-002610US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 611:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1154 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..1154
; OTHER INFORMATION: /note= "fusion protein composed of hTERT
; protein sequence, vector sequences, the
; Myc epitope and His6 tag"
; SEQUENCE DESCRIPTION: SEQ ID NO: 611:
US-10-877-146-611

Query Match 100.0%; Score 5961; DB 17; Length 1154;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MPRAPRCRAVRSLLRSHYREVLPPLATEFVRLRGQWRLVQGPAAFPALVAOCLVCPW 60
Db 1 MPRAPRCRAVRSLLRSHYREVLPPLATEFVRLRGQWRLVQGPAAFPALVAOCLVCPW 60
Qy 61 DARPPPAAPSFQVSCLELVARVQLRCERGANVLAFGFALLDARGGPPPEAFTTSVR 120
Db 61 DARPPPAAPSFQVSCLELVARVQLRCERGANVLAFGFALLDARGGPPPEAFTTSVR 120
Qy 121 SYLPNTVTDALRGSGAWGLLRVGGDVLVHLARCALFVLVAPSCAYQVCGPPLYQLGA 180
Db 121 SYLPNTVTDALRGSGAWGLLRVGGDVLVHLARCALFVLVAPSCAYQVCGPPLYQLGA 180
Qy 181 ATQARPPPHASGPRRRIGCERAWNHSVREAGVPLGLPAPGARRRGGSSASRSLPLPKPRR 240
Db 181 ATQARPPPHASGPRRRIGCERAWNHSVREAGVPLGLPAPGARRRGGSSASRSLPLPKPRR 240
Qy 241 GAPEPERTVQGSWAHPGRTGSDRGFCVVSPPARPAEATSEALSGSTRHSHPVG 300
Db 241 GAPEPERTVQGSWAHPGRTGSDRGFCVVSPPARPAEATSEALSGSTRHSHPVG 300
Qy 301 RQHHAGPSTSRPPRPMWDTPCPPVYAEVKHFLYSSGDKQELRPSFLLSSLRPSLTGARRL 360
Db 301 RQHHAGPSTSRPPRPMWDTPCPPVYAEVKHFLYSSGDKQELRPSFLLSSLRPSLTGARRL 360
Qy 361 VETIFLGSRPWMEGTPTRRLLPRLPQRYWQMRPLFLELLGNHAQCPYGVLLKTHCPLRAAVT 420
Db 361 VETIFLGSRPWMEGTPTRRLLPRLPQRYWQMRPLFLELLGNHAQCPYGVLLKTHCPLRAAVT 420
Qy 421 PAAGVCAREKPGQSVAAPEEEDTPRLVOLLQHSHPWQYGVFVACLRRLVPPGLWGS 480
Db 421 PAAGVCAREKPGQSVAAPEEEDTPRLVOLLQHSHPWQYGVFVACLRRLVPPGLWGS 480
Qy 481 RHNERRFLRNTKKFISLGKHAQLSLQELTWKMSVRDCAWLRRSPGVGCVPAAEHRLREEI 540
Db 481 RHNERRFLRNTKKFISLGKHAQLSLQELTWKMSVRDCAWLRRSPGVGCVPAAEHRLREEI 540
Qy 541 LAKFLHLMMSVYVVELLRSFFYVTTFTFQKNRLFYFKRSVMSKLSQSIGIRGHLKRVQLRE 600
Db 541 LAKFLHLMMSVYVVELLRSFFYVTTFTFQKNRLFYFKRSVMSKLSQSIGIRGHLKRVQLRE 600
Qy 601 LSEAEVQHREARPAALITSLRFTPKDDGLRPINMDYVVGARTFREKRAERLTSRVKA 660
Db 601 LSEAEVQHREARPAALITSLRFTPKDDGLRPINMDYVVGARTFREKRAERLTSRVKA 660
Qy 661 LFSVLNYERARRPGILGASVLGLDDIHRWRTFVLVRADQPPPELVFVKVVDVTVGADYTI 720
Db 661 LFSVLNYERARRPGILGASVLGLDDIHRWRTFVLVRADQPPPELVFVKVVDVTVGADYTI 720

661 LFSVLNYERARRPGLLGASVGLDLDIHRWRTFVLVRVRAQDPPELYFVKVDVGTAYDTI 720
721 PDRLTEVIASIIKPQNTYCVRYAVVQAAHGHVKAFKSHVSTLTDLPYMRQFVAHL 780
721 PDRLTEVIASIIKPQNTYCVRYAVVQAAHGHVKAFKSHVSTLTDLPYMRQFVAHL 780
781 QETSPRDVAVVIOSSSLNEASSGLFDVFLRFCHHAVIRGKSYVQCOGIPGOSILSTL 840
781 QETSPRDVAVVIOSSSLNEASSGLFDVFLRFCHHAVIRGKSYVQCOGIPGOSILSTL 840
841 LCLSCYGDMEKLFAGIRRDGLLRLVDPLVTPHILTHAKTFLRTLVRGVPYGCVMNL 900
841 LCLSCYGDMEKLFAGIRRDGLLRLVDPLVTPHILTHAKTFLRTLVRGVPYGCVMNL 900
901 RKTVMNFPVEDEALGTAFAVQMPAHGLFPWCGLLDTRTLEVOSSDYSSYARTSIRASLTF 960
901 RKTVMNFPVEDEALGTAFAVQMPAHGLFPWCGLLDTRTLEVOSSDYSSYARTSIRASLTF 960
961 NRGFKAGRNMRRLFGVLRILKCHSLFDLDQVNSLQTVCTNIYKILLQAYRFHACVQLQP 1020
961 NRGFKAGRNMRRLFGVLRILKCHSLFDLDQVNSLQTVCTNIYKILLQAYRFHACVQLQP 1020
1021 FHOQVWKNPTFFLRLVSDTASLCYSILKAKNAGMSIGAKGAGPLPSEAVQMLCHQAFLL 1080
1021 FHOQVWKNPTFFLRLVSDTASLCYSILKAKNAGMSIGAKGAGPLPSEAVQMLCHQAFLL 1080
1081 KLTHRTVTVPLGLSLRTAQTLRSKLPGLTTLTALEAAANPALPSDFKTILD 1132
1081 KLTHRTVTVPLGLSLRTAQTLRSKLPGLTTLTALEAAANPALPSDFKTILD 1132

RESULT 37

US-10-044-692-325
; Sequence 325, Application US/10044692
; Publication No. US20030096344A1

GENERAL INFORMATION:

APPLICANT: Cech, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin
Andrews, William H.

TITLE OF INVENTION: HUMAN TELOMERASE CATALYTIC SUBUNIT: DIAGNOSTIC AND THERAPEUTIC METHODS

NUMBER OF SEQUENCES: 335

CORRESPONDENCE ADDRESS:

ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: United States of America
ZIP: 94111

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/044,692
FILING DATE: 11-Jan-2002
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/912,951
FILING DATE: <Unknown>
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997

APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002600US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 325:
SEQUENCE CHARACTERISTICS:
LENGTH: 1189 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 325:
US-10-044-692-325

Query Match 100.0%; Score 5961; DB 14; Length 1189;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPAPRCRAVRSLRSHYREVLPATFVRRLPQGWRLVQRGDPAAFRALVAQCLVCVPW 60
DB 58 MPAPRCRAVRSLRSHYREVLPATFVRRLPQGWRLVQRGDPAAFRALVAQCLVCVPW 117
QY 61 DARPPAAPSPQVSCLEKELVARVQLRCERGAKNVLAFGFALLDGAAGGPPPEAFTTSVR 120
DB 118 DARPPAAPSPQVSCLEKELVARVQLRCERGAKNVLAFGFALLDGAAGGPPPEAFTTSVR 177
QY 121 SYLNTVTDALRGSGAWGLLRRVGGDVLVHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180
DB 178 SYLNTVTDALRGSGAWGLLRRVGGDVLVHLLARCALFVLVAPSCAYQVCGPPLYQLGA 237
QY 181 ATQARPPPHASGPRRLRCERAWNHSVREAGVPLGLPAPGARRRGSGASRSLPLPKRPRR 240
DB 238 ATQARPPPHASGPRRLRCERAWNHSVREAGVPLGLPAPGARRRGSGASRSLPLPKRPRR 297
QY 241 GAAPERTPVCGGSAWHPGRTGRGSDRGFCVVSAPARPAEATSLRGALSGTHSHPSVVG 300
DB 298 GAAPERTPVCGGSAWHPGRTGRGSDRGFCVVSAPARPAEATSLRGALSGTHSHPSVVG 357
QY 301 RQHAGPSTSRPPRPWDTPCPVVAETKHFLYSSGDKEQLRPSFLLSSLRSLTGARRL 360
DB 358 RQHAGPSTSRPPRPWDTPCPVVAETKHFLYSSGDKEQLRPSFLLSSLRSLTGARRL 417
QY 361 VETIFLGSRPWMPGTTPRRLPRLPQRYQWRPLFLELLGNHACQPYGVLLKTHCPLRAAVT 420
DB 418 VETIFLGSRPWMPGTTPRRLPRLPQRYQWRPLFLELLGNHACQPYGVLLKTHCPLRAAVT 477
QY 421 PAAGVCAREKPGQSVAAPEEEDTPRRLVOLLROHSSPMQVYGFVACLRRLVPPGLWGS 480
DB 478 PAAGVCAREKPGQSVAAPEEEDTPRRLVOLLROHSSPMQVYGFVACLRRLVPPGLWGS 537
QY 481 RINERRFLRNTKFTISLGKHAQLSQELTKWMSVRDCAWLRSRSPGVGCVPAAEHRLREEI 540
DB 538 RINERRFLRNTKFTISLGKHAQLSQELTKWMSVRDCAWLRSRSPGVGCVPAAEHRLREEI 597
QY 541 LAKFLHMLMSVYVVELLSRFFVYVTTTFOKNRLLFFYRKSVMWSKLQSIGIRQHLKRVLRE 600
DB 598 LAKFLHMLMSVYVVELLSRFFVYVTTTFOKNRLLFFYRKSVMWSKLQSIGIRQHLKRVLRE 657
QY 601 LSEAEVRQHREARPAALLTSRLRFPKPDGLRIRVNMVYVGARTFRREKRAERLTSRVKA 660
DB 658 LSEAEVRQHREARPAALLTSRLRFPKPDGLRIRVNMVYVGARTFRREKRAERLTSRVKA 717
QY 661 LFSVLNYERARRPGLLGASVGLDLDIHRWRTFVLVRVRAQDPPELYFVKVDVGTAYDTI 720
DB 718 LFSVLNYERARRPGLLGASVGLDLDIHRWRTFVLVRVRAQDPPELYFVKVDVGTAYDTI 777
QY 721 PODRLTEVIASIIKPQNTYCVRYAVVQAAHGHVKAFKSHVSTLTDLPYMRQFVAHL 780

Db 778 PODRLTEVIASIIKPNQTYCYRRYAVQKAAHGHVIRKAFKSHVSTLTDLPYMRQFVAHL 837
Qy 781 QETSPLRDAVTEQSSSINEASSGLFDVFLRPMCHHVRIRKGSYVQCQGIPOGSILSTL 840
Db 838 QETSPLRDAVTEQSSSINEASSGLFDVFLRPMCHHVRIRKGSYVQCQGIPOGSILSTL 897
Qy 841 LCSLCYGDMEKLFAGIRDDGLLRVDDFLVTLPHLTHAKTFLTLVRGVPEYGCVVNL 900
Db 898 LCSLCYGDMEKLFAGIRDDGLLRVDDFLVTLPHLTHAKTFLTLVRGVPEYGCVVNL 957
Qy 901 RKTUVNFFVEALGCTAFVQMPAHGLFPWCGLLDDTRTLEQSDYSSYARTSIRASLTF 960
Db 958 RKTUVNFFVEALGCTAFVQMPAHGLFPWCGLLDDTRTLEQSDYSSYARTSIRASLTF 1017
Qy 961 NRGFKAGNRMRKLFVLRKLSHSLFDLQVNSLQTVCTNIIKILLQAYRPHACVLQLP 1020
Db 1018 NRGFKAGNRMRKLFVLRKLSHSLFDLQVNSLQTVCTNIIKILLQAYRPHACVLQLP 1077
Qy 1021 FHOQVWKNPFFLRVISTASLCYSLKAKNAGMSLGAKGAGPLPSEAVQWLCHOAFLL 1080
Db 1078 FHOQVWKNPFFLRVISTASLCYSLKAKNAGMSLGAKGAGPLPSEAVQWLCHOAFLL 1137
Qy 1081 KLTRHRVTYVPLLSLRTAQTLRSKLPCTTLTALAAAANPALPSDFKTILD 1132
Db 1138 KLTRHRVTYVPLLSLRTAQTLRSKLPCTTLTALAAAANPALPSDFKTILD 1189

RESULT 38

US-10-044-539-325

; Sequence 325, Application US/10044539

; Publication No. US2003010093A1

GENERAL INFORMATION:

; APPLICANT: Cech, Thomas R.

; Lingner, Joachim

; Nakamura, Toru

; Chapman, Karen B.

; Morin, Gregg B.

; Harley, Calvin

; Andrews, William H.

; TITLE OF INVENTION: HUMAN TELOMERASE CATALYTIC SUBUNIT: DIAGNOSTIC AND

; THERAPEUTIC METHODS

; NUMBER OF SEQUENCES: 335

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Townsend and Townsend and Crew LLP

; STREET: Two Embarcadero Center, 8th Floor

; CITY: San Francisco

; STATE: California

; COUNTRY: United States of America

; ZIP: 94111

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent In Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/10/044,539

; FILING DATE: 11-Jan-2002

; CLASSIFICATION DATA:

; PRIORITY APPLICATION DATA:

; FILING DATE: 08/912,951

; APPLICATION NUMBER: US 08/854,050

; FILING DATE: 09-MAY-1997

; APPLICATION NUMBER: US 08/851,843

; FILING DATE: 06-MAY-1997

; APPLICATION NUMBER: US 08/846,017

; FILING DATE: 25-APR-1997

; APPLICATION NUMBER: US 08/844,419

; FILING DATE: 18-APR-1997

; APPLICATION NUMBER: US 08/724,643

; FILING DATE: 01-OCT-1996

; ATTORNEY/AGENT INFORMATION:

; NAME: Apple, Randolph T.

; ; REGISTRATION NUMBER: 36,429

; REFERENCE/DOCKET NUMBER: 015389-002600US

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (415) 576-0200

; TELEFAX: (415) 576-0300

; INFORMATION FOR SEQ ID NO: 325:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 1189 amino acids

; TYPE: amino acid

; STRANDEDNESS: <Unknown>

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; SEQUENCE DESCRIPTION: SEQ ID NO: 325:

US-10-044-539-325

Query Match 100.0%; Score 5961; DB 14; Length 1189;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MPRAPRCRAVRSLLRSHYREVLPATFVRRLLGPOGWRLVQRGDPAAFPALVAQCLVCPWP 60

Db 58 MPRAPRCRAVRSLLRSHYREVLPATFVRRLLGPOGWRLVQRGDPAAFPALVAQCLVCPWP 117

Qy 61 DARPPPAAPSPROVSKLKLVARVLQRLCERGAKNVLAFFALLDGGRGPEAFTTSVR 120

Db 118 DARPPPAAPSFRQVSKLKLVARVLQRLCERGAKNVLAFFALLDGGRGPEAFTTSVR 177

Qy 121 SYLENTVTDLRSGGAWGLLLRRVDDVLVHLLARCALFVLVAPSCAYQVCGPPLYLGA 180

Db 178 SYLENTVTDLRSGGAWGLLLRRVDDVLVHLLARCALFVLVAPSCAYQVCGPPLYLGA 237

Qy 181 ATQARPPPHASGPRRRRLGCERAWNHSVREAGVPLGAPGARRRGGSASRSLPLPKRRR 240

Db 238 ATQARPPPHASGPRRRRLGCERAWNHSVREAGVPLGAPGARRRGGSASRSLPLPKRRR 297

Qy 241 GAAPERTPVQGSWAHPGTRGSDRGFCVSPARPAEATSLLEGALSCTRHSHPVSG 300

Db 298 GAAPERTPVQGSWAHPGTRGSDRGFCVSPARPAEATSLLEGALSCTRHSHPVSG 357

Qy 301 RQHAGPSTSRPPRMDTPCPVYAEIKHFLYSYSGDKQLRPSFLLSRPSLTGARRL 360

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Db 418 VETIFLGSRPWMPGTPRRLPRLPQRYQWMLPFLLELGNHACCPYGVLLKTHCPLRAAVT 477

Qy 421 PAAGVCAREKPGQSVAAPEEEDTPRRLVQLLRHSSPWQVYGFVRACLRLVPPGLWGS 480

Db 478 PAAGVCAREKPGQSVAAPEEEDTPRRLVQLLRHSSPWQVYGFVRACLRLVPPGLWGS 537

Qy 481 RHNERRFLRNTKFTISLGKHAQLSLOELTWKMSVRDCAWLRSPGVGCVPAAEHRLREI 540

Db 538 RHNERRFLRNTKFTISLGKHAQLSLOELTWKMSVRDCAWLRSPGVGCVPAAEHRLREI 597

Qy 541 LAKFLHMLMSYVVVELLSRFFYVTTFTFQKRLFFYRKSVMKLSQISIGIRHQLKRVQLRE 600

Db 598 LAKFLHMLMSYVVVELLSRFFYVTTFTFQKRLFFYRKSVMKLSQISIGIRHQLKRVQLRE 657

Qy 601 LSEAEVQRHREARPAALLTSRLRFIPKPDGLRPIVNMDDYVVGARTFRREKRAERLTSRVKA 660

Db 658 LSEAEVQRHREARPAALLTSRLRFIPKPDGLRPIVNMDDYVVGARTFRREKRAERLTSRVKA 717

Qy 661 LFSVLNYERARRPGLLGASVLGLDDIHRAMRTFVLVRVAQDPPPPPELYFVKVDVTGAYDTI 720

Db 718 LFSVLNYERARRPGLLGASVLGLDDIHRAMRTFVLVRVAQDPPPPPELYFVKVDVTGAYDTI 777

Qy 721 PODRLTEVIASIIKPNQTYCYRRYAVQKAAHGHVIRKAFKSHVSTLTDLPYMRQFVAHL 780

Db 778 PODRLTEVIASIIKPNQTYCYRRYAVQKAAHGHVIRKAFKSHVSTLTDLPYMRQFVAHL 837

Qy 781 QETSPLRDAVTEQSSSINEASSGLFDVFLRPMCHHVRIRKGSYVQCQGIPOGSILSTL 840

Db 838 QETSLRDAVIEQSSLINEASSGLFDVFLRPMCHAVRIKSVQCGIPIQGSILSTL 897
Qy 841 LCSLCYGMENKLFAGIRRDGLLLRLVDDFLVTTPLHAKTFLRLTVRGVPEYGCVVNL 900
Db 898 LCSLCYGMENKLFAGIRRDGLLLRLVDDFLVTTPLHAKTFLRLTVRGVPEYGCVVNL 957
Qy 901 KTVNVPFVEDALGCTAFVQMPAHGLFPWCGLLLDTRTLEVQSDYSSYARTSIRASLTF 960
Db 958 KTVNVPFVEDALGCTAFVQMPAHGLFPWCGLLLDTRTLEVQSDYSSYARTSIRASLTF 1017
Qy 961 NRGFKAGNRKRLFGVLRKCHSLFLDLQVNSLQVCTNIYKILLQAYRPHACVQLP 1020
Db 1018 NRGFKAGNRKRLFGVLRKCHSLFLDLQVNSLQVCTNIYKILLQAYRPHACVQLP 1077
Qy 1021 FHOQWKNPFFLRFVISDTASLCYSILKAKNAGMSLGAKGAGPLPSEAVQWLCHQAFLL 1080
Db 1078 FHOQWKNPFFLRFVISDTASLCYSILKAKNAGMSLGAKGAGPLPSEAVQWLCHQAFLL 1137
Qy 1081 KLTRHRVTVPLLSRLTAQTLQSLKPLGTTTLTALEAAANPALPSDFKTILD 1132
Db 1138 KLTRHRVTVPLLSRLTAQTLQSLKPLGTTTLTALEAAANPALPSDFKTILD 1189

RESULT 39
US-10-325-810-613
; Sequence 613, Application US/10325810
; Publication No. US20030204069A1
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; Lingner, Joachim
; Nakamura, Toru
; Chapman, Karen B.
; Morin, Gregg B.
; Harley, Calvin B.
; Andrews, William H.
; TITLE OF INVENTION: Human Telomerase Catalytic Subunit
; NUMBER OF SEQUENCES: 633
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/325,810
; FILING DATE: 20-Dec-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/402,181
; FILING DATE: 29-Sep-1997
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; APPLICATION NUMBER: US 08/851,843
; FILING DATE: 06-MAY-1997
; APPLICATION NUMBER: US 08/854,050
; FILING DATE: 09-MAY-1997
; APPLICATION NUMBER: US 08/911,312
; FILING DATE: 14-AUG-1997
; APPLICATION NUMBER: US 08/912,951
; FILING DATE: 14-AUG-1997
; APPLICATION NUMBER: US 08/915,503
; FILING DATE: 14-AUG-1997
; APPLICATION NUMBER: WO PCT/US97/17885

; FILING DATE: 01-OCT-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Ausenhus, Scott L.
; REGISTRATION NUMBER: 42,271
; REFERENCE/DOCKET NUMBER: 015389-0026200S
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 613:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1189 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..1189
; OTHER INFORMATION: /note= "fusion protein composed of
; melittin signal sequence and full length
; hTERT protein"
; SEQUENCE DESCRIPTION: SEQ ID NO: 613:
; US-10-325-810-613
; Query Match 100.0%; Score 5961; DB 15; Length 1189;
; Best Local Similarity 100.0%; Pred. No. 0;
; Matches 1132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MPAPRCRAVRSLLRSHYREVLPLATFVRRILGPGWRLVQRGDPAAPFALVAQCLVCVPW 60
Db 58 MPAPRCRAVRSLLRSHYREVLPLATFVRRILGPGWRLVQRGDPAAPFALVAQCLVCVPW 117
Qy 61 DARPPAAPSPROVSCLELVARVLQRLCERGANVLAFLGALLDGGARGGPEAFTTSVR 120
Db 118 DARPPAAPSPROVSCLELVARVLQRLCERGANVLAFLGALLDGGARGGPEAFTTSVR 177
Qy 121 SYLENTVTDALRGSGANGLLRLRVGDDVLVHLLARCALFVLVAFSCAYQVCGPPLYQLGA 180
Db 178 SYLENTVTDALRGSGANGLLRLRVGDDVLVHLLARCALFVLVAFSCAYQVCGPPLYQLGA 237
Qy 181 ATQARPPPHASGPRRLGCRANWHSVREAGVPLGLPAGARRGGGSASRLPLPKRRR 240
Db 238 ATQARPPPHASGPRRLGCRANWHSVREAGVPLGLPAGARRGGGSASRLPLPKRRR 297
Qy 241 GAAPERTPVQGSWAHPGRTGCRSDRGFCVSPAPAEATSLGALSCTRSHSPSVG 300
Db 298 GAAPERTPVQGSWAHPGRTGCRSDRGFCVSPAPAEATSLGALSCTRSHSPSVG 357
Qy 301 RQHAGPPSTSRPPRPMDTPCPVYAEYTKHFLYSSGDKQLRPSFLSLSPSLTGARRL 360
Db 358 RQHAGPPSTSRPPRPMDTPCPVYAEYTKHFLYSSGDKQLRPSFLSLSPSLTGARRL 417
Qy 361 VETIFLGSRPMPGTPRRLPRLPQRYWQMRPLFLELLGNHAQCPYGVLLKTHCPFLRAAVT 420
Db 418 VETIFLGSRPMPGTPRRLPRLPQRYWQMRPLFLELLGNHAQCPYGVLLKTHCPFLRAAVT 477
Qy 421 PAAGVCAREKPGQSVAAPEEDTDPRLVOLLROHSSFPWQYVGFVACRLRLVPPGLWGS 480
Db 478 PAAGVCAREKPGQSVAAPEEDTDPRLVOLLROHSSFPWQYVGFVACRLRLVPPGLWGS 537
Qy 481 RHNERRFLRNTKFI SLGKIAKLSLOELTWKMSVDCAWLRSSPGVGVCPAAEHLRLEEI 540
Db 538 RHNERRFLRNTKFI SLGKIAKLSLOELTWKMSVDCAWLRSSPGVGVCPAAEHLRLEEI 597
Qy 541 LAKEFLHLMSSVYVVELLRSFFYVTTTFFQKNRLFYFKSVMSKLSQSIGIRHLLKRVQRE 600
Db 598 LAKEFLHLMSSVYVVELLRSFFYVTTTFFQKNRLFYFKSVMSKLSQSIGIRHLLKRVQRE 657
Qy 601 LSEAEVQHREARPAALLTSRLRFPKPDGLRPIVNDYVVGARTFREKRAERLTSRVKA 660
Db 658 LSEAEVQHREARPAALLTSRLRFPKPDGLRPIVNDYVVGARTFREKRAERLTSRVKA 717
Qy 661 LFSVLNYERARRPGLLGASVLGLDDIHRAWRTFVLVRQAQDPPPELYFVKVDVTGAYDTI 720

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Db 718 LFSVLYERARRGLLGASVGLDDIHRARWIFVLRVRAQDPPPELYFVKVDVTGAYDI 777
Qy 721 PQDLTEVIASIIKPONTYCVRRYAVVQAAHGHVKAFKSHVSTLTDLPYMRQFVAHL 780
Db 778 PQDLTEVIASIIKPONTYCVRRYAVVQAAHGHVKAFKSHVSTLTDLPYMRQFVAHL 837
Qy 781 QETSPURDAVVIQSSSLNEASSGLFDVFLRFMCHHAVIRKGSYVQCGIIPQGSITLSTL 840
Db 838 QETSPURDAVVIQSSSLNEASSGLFDVFLRFMCHHAVIRKGSYVQCGIIPQGSITLSTL 897
Qy 841 LCSLCYGDMEKFLFAGIRRDGLLLRLVDDFLVPLTHAKTFLRLTVRGVPEYGCVNL 900
Db 898 LCSLCYGDMEKFLFAGIRRDGLLLRLVDDFLVPLTHAKTFLRLTVRGVPEYGCVNL 957
Qy 901 RKTVMNPFVEDEALGTAFOVMPAHGLFPWCGLLDTRTLEVQSDYSSVARTSIRASLTF 960
Db 958 RKTVMNPFVEDEALGTAFOVMPAHGLFPWCGLLDTRTLEVQSDYSSVARTSIRASLTF 1017
Qy 961 NRGFKAQRNRRKLFGLVRLKCHSLFDLDQVNSLQTVCTNIYKILLQAYRHACVLQLP 1020
Db 1018 NRGFKAQRNRRKLFGLVRLKCHSLFDLDQVNSLQTVCTNIYKILLQAYRHACVLQLP 1077
Qy 1021 FHQVQWKNPTFFLRVISDTSASLCYSILKAKNAGMSLGAKGAGPLPSEAVQWLCHQAFLL 1080
Db 1078 FHQVQWKNPTFFLRVISDTSASLCYSILKAKNAGMSLGAKGAGPLPSEAVQWLCHQAFLL 1137
Qy 1081 KLTHRVTVYVPLLGSLRTAQTSRLKPGTTLTALEAANPALPSPDKTILD 1132
Db 1138 KLTHRVTVYVPLLGSLRTAQTSRLKPGTTLTALEAANPALPSPDKTILD 1189

RESULT 40
US-10-877-124-613
; Sequence 613, Application US/10877124
; Publication No. US20040242529A1
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; Lingner, Joachim
; Nakamura, Toru
; Chapman, Karen B.
; Morin, Gregg B.
; Harley, Calvin B.
; Andrews, William H.
; TITLE OF INVENTION: Human Telomerase Catalytic Subunit
; NUMBER OF SEQUENCES: 727
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/877,124
; FILING DATE: 24-Jun-2004
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/432,503
; FILING DATE: 02-Nov-1999
; APPLICATION NUMBER: 08/974,549
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; APPLICATION NUMBER: US 08/851,843
; FILING DATE: 06-MAY-1997
```

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; APPLICATION NUMBER: US 08/854,050
; FILING DATE: 09-MAY-1997
; APPLICATION NUMBER: US 08/911,312
; FILING DATE: 14-AUG-1997
; APPLICATION NUMBER: US 08/912,951
; FILING DATE: 14-AUG-1997
; APPLICATION NUMBER: US 08/915,503
; FILING DATE: 14-AUG-1997
; APPLICATION NUMBER: WO PCT/US97/17618
; FILING DATE: 01-OCT-1997
; APPLICATION NUMBER: WO PCT/US97/17885
; FILING DATE: 01-OCT-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph, Ted
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-002610US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 613:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1189 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..1189
; OTHER INFORMATION: /note= "fusion protein composed of
; melittin signal sequence and full length
; hTERT protein"
; SEQUENCE DESCRIPTION: SEQ ID NO: 613:
US-10-877-124-613

Query Match 100.0%; Score 5961; DB 16; Length 1189;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MPRAPRCRAVRSLLSHYREVLPVPLATFVRRLLGPGQWRLVORGDPAAFRALVAQCLVCVW 60
Db 58 MPRAPRCRAVRSLLSHYREVLPVPLATFVRRLLGPGQWRLVORGDPAAFRALVAQCLVCVW 117
Qy 61 DARPPPAAPSQVSVCKELVARVQLRQCERAKNVAFGFALLDGCARGGPEAFVTSVR 120
Db 118 DARPPPAAPSQVSVCKELVARVQLRQCERAKNVAFGFALLDGCARGGPEAFVTSVR 177
Qy 121 SYLPNTVTDALRGSGAWGLLLRRVGDVVLVHLLARCALPVLVAPSCAYVCGPPLYQLGA 180
Db 178 SYLPNTVTDALRGSGAWGLLLRRVGDVVLVHLLARCALPVLVAPSCAYVCGPPLYQLGA 237
Qy 181 ATQARPPPHASGPRRLGCERAWNHSVREAGVPLGLPAPGARRRGGSASRSLPLKPRR 240
Db 238 ATQARPPPHASGPRRLGCERAWNHSVREAGVPLGLPAPGARRRGGSASRSLPLKPRR 297
Qy 241 GAAPPERTPVQGSWAHPGTRGSPDRGFCVVSPPARPAEAEATSEALSGTRHSHPSVG 300
Db 298 GAAPPERTPVQGSWAHPGTRGSPDRGFCVVSPPARPAEAEATSEALSGTRHSHPSVG 357
Qy 301 RQHAGPPSTSRPPRWDTPCPVVAETHGFHYSSGDKQLRPSFLLSLRSLTGARRL 360
Db 358 RQHAGPPSTSRPPRWDTPCPVVAETHGFHYSSGDKQLRPSFLLSLRSLTGARRL 417
Qy 361 VETIFLGSPPWMPGTPRRLPRLPQRYQWQMRPLFLELLGNHACPCYGVLLKTHCPLRAAVT 420
Db 418 VETIFLGSPPWMPGTPRRLPRLPQRYQWQMRPLFLELLGNHACPCYGVLLKTHCPLRAAVT 477
Qy 421 PAAGVCAREKPOGSSVAAPPEEDTDPRRLVQLLRQHSPPMQVYGFVRACLRLRVLPPGLWGS 480
Db 478 PAAGVCAREKPOGSSVAAPPEEDTDPRRLVQLLRQHSPPMQVYGFVRACLRLRVLPPGLWGS 537
Qy 481 RINERRFLENTKFTISLGHAKLSLOELTWKQSVRDCAWLRRSPGVGCVPAAEHRLREEI 540
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Db 538 RHNERFURNTKFKTSLGKHAKLSQELTWKMSVRDCAWLRSPGVGCPAAEHLRBEI 597
Qy 541 LAKFLHLMMSVYVVELLRSFFVYVTTTTPQKNLFYRKSVKSLQSIGIRHKLKVOLRE 600
Db 598 LAKFLHLMMSVYVVELLRSFFVYVTTTTPQKNLFYRKSVKSLQSIGIRHKLKVOLRE 657
Qy 601 LSEAEVROHREARPAALLTSRLRFTPKPDGLRPIVNMDDVVGARTFRKRAERLTSRVKA 660
Db 658 LSEAEVROHREARPAALLTSRLRFTPKPDGLRPIVNMDDVVGARTFRKRAERLTSRVKA 717
Qy 661 LFSVLNTERARRPGLGASVGLDDIHRATWTEVLVRPAODPPPELVFKVDVTVGAYDTI 720
Db 718 LFSVLNTERARRPGLGASVGLDDIHRATWTEVLVRPAODPPPELVFKVDVTVGAYDTI 777
Qy 721 PODRLTEVIASIIKPQNTYCVRRYAVVQKAAHGHVRKAFKSHVSTLTDLPYMQFVAHL 780
Db 778 PODRLTEVIASIIKPQNTYCVRRYAVVQKAAHGHVRKAFKSHVSTLTDLPYMQFVAHL 837
Qy 781 QETSPLRDVAVIEOSSSINEASSGLFDVFLRFMCHHAVIRGKSYVQCQIGIPQGSILSTL 840
Db 838 QETSPLRDVAVIEOSSSINEASSGLFDVFLRFMCHHAVIRGKSYVQCQIGIPQGSILSTL 897
Qy 841 LCSLCYGDMEKNLFGIRRDGLLRVDDFLVTPHLLTHAKTFLRTLVRGVPEYGCVVNL 900
Db 898 LCSLCYGDMEKNLFGIRRDGLLRVDDFLVTPHLLTHAKTFLRTLVRGVPEYGCVVNL 957
Qy 901 RKTVNFPEDEALGGTAFVQMPAHGLFPWCGLLDTRTLEVSQDYSYARTSIRASLTF 960
Db 958 RKTVNFPEDEALGGTAFVQMPAHGLFPWCGLLDTRTLEVSQDYSYARTSIRASLTF 1017
Qy 961 NRGFKAGNMRKLFVGLRLKCHSLFDLDQVNSIQTVCTNIYKILLQAVRFHACVLOLP 1020
Db 1018 NRGFKAGNMRKLFVGLRLKCHSLFDLDQVNSIQTVCTNIYKILLQAVRFHACVLOLP 1077
Qy 1021 FHOQVWKNPTFLRAVISTASLCYSILKAKNAGSLGAKGAGPLPSEAVOMLCHOAFIL 1080
Db 1078 FHOQVWKNPTFLRAVISTASLCYSILKAKNAGSLGAKGAGPLPSEAVOMLCHOAFIL 1137
Qy 1081 KLTHRYVYVPLGLSLRTAQTOLSRKLPGLTTLTALEAANPALPSPDKTILD 1132
Db 1138 KLTHRYVYVPLGLSLRTAQTOLSRKLPGLTTLTALEAANPALPSPDKTILD 1189

RESULT 41

US-10-877-022-613
; Sequence 613, Application US/10877022
; Publication No. US20040247613A1

GENERAL INFORMATION:

APPLICANT: Cech, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin B.
Andrews, William H.

TITLE OF INVENTION: Human Telomerase Catalytic Subunit

NUMBER OF SEQUENCES: 727

CORRESPONDENCE ADDRESS:

ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
City: San Francisco
STATE: California
COUNTRY: USA

ZIP: 94111-3834

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/877,022

FILING DATE: 24-Jun-2004

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/432,503
FILING DATE: 02-Nov-1999
APPLICATION NUMBER: 08/974,549
FILING DATE: <Unknown>
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/911,312
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: WO PCT/US97/17618
FILING DATE: 01-OCT-1997
APPLICATION NUMBER: WO PCT/US97/17885
FILING DATE: 01-OCT-1997

ATTORNEY/AGENT INFORMATION:

NAME: Apple, Randolph Ted
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002610US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300

INFORMATION FOR SEQ ID NO: 613:

SEQUENCE CHARACTERISTICS:
LENGTH: 1189 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:

NAME/KEY: Protein

LOCATION: 1..1189

OTHER INFORMATION: /note= "fusion protein composed of
melittin signal sequence and full length
hTERT protein"

SEQUENCE DESCRIPTION: SEQ ID NO: 613:

US-10-877-022-613

Query Match 100.0%; Score 5961; DB 16; Length 1189;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MPRAPRCRAVRSLLRSHYREVLP	1189
Db	58	MPRAPRCRAVRSLLRSHYREVLP <td>117</td>	117
Qy	61	DARPPPAAPSFQVSCCLKELVARV <td>120</td>	120
Db	118	DARPPPAAPSFQVSCCLKELVARV <td>177</td>	177
Qy	121	SYLPTNTVDALRGSGAWGLLLRRV <td>180</td>	180
Db	178	SYLPTNTVDALRGSGAWGLLLRRV <td>237</td>	237
Qy	181	ATQARPPPHASGPRRLGGERAWNH <td>240</td>	240
Db	238	ATQARPPPHASGPRRLGGERAWNH <td>297</td>	297
Qy	241	GAAPEDERTPVGQSWAHPGRTRG <td>300</td>	300
Db	298	GAAPEDERTPVGQSWAHPGRTRG <td>357</td>	357
Qy	301	RQHAGPPSTSRPPRPWDTPCPPV <td>360</td>	360
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QY 361 VETIFLGSRWMPGTPRRRLPRLPQRYQWMEPLFLELLGNHAQCPYGVLLKTHCPRAAVT 420
DB 418 VETIFLGSRWMPGTPRRRLPRLPQRYQWMEPLFLELLGNHAQCPYGVLLKTHCPRAAVT 477
QY 421 PAAGVCAREKPGQSVAAPEEEDTDPRLVOLLQHSPPQWYGVFVACLRRLVPPGLMGS 480
DB 478 PAAGVCAREKPGQSVAAPEEEDTDPRLVOLLQHSPPQWYGVFVACLRRLVPPGLMGS 537
QY 481 RHNERFLRNTKFIISGKHAKLSLOELTWKMSVRCDCAWLRSPGVGCVPAEHRRLREI 540
DB 538 RHNERFLRNTKFIISGKHAKLSLOELTWKMSVRCDCAWLRSPGVGCVPAEHRRLREI 597
QY 541 LAKFLHLMVSVVVELLRSFFYTTTFOKNRFFFYRKSVWSKLQSIGIRQHILKRVQLRE 600
DB 598 LAKFLHLMVSVVVELLRSFFYTTTFOKNRFFFYRKSVWSKLQSIGIRQHILKRVQLRE 657
QY 601 LSAEVRQHRREARPAALLTSRLRIFPKPDGLRPIVNDYVVGARTFREKKAERLTSRVKA 660
DB 658 LSAEVRQHRREARPAALLTSRLRIFPKPDGLRPIVNDYVVGARTFREKKAERLTSRVKA 717
QY 661 LFSVLYNERARRRGLLGASVLGDDIHRARWTFVLRVRAODPPELYFVKVDVVTGAYDTI 720
DB 718 LFSVLYNERARRRGLLGASVLGDDIHRARWTFVLRVRAODPPELYFVKVDVVTGAYDTI 777
QY 721 PQDLTEVIASIIKPQNTYCVRRYAVVQKAAHGHVRKAFKSHVSTLTLDLPYMRQFVAHL 780
DB 778 PQDLTEVIASIIKPQNTYCVRRYAVVQKAAHGHVRKAFKSHVSTLTLDLPYMRQFVAHL 837
QY 781 QETSPLRDVAVVIEQSSSLNEASSGLFDVFLRFMCHAVRIRGKSVYQCQIPIQGSILSTL 840
DB 838 QETSPLRDVAVVIEQSSSLNEASSGLFDVFLRFMCHAVRIRGKSVYQCQIPIQGSILSTL 897
QY 841 LCSLCYGDMEKLFAGIRRGGLLRLLVDDFLVTPHLLTHAKTFLRTLVRCVPYGCVNIL 900
DB 898 LCSLCYGDMEKLFAGIRRGGLLRLLVDDFLVTPHLLTHAKTFLRTLVRCVPYGCVNIL 957
QY 901 RKTWNPNPVEDEALGGTAFVQMPAHGLFPWCGLLDTRTLEVDSSYSSVARTSIRASLTF 960
DB 958 RKTWNPNPVEDEALGGTAFVQMPAHGLFPWCGLLDTRTLEVDSSYSSVARTSIRASLTF 1017
QY 961 NRGFKAGNRMRKLFVGLRLKCHSLFDLDQVNSLQTVCTNIYKILLQAYRFHACVQLQP 1020
DB 1018 NRGFKAGNRMRKLFVGLRLKCHSLFDLDQVNSLQTVCTNIYKILLQAYRFHACVQLQP 1077
QY 1021 FHOQVKNPTFFLRVSDTASLCYSILKAKNAGSLGAKGAGPLSEAVQWLCHQAFLL 1080
DB 1078 FHOQVKNPTFFLRVSDTASLCYSILKAKNAGSLGAKGAGPLSEAVQWLCHQAFLL 1137
QY 1081 KLTRHRVTVYVPLGLSLRTAQTLRSKLPGLTTLTALEAAANPALPSPDKTILD 1132
DB 1138 KLTRHRVTVYVPLGLSLRTAQTLRSKLPGLTTLTALEAAANPALPSPDKTILD 1189

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RESULT 42

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US-10-877-146-613
; Sequence 613, Application US/10877146
; Publication No. US20050013825A1
; GENERAL INFORMATION:
; APPLICANT: Cecch, Thomas R.
;             Lingner, Joachim
;             Nakamura, Toru
;             Chapman, Karen B.
;             Morin, Gregg B.
;             Harley, Calvin B.
;             Andrews, William H.
; TITLE OF INVENTION: Human Telomerase Catalytic Subunit
; NUMBER OF SEQUENCES: 727
; CORRESPONDENCE ADDRESS:
; STREET: Townsend and Townsend and Crew LLP
; CITY: San Francisco
; STATE: California

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; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/877,146
; FILING DATE: 24-Jun-2004
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/432,503
; FILING DATE: 02-Nov-1999
; APPLICATION NUMBER: 08/974,549
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; APPLICATION NUMBER: US 08/851,843
; FILING DATE: 06-MAY-1997
; APPLICATION NUMBER: US 08/854,050
; FILING DATE: 09-MAY-1997
; APPLICATION NUMBER: US 08/911,312
; FILING DATE: 14-AUG-1997
; APPLICATION NUMBER: US 08/912,951
; FILING DATE: 14-AUG-1997
; APPLICATION NUMBER: US 08/915,503
; FILING DATE: 14-AUG-1997
; APPLICATION NUMBER: WO PCT/US97/17618
; FILING DATE: 01-OCT-1997
; APPLICATION NUMBER: WO PCT/US97/17885
; FILING DATE: 01-OCT-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph Ted
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-002610US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 613:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1189 amino acids
; TYPE: amino acid
; STRANDEDNESS: <unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..1189
; OTHER INFORMATION: /note= "fusion protein composed of
; melittin signal sequence and full length
; hirt protein"
; SEQUENCE DESCRIPTION: SEQ ID NO: 613:
; US-10-877-146-613

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Query Match 100.0%; Score 5961; DB 17; Length 1189;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MPRAPRCRAVRSLLRSHYREVLPPLATFVRRLGPGQWRVLVQRPDPAAFRALVAQCLVCPW 60
DB 58 MPRAPRCRAVRSLLRSHYREVLPPLATFVRRLGPGQWRVLVQRPDPAAFRALVAQCLVCPW 117
QY 61 DARPPPAAPSFQVSCLEKELVARVLRQRCERKAKNVLAFGFALLDARGCPPPEAFTTSVR 120
DB 118 DARPPPAAPSFQVSCLEKELVARVLRQRCERKAKNVLAFGFALLDARGCPPPEAFTTSVR 177
QY 121 SYLPTNTVDALRGSGAWGLLRRVGDVLLVHLLARCALFVLVAPSCAYOVCGPPLYQLGA 180
DB 178 SYLPTNTVDALRGSGAWGLLRRVGDVLLVHLLARCALFVLVAPSCAYOVCGPPLYQLGA 237

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181	QY	ATQARPPPHASGPRRRRLCCERAWNHVSREAGVPLGLPAPGARRRGGSASRSLSLPLPKRPRR	240
238	Db	ATQARPPPHASGPRRRRLCCERAWNHVSREAGVPLGLPAPGARRRGGSASRSLSLPLPKRPRR	297
241	QY	GAAPPEPRTPVQCGSWAHPGRTGRPSDRGFCVWSPARPAEBAATSLLEGALSCTRSHSPVG	300
298	Db	GAAPPEPRTPVQCGSWAHPGRTGRPSDRGFCVWSPARPAEBAATSLLEGALSCTRSHSPVG	357
301	QY	ROHAGPPSTSRPPRPMDTPCPPIVAAETKHFPLYSSGDKEQURPSPFLSSLSRPSLTGARRL	360
358	Db	ROHAGPPSTSRPPRPMDTPCPPIVAAETKHFPLYSSGDKEQURPSPFLSSLSRPSLTGARRL	417
361	QY	VETIFLGSRPMWPGTPRRLPLRPORYWQMRPLFLELLGNHQAOCPVGLLTKTCHPLRAAVT	420
418	Db	VETIFLGSRPMWPGTPRRLPLRPORYWQMRPLFLELLGNHQAOCPVGLLTKTCHPLRAAVT	477
421	QY	PAAGVCAREKPOGQSWAAPEEEDTPRRLVOLLROHSSPWQYVGFVRACLRRLVPPGLWGS	480
478	Db	PAAGVCAREKPOGQSWAAPEEEDTPRRLVOLLROHSSPWQYVGFVRACLRRLVPPGLWGS	537
481	QY	RHNERRFLRNTKFTISLGKHAKLSLOBLTWKQSVRDCAWLRRSPGVGCVPAAEHRLREEI	540
538	Db	RHNERRFLRNTKFTISLGKHAKLSLOBLTWKQSVRDCAWLRRSPGVGCVPAAEHRLREEI	597
541	QY	LAKFLHLMWSYVVVELLARSFPYVTTTFQKNRLFYFKSVWSKLSQSIGROHLKRVQURE	600
598	Db	LAKFLHLMWSYVVVELLARSFPYVTTTFQKNRLFYFKSVWSKLSQSIGROHLKRVQURE	657
601	QY	LSEAEVQHREARPALITSRLRFTPKPDGLRPIVNMDYVVGARTFREKRAERLTSRVKA	660
658	Db	LSEAEVQHREARPALITSRLRFTPKPDGLRPIVNMDYVVGARTFREKRAERLTSRVKA	717
661	QY	LFSVLNTERARRPGLLGASVLGLDDIHRWRTFVLVRAODPPPELYFVKVDVTGAYDTI	720
718	Db	LFSVLNTERARRPGLLGASVLGLDDIHRWRTFVLVRAODPPPELYFVKVDVTGAYDTI	777
721	QY	PODELTEVIASIIKPONTYCVRRYAVVQKAAGHVRAKAFKSHVSLTDLQPYMRQFVAHL	780
778	Db	PODELTEVIASIIKPONTYCVRRYAVVQKAAGHVRAKAFKSHVSLTDLQPYMRQFVAHL	837
781	QY	QETSPLRDAVVEIOSSLINEASSGLFDVFLRFMCHHAVIRIGKSYVOCQGIPOGSIISLT	840
838	Db	QETSPLRDAVVEIOSSLINEASSGLFDVFLRFMCHHAVIRIGKSYVOCQGIPOGSIISLT	897
841	QY	LCSLCYGD MENKLPAGIRRDGLLRLVDDFLLVTPHLTHAKTFLRTLVRGPVEYGCVVNL	900
898	Db	LCSLCYGD MENKLPAGIRRDGLLRLVDDFLLVTPHLTHAKTFLRTLVRGPVEYGCVVNL	957
901	QY	RKTVNVNPFVEDEALGGTAFVQMPAHGLFPWCGLLLDTRTLEQSDYSYARTSTRASLTFF	960
958	Db	RKTVNVNPFVEDEALGGTAFVQMPAHGLFPWCGLLLDTRTLEQSDYSYARTSTRASLTFF	1017
961	QY	NRGFKAGNRMRKLFVGLRLKCHSLFDLQVNSLQVCTNIIYKILLQAVRFHACVQLQP	1020
1018	Db	NRGFKAGNRMRKLFVGLRLKCHSLFDLQVNSLQVCTNIIYKILLQAVRFHACVQLQP	1077
1021	QY	FHQQVKNPFTFFLRVISDTASLCSYILKAKNAGSLGAKGAAGPLPSEAVQWLCHQAFLL	1080
1078	Db	FHQQVKNPFTFFLRVISDTASLCSYILKAKNAGSLGAKGAAGPLPSEAVQWLCHQAFLL	1137
1081	QY	KLTRHRYVYVPLLGSLRTAQQLSRKLP GTGTLTALAEAAANPALPSPDFTILD	1132
1138	Db	KLTRHRYVYVPLLGSLRTAQQLSRKLP GTGTLTALAEAAANPALPSPDFTILD	1189

RESIN.T 43

RESULT 43
IIS-10-044-692-324

US-10-044-892-324
: Sequence 324. Application US/10044692

Publication No. US20030096344A1

; FACTICATIO NO: 092003
; GENERAL INFORMATION:

APPLICANT: Cech, Thomas R.

Lingner, Joachim

Nakamura, Toru

Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin
Andrews, William H.

TITLE OF INVENTION: HUMAN TELOMERASE CATALYTIC SUBUNIT: DIAGNOSTIC AND THERAPEUTIC METHODS

```
Query Match      100.0%; Score 5961; DB 14; Length 1200;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy Dk

QY 241 GAAPEPERTVPGQSWAHPCGTRGSDRGFCVVPSPARPAEATSLGALSGLTRHSPSVG 300
Db 309 GAAPEPERTVPGQSWAHPCGTRGSDRGFCVVPSPARPAEATSLGALSGLTRHSPSVG 368
QY 301 ROHAGPPSTRPRPMDTPCPVYAEKFLYSKGDKEQLRSPFLSSLRPSLTGARRL 360
Db 369 ROHAGPPSTRPRPMDTPCPVYAEKFLYSKGDKEQLRSPFLSSLRPSLTGARRL 428
QY 361 VETIFLGRSPWMPCTPRRLPRLPQRYWQMRPLFLELLGNHAQCPYGVLLKTHCPLRAAVT 420
Db 429 VETIFLGRSPWMPCTPRRLPRLPQRYWQMRPLFLELLGNHAQCPYGVLLKTHCPLRAAVT 488
QY 421 PAAGVCAREKPOGSVAPEEEDTPRLVLQLLRQHSSPMQVYFVRACLRRLVPPGLWGS 480
Db 489 PAAGVCAREKPOGSVAPEEEDTPRLVLQLLRQHSSPMQVYFVRACLRRLVPPGLWGS 548
QY 481 RHNERFLRNTKXFSISLKGAKLSLQBLTWKMSVRDCAMLRSPGVGCVPAAEHRLREEI 540
Db 549 RHNERFLRNTKXFSISLKGAKLSLQBLTWKMSVRDCAMLRSPGVGCVPAAEHRLREEI 608
QY 541 LAKFLHLMWSVYVVELLRSFYVETTFQKNRLFYVRKSVMSKLSQSIGIRQHILKRVOLRE 600
Db 609 LAKFLHLMWSVYVVELLRSFYVETTFQKNRLFYVRKSVMSKLSQSIGIRQHILKRVOLRE 668
QY 601 LSEAEVRQREARPALITSRLRPIPKDGLRPIVNM DYVVGARTFRREKAEALTSRVKA 660
Db 669 LSEAEVRQREARPALITSRLRPIPKDGLRPIVNM DYVVGARTFRREKAEALTSRVKA 728
QY 661 LFSVLNTERARRPGLLGASVLGDDIHRWRTFVLVRADPPPELYFVKVDTGAYDTI 720
Db 729 LFSVLNTERARRPGLLGASVLGDDIHRWRTFVLVRADPPPELYFVKVDTGAYDTI 788
QY 721 PQRLTEVIASIIKPQNTYCVRRYAVVQKAAHGHVRKAFKSHVSTLTDLOPNRQFVAHL 780
Db 789 PQRLTEVIASIIKPQNTYCVRRYAVVQKAAHGHVRKAFKSHVSTLTDLOPNRQFVAHL 848
QY 781 QETSPLRDVAVIEQSSSLNEASSGLFDVFLRFMCHAVRIRGKSVYQCQIPOGSIILSTL 840
Db 849 QETSPLRDVAVIEQSSSLNEASSGLFDVFLRFMCHAVRIRGKSVYQCQIPOGSIILSTL 908
QY 841 LCSLCYGDMMENKLFAGIRRDGLLRLVDDFLVTPHLLTHAKTFLRLTVRGVPYGCVNL 900
Db 909 LCSLCYGDMMENKLFAGIRRDGLLRLVDDFLVTPHLLTHAKTFLRLTVRGVPYGCVNL 968
QY 901 RKTVMNPFVDEALGGTAFVQMPAHGLFPWCGLLDDTRTLEVDYSSYARTSIRASLTF 960
Db 969 RKTVMNPFVDEALGGTAFVQMPAHGLFPWCGLLDDTRTLEVDYSSYARTSIRASLTF 1028
QY 961 NRGFKAGNNRRKLFVGLRLKCHSLFLLDQVNSLQTVCTNIYKILLQAYRPHACVLQLP 1020
Db 1029 NRGFKAGNNRRKLFVGLRLKCHSLFLLDQVNSLQTVCTNIYKILLQAYRPHACVLQLP 1088
QY 1021 FHOQVKNPFTFLRVIDSTASLCYSILKAKNAGMSLGAKAAGPLPSEAVQWVCHQAFLL 1080
Db 1089 FHOQVKNPFTFLRVIDSTASLCYSILKAKNAGMSLGAKAAGPLPSEAVQWVCHQAFLL 1148
QY 1081 KLTRHRVTVYVPLLGSLRTAQTLRSKLPGLTTLTALEAAANPALPSDFKTLTD 1132
Db 1149 KLTRHRVTVYVPLLGSLRTAQTLRSKLPGLTTLTALEAAANPALPSDFKTLTD 1200

RESULT 44

US-10-044-539-324
; Sequence 324, Application US/10044539
; Publication No. US20030100093A1
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; ; Lingner, Joachim
; ; Nakamura, Toru
; ; Chapman, Karen B.
; ; Morin, Gregg B.
; ; Harley, Calvin
; ; Andrews, William H.

; TITLE OF INVENTION: HUMAN TELOMERASE CATALYTIC SUBUNIT: DIAGNOSTIC AND
; THERAPEUTIC METHODS
; NUMBER OF SEQUENCES: 335
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/044,539
; FILING DATE: 11-Jan-2002
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/912,951
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US 08/854,050
; FILING DATE: 09-MAY-1997
; APPLICATION NUMBER: US 08/851,843
; FILING DATE: 06-MAY-1997
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph T.
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-002600US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 324:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1200 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 324:
; US-10-044-539-324

Query Match 100.0%; Score 5961; DB 14; Length 1200;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MPRAPRCRAVRSLRSHYREVLPATFVRRLPGQWRLVORGDPAAFRALVAOCLVCVPW 60
Db 69 MPRAPRCRAVRSLRSHYREVLPATFVRRLPGQWRLVORGDPAAFRALVAOCLVCVPW 128
QY 61 DARPPAAPSRFQVSCLELVARVLQRLCERGAKNVLAEGFALLDGCARGGPPPEAFTTSVR 120
Db 129 DARPPAAPSRFQVSCLELVARVLQRLCERGAKNVLAEGFALLDGCARGGPPPEAFTTSVR 188
QY 121 SYLPTNTVDALRGSGAWGLLRRVGGDVLVHLIARCALFVLVAPSCAYQVCGPPLYQLGA 180
Db 189 SYLPTNTVDALRGSGAWGLLRRVGGDVLVHLIARCALFVLVAPSCAYQVCGPPLYQLGA 248
QY 181 ATQARPPPHASGPRRLRGGERAWNHSVRAGVPLGLPAPGARRRGGSASRSLPLPKRPRR 240
Db 249 ATQARPPPHASGPRRLRGGERAWNHSVRAGVPLGLPAPGARRRGGSASRSLPLPKRPRR 308
QY 241 GAAPEPERTVPGQSWAHPCGTRGSDRGFCVVPSPARPAEATSLGALSGLTRHSPSVG 300
Db 309 GAAPEPERTVPGQSWAHPCGTRGSDRGFCVVPSPARPAEATSLGALSGLTRHSPSVG 368

301 ROHAGPSTSRPPMDTPCPVVAETKHFYSSGDKQURPSFLSSLSPLSTGARRL 360
 369 ROHAGPSTSRPPMDTPCPVVAETKHFYSSGDKQURPSFLSSLSPLSTGARRL 428
 361 VETIFLGSRPWMPGTRELRLPORYWQMRPLFLELLGNHQAOCYGVLLKTHCPRAVY 420
 429 VETIFLGSRPWMPGTRELRLPORYWQMRPLFLELLGNHQAOCYGVLLKTHCPRAVY 488
 421 PAAGVCAREKPOGSAVAPEEDTDPRLVQLLRQHSFPWQYGVFVRACLRLRVPGLWGS 480
 489 PAAGVCAREKPOGSAVAPEEDTDPRLVQLLRQHSFPWQYGVFVRACLRLRVPGLWGS 548
 481 RHNERFLRWTKFISLGKHAKLISOELTWKMSVDCAWLRSPGVGCVPAAEHRLREEI 540
 549 RHNERFLRWTKFISLGKHAKLISOELTWKMSVDCAWLRSPGVGCVPAAEHRLREEI 608
 541 LAKFLHLMMSVYVVELLRSPPVTTETFOKNRLFYKRSVMSKLSQSIGIRHKLKVQRE 600
 609 LAKFLHLMMSVYVVELLRSPPVTTETFOKNRLFYKRSVMSKLSQSIGIRHKLKVQRE 668
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 669 LSEAEVRQREARPAALTSRLRFIPKPDGLRPIVNMDDYVVGARTFREKRAERLTSRVKA 728
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 781 QETSPLRDVAVIEQSSLINEASSGLFDVFLRFMCHHVRIRGKSVYVOCQIGIPQGSILSTL 840
 849 QETSPLRDVAVIEQSSLINEASSGLFDVFLRFMCHHVRIRGKSVYVOCQIGIPQGSILSTL 908
 841 LCSICYGDMENKLPAGIRRDGLLRLVDDFLVTPHLLTHAKTFRLTLVRGVPEYGCVVNL 900
 909 LCSICYGDMENKLPAGIRRDGLLRLVDDFLVTPHLLTHAKTFRLTLVRGVPEYGCVVNL 968
 901 RKTVVNPFVEDEALGTAFAVQMPAHGLFPWCGLLLDTRTLEVOQSDYSSYARTSIRASLT 960
 969 RKTVVNPFVEDEALGTAFAVQMPAHGLFPWCGLLLDTRTLEVOQSDYSSYARTSIRASLT 1028
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 1029 NRGFKAGNRWRKLFVGLRKLCHSLFDLQVNSLQVCTWIKYIKLLQAYREHACVLQLP 1088
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 1081 KLTHRVYVPLGSLTAQTLRSKLPGLTTLTALEAANPALPSDFKTILD 1132
 1149 KLTHRVYVPLGSLTAQTLRSKLPGLTTLTALEAANPALPSDFKTILD 1200

RESULT 45

US-10-325-810-612
 ; Sequence 612, Application US/10325810
 ; Publication No. US20030204069A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Cech, Thomas R.
 ; Lingner, Joachim
 ; Nakamura, Toru
 ; Chapman, Karen B.
 ; Morin, Gregg B.
 ; Harley, Calvin B.
 ; Andrews, William H.
 ; TITLE OF INVENTION: Human Telomerase Catalytic Subunit
 ; NUMBER OF SEQUENCES: 633
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Townsend and Townsend and Crew LLP

Query Match 100.0%; Score 5961; DB 15; Length 1200;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPRAPRCRAVRSLLRSHYREVLPATFVRRLGQGWRLVQRGDPAAFRALVAQCLVCVPW 60
 DB 69 MPRAPRCRAVRSLLRSHYREVLPATFVRRLGQGWRLVQRGDPAAFRALVAQCLVCVPW 128
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 QY 121 SYLPTNTVTDALRGSGAWGLLRVGGDDVLVHLARCALFVLVAPSCAYQVCGPPLYOLGA 180

STREET: Two Embarcadero Center, Eighth Floor
 CITY: San Francisco
 STATE: California
 COUNTRY: USA
 ZIP: 94111-3834
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent in Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/10/325,810
 FILING DATE: 20-Dec-2002
 CLASSIFICATION: <Unknown>
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/09/402,181
 FILING DATE: 29-Sep-1997
 APPLICATION NUMBER: US 08/724,643
 FILING DATE: 01-OCT-1996
 APPLICATION NUMBER: US 08/844,419
 FILING DATE: 18-APR-1997
 APPLICATION NUMBER: US 08/846,017
 FILING DATE: 25-APR-1997
 APPLICATION NUMBER: US 08/851,843
 FILING DATE: 06-MAY-1997
 APPLICATION NUMBER: US 08/854,050
 FILING DATE: 09-MAY-1997
 APPLICATION NUMBER: US 08/911,312
 FILING DATE: 14-AUG-1997
 APPLICATION NUMBER: US 08/912,951
 FILING DATE: 14-AUG-1997
 APPLICATION NUMBER: US 08/915,503
 FILING DATE: 14-AUG-1997
 APPLICATION NUMBER: WO PCT/US97/17885
 FILING DATE: 01-OCT-1997
 ATTORNEY/AGENT INFORMATION:
 NAME: Ausenhus, Scott L.
 REGISTRATION NUMBER: 42,271
 REFERENCE/DOCKET NUMBER: 015389-002620US
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 576-0200
 TELEFAX: (415) 576-0300
 INFORMATION FOR SEQ ID NO: 612:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1200 amino acids
 TYPE: amino acid
 STRANDEDNESS: <Unknown>
 MOLECULE TYPE: protein
 FEATURE:
 NAME/KEY: Protein
 LOCATION: 1..1200
 OTHER INFORMATION: /note= "fusion protein composed of His6 and Anti-Xpress tags, enterokinase cleavage site and full length hTERT protein"
 SEQUENCE DESCRIPTION: SEQ ID NO: 612:
 US-10-325-810-612

Db 189 SYLPTNTVTDALRGSGAWGLLRRVGGDVLVHLLARCALFVLVAPSCAYVCGPPLYQLGA 248
Qy 181 ATCARPPPHASGRRRLRCERANHNSVREAGVPLGLPAPCARRRGGSASRLPLPKPRR 240
Db 249 ATQARPPPHASGRRRLRCERANHNSVREAGVPLGLPAPCARRRGGSASRLPLPKPRR 308
Qy 241 GAAPERTPVGGGSAHPCRTGSDRGFCVSPARPAREATSLGALSGLTSHSPSVG 300
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Qy 301 ROHAGPPSTRPPRWDTPCPPIYATKHFLYSSGDKQOLRPSFLLSSLRPLSLTGARRL 360
Db 369 ROHAGPPSTRPPRWDTPCPPIYATKHFLYSSGDKQOLRPSFLLSSLRPLSLTGARRL 428
Qy 361 VETIFLGSRRPMPCTPRRLPRLPORVWQMPLELLGNHAOCYPYVLLKTKHCPLRAAVT 420
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Qy 421 PAAGVCAREXPQGSVAAPBEDDTPRLVQLLRQHSPPWQVYGFVRACLRLVPPGLWGS 480
Db 489 PAAGVCAREXPQGSVAAPBEDDTPRLVQLLRQHSPPWQVYGFVRACLRLVPPGLWGS 548
Qy 481 RHNERPLRNTKKFISLGKHAQLSQELTWKMSVRDCAMLRSPGVCVPAABHRLREEI 540
Db 549 RHNERPLRNTKKFISLGKHAQLSQELTWKMSVRDCAMLRSPGVCVPAABHRLREEI 608
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Qy 601 LSAEVRQHEARPAALTSRLRTPKPDGLRPVNDYVVGARTFRREKRAELTTSRVKA 660
Db 669 LSAEVRQHEARPAALTSRLRTPKPDGLRPVNDYVVGARTFRREKRAELTTSRVKA 728
Qy 661 LFSVLNYERARRPGLIGASVLGDDIHRWRTFVLVRVRAQDPPPELYFVKVDVTGAYDTI 720
Db 729 LFSVLNYERARRPGLIGASVLGDDIHRWRTFVLVRVRAQDPPPELYFVKVDVTGAYDTI 788
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Db 789 PODELTEVIASIIKPQNTYCVRRYAVVQKAAGHVRKAFKSHVSTLTDLPQYMRQFVAHL 848
Qy 781 QETSPLRDAVVIQSSSLNEASSGLFDVFLRFMCHAVRIRGKSYVQCQIPOGSIILSTL 840
Db 849 QETSPLRDAVVIQSSSLNEASSGLFDVFLRFMCHAVRIRGKSYVQCQIPOGSIILSTL 908
Qy 841 LCSLCYGDMMENKLFAGIRRDGLLRLVDDFLVTPHLTHAKTFLRTLVRGVPYGCVVNL 900
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Db 969 RKTVVNFPVDEALGGTAFVQMPAHGLFPWCGLLDTRTLEVDSDYSSYARTSIRASLTF 1028
Qy 961 NRGFKAGNRRKLFVGLRLKCHSLFDLDQVNSIQVTCTNIYKILLIQAYRFHACVQLQP 1020
Db 1029 NRGFKAGNRRKLFVGLRLKCHSLFDLDQVNSIQVTCTNIYKILLIQAYRFHACVQLQP 1088
Qy 1021 FHOQVWKNPTFFLRVISTASLCYSILKAKNAGMSLGAKAAGPLPSEAVQWICHQAFLL 1080
Db 1089 FHOQVWKNPTFFLRVISTASLCYSILKAKNAGMSLGAKAAGPLPSEAVQWICHQAFLL 1148
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Db 1149 KLTRHRVTVYVPLLSLRTAQTQLSRKLPGTTLTALEAANPALPSPDKTILD 1200

RESULT 46

US-10-877-124-612
; Sequence 612, Application US/10877124
; Publication No. US20040242529A1
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.

Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin B.
Andrews, William H.
TITLE OF INVENTION: Human Telomerase Catalytic Subunit
NUMBER OF SEQUENCES: 727
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA: US/10/877,124
FILING DATE: 24-Jun-2004
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/432,503
FILING DATE: 02-Nov-1999
APPLICATION NUMBER: 08/974,549
FILING DATE: <Unknown>
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/911,312
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: WO PCT/US97/17618
FILING DATE: 01-OCT-1997
APPLICATION NUMBER: WO PCT/US97/17885
FILING DATE: 01-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph Ted
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002610US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 612:
SEQUENCE CHARACTERISTICS:
LENGTH: 1200 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
NAME/KEY: Protein
LOCATION: 1..1200
OTHER INFORMATION: /note= "fusion protein composed of His6
and Anti-Xpress tags, enterokinase
cleavage site and full length hTERT
protein"
SEQUENCE DESCRIPTION: SEQ ID NO: 612:
US-10-877-124-612

Query Match 100.0%; Score 5961; DB 16; Length 1200;
Best Local Similarity 100.0%; Pred. No. 0;

Matches 1132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 Db |||||
 Qy 121 SYLPTNTVDALRGSGAGLLRRVDDVLVHLLARCALFVLVAPSCAYOVCPPYLQGA 180
 Db |||||
 Qy 189 SYLPTNTVDALRGSGAGLLRRVDDVLVHLLARCALFVLVAPSCAYOVCPPYLQGA 248
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 Qy 181 ATQARPPPHASGPRRLRCERAMNHSVREAGVPLGLPAPGARRRGSGASRSPLPKPRR 240
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 Qy 249 ATQARPPPHASGPRRLRCERAMNHSVREAGVPLGLPAPGARRRGSGASRSPLPKPRR 308
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 Qy 241 GAAPERTPVQGSWAHPGTRGSDRGFCVSPAPAEATSLGALSGTRHSHPSVG 300
 Db |||||
 Qy 309 GAAPERTPVQGSWAHPGTRGSDRGFCVSPAPAEATSLGALSGTRHSHPSVG 368
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 Qy 301 RQHAGPSTSRPRPDWTPCPVYATKHPLYSSGDKQELRPSFLASSLRPSLTGARRL 360
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 Qy 361 VETIFLGSRRPMPGTPRRLPRLPORYQWMRPLFLELLGNHAQCPYGVLLKTHCPLRAVT 420
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 Qy 481 RHNERFLRNTKKISLGKHAQLSLOELTWKMSVRDCAWLRSPGVCVPAAEHRLREI 540
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 Qy 541 LAKEFLHLMMSVYVVELLRSFPYVTTTFQKRLFFYKSVMSKQSIGIRQHLKRVOLRE 600
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 Qy 601 LSEAEVQREARPAALLTSRLRPIKPDGLRPIVNDYVVGARTFREKRAERLTSRVKA 660
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 Qy 669 LSEAEVQREARPAALLTSRLRPIKPDGLRPIVNDYVVGARTFREKRAERLTSRVKA 728
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 Qy 661 LFSVINTERRARRPGLGASVGLDDIHRWRTFVLVRADPPPELYFVKVDVTGAYDTI 720
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 Qy 721 PODRLTEVIASIIKPNQTYCVRVAVVQKAHGHVRAFKSHVSTLTDLOPYMFOVAHL 780
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 Qy 781 QETSPLRDVAVIEOSSLINEASSGLFDVFLRPMCHAVIRGKSVQCGIPQGSILSTL 840
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 Qy 841 LCSICYGDMENKLPAGIRRDGLLRLVDDFLVTPHPTHAKTFTLRTLVRGVPEYGCVVNL 900
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 Qy 909 LCSICYGDMENKLPAGIRRDGLLRLVDDFLVTPHPTHAKTFTLRTLVRGVPEYGCVVNL 968
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 Qy 901 RKTVVNPFVEALGGTAFVOMPAGHLPFPGGLLDDRTLEVDQSDYSYARTSRASLTFF 960
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 Qy 969 RKTVVNPFVEALGGTAFVOMPAGHLPFPGGLLDDRTLEVDQSDYSYARTSRASLTFF 1028
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 Qy 961 NRGFKAGNMRKLPFGVRLKCHSLFLDLQVNSLQTVCTNIYKILLQAVRFHACVQLP 1020
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 Db 1149 KLTHRRVTVVPLLGSLRTAQTOLSRKLPGLTTLTALAAANPALPSPDFKTILD 1200

RESULT 47

US-10-877-022-612
 ; Sequence 612, Application US/10877022
 ; Publication No. US20040247613A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Cech, Thomas R.
 ; Lingner, Joachim
 ; Nakamura, Toru
 ; Chapman, Karen B.
 ; Morin, Gregg B.
 ; Harley, Calvin B.
 ; Andrews, William H.
 ; TITLE OF INVENTION: Human Telomerase Catalytic Subunit
 ; NUMBER OF SEQUENCES: 727
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Townsend and Townsend and Crew LLP
 ; STREET: Two Embarcadero Center, Eighth Floor
 ; CITY: San Francisco
 ; STATE: California
 ; COUNTRY: USA
 ; ZIP: 94111-3834
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/10/877,022
 ; FILING DATE: 24-Jun-2004
 ; CLASSIFICATION: <Unknown>
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/432,503
 ; FILING DATE: 02-Nov-1999
 ; APPLICATION NUMBER: 08/974,549
 ; FILING DATE: <Unknown>
 ; APPLICATION NUMBER: US 08/844,419
 ; FILING DATE: 18-APR-1997
 ; APPLICATION NUMBER: US 08/846,017
 ; FILING DATE: 25-APR-1997
 ; APPLICATION NUMBER: US 08/851,843
 ; FILING DATE: 06-MAY-1997
 ; APPLICATION NUMBER: US 08/854,050
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 ; APPLICATION NUMBER: US 08/912,951
 ; FILING DATE: 14-AUG-1997
 ; APPLICATION NUMBER: US 08/915,503
 ; FILING DATE: 14-AUG-1997
 ; APPLICATION NUMBER: WO PCT/US97/17618
 ; FILING DATE: 01-OCT-1997
 ; APPLICATION NUMBER: WO PCT/US97/17885
 ; FILING DATE: 01-OCT-1997
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Apple, Randolph Ted
 ; REGISTRATION NUMBER: 36,429
 ; REFERENCE/DOCKET NUMBER: 015389-002610US
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (415) 576-0200
 ; TELEFAX: (415) 576-0300
 ; INFORMATION FOR SEQ ID NO: 612:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 1200 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: <Unknown>
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein

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; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..1200
; OTHER INFORMATION: /note="fusion protein composed of His6
; and Anti-Xpress tags, enterokinase
; cleavage site and full length htkr
; protein"
; SEQUENCE DESCRIPTION: SEQ ID NO: 612:
; US-10-877-022-612

Query Match 100.0%; Score 5961; DB 16; Length 1200;
Best local Similarity 100.0%; Pred. No. 0;
Matches 1132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPAPRCRAVRSLLRSHYREVLPLATFVRLPGQWRLVORGPPAAAFRALVAOCLVCVPW 60
DB 69 MPAPRCRAVRSLLRSHYREVLPLATFVRLPGQWRLVORGPPAAAFRALVAOCLVCVPW 128

QY 61 DARPPPAAPSFQVSCILKELVARVLQRLCERGAQNVLAQFALLDGAAGGPPPEAFTTSVR 120
DB 129 DARPPPAAPSFQVSCILKELVARVLQRLCERGAQNVLAQFALLDGAAGGPPPEAFTTSVR 188

QY 121 SYLPNTVTDALRSGAGLLRRVGGDDVLVHLLARCALFVLVAPSCAYQVCGPPLYLGA 180
DB 189 SYLPNTVTDALRSGAGLLRRVGGDDVLVHLLARCALFVLVAPSCAYQVCGPPLYLGA 248

QY 181 ATQARPPPHASGPRRLRCERAWNHSVREAGVPLGLPAPGARRRGGASRSLSPLPKPRR 240
DB 249 ATQARPPPHASGPRRLRCERAWNHSVREAGVPLGLPAPGARRRGGASRSLSPLPKPRR 308

QY 241 GAAPERTPVQGSWAHPGRTGPRSDRGFCVSPAPAEATSLLEGALSGTRHSHPSVG 300
DB 309 GAAPERTPVQGSWAHPGRTGPRSDRGFCVSPAPAEATSLLEGALSGTRHSHPSVG 368

QY 301 ROHAGAPTSRPPRPHDTPCPVYATKHLFVSSGDKQELRPSFLSSLRPSLTGARRL 360
DB 369 ROHAGAPTSRPPRPHDTPCPVYATKHLFVSSGDKQELRPSFLSSLRPSLTGARRL 428

QY 361 VETIFLGRSPWMPCTPRRLPRLPQRYWQMPPLFLELGNHAQCPYGVLLKTHCPLRAAVT 420
DB 429 VETIFLGRSPWMPCTPRRLPRLPQRYWQMPPLFLELGNHAQCPYGVLLKTHCPLRAAVT 488

QY 421 PAAGVCAREKPGQSVAAPEEEDTPRLVLQRLQHSPPWQVYGFVRACLRLVPPGLMGS 480
DB 489 PAAGVCAREKPGQSVAAPEEEDTPRLVLQRLQHSPPWQVYGFVRACLRLVPPGLMGS 548

QY 481 RHNERFLRNTKFIISLGHAKLSLQELTWKMSVRDCAWLRRSPGVCVPAAEHRLREEI 540
DB 549 RHNERFLRNTKFIISLGHAKLSLQELTWKMSVRDCAWLRRSPGVCVPAAEHRLREEI 608

QY 541 LAKFLHLMWSYVVELLRSFYVTTFTFQKNRLFYRKSVWSKLQSIGIRQHLKRVOLRE 600
DB 609 LAKFLHLMWSYVVELLRSFYVTTFTFQKNRLFYRKSVWSKLQSIGIRQHLKRVOLRE 668

QY 601 LSEAEVQREARFALLTSRLFTPKPDGLRPIVNMDDYVVGARTFREKEAERLTSRVKA 660
DB 669 LSEAEVQREARFALLTSRLFTPKPDGLRPIVNMDDYVVGARTFREKEAERLTSRVKA 728

QY 661 LFSVLNTERARRPGLLGASVLGLDDIHRWRTFVLVRAQDPPPELYFVKVDVTGAYDTI 720
DB 729 LFSVLNTERARRPGLLGASVLGLDDIHRWRTFVLVRAQDPPPELYFVKVDVTGAYDTI 788

QY 721 PQDLTEVIASIIKQNTYCVRRYAVVQKAHGHVKAFAKSHVSTLTDLOPYNRQFVAHL 780
DB 789 PQDLTEVIASIIKQNTYCVRRYAVVQKAHGHVKAFAKSHVSTLTDLOPYNRQFVAHL 848

QY 781 QETSPLRDVAVIEQSSLSNASSGLFDVFLRFMCHHAVIRIGKSVYQCQIPQGSILSTL 840
DB 849 QETSPLRDVAVIEQSSLSNASSGLFDVFLRFMCHHAVIRIGKSVYQCQIPQGSILSTL 908

QY 841 LCSICYGDMENKLFAGIRRDGLLIRLVDDLLVTPHLTHAKTFLRTLVRGVPYGCVVNL 900
DB 909 LCSICYGDMENKLFAGIRRDGLLIRLVDDLLVTPHLTHAKTFLRTLVRGVPYGCVVNL 968
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RESULT 48
US-10-877-146-612
; Sequence 612, Application US/10877146
; Publication No. US20050013825A1
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; Lingner, Joachim
; Nakamura, Toru
; Chapman, Karen B.
; Morin, Gregg B.
; Harley, Calvin B.
; Andrews, William H.
; TITLE OF INVENTION: Human Telomerase Catalytic Subunit
; NUMBER OF SEQUENCES: 727
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/877,146
; FILING DATE: 24-Jun-2004
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/432,503
; FILING DATE: 02-Nov-1999
; APPLICATION NUMBER: 08/974,549
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; APPLICATION NUMBER: US 08/851,843
; FILING DATE: 06-MAY-1997
; APPLICATION NUMBER: US 08/854,050
; FILING DATE: 09-MAY-1997
; APPLICATION NUMBER: US 08/911,312
; FILING DATE: 14-AUG-1997
; APPLICATION NUMBER: US 08/912,951
; FILING DATE: 14-AUG-1997
; APPLICATION NUMBER: US 08/915,503
; FILING DATE: 14-AUG-1997
; APPLICATION NUMBER: WO PCT/US97/17618
; FILING DATE: 01-OCT-1997
; APPLICATION NUMBER: WO PCT/US97/17885
; FILING DATE: 01-OCT-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph Ted
```

```
;
;
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-002610US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
;
; INFORMATION FOR SEQ ID NO: 612:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1200 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..1200
; OTHER INFORMATION: /note= "fusion protein composed of His6
; and Anti-Xpress tags, enterokinase
; cleavage site and full length hTERT
; protein"
;
; SEQUENCE DESCRIPTION: SEQ ID NO: 612:
US-10-877-146-612

Query Match 100.0%; Score 5961; DB 17; Length 1200;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MPAPRCRAVRSLLRSYREVLPLATFVRRLLGPOQWRLVQRGDPAAPFALVAQCLVCVPW 60
Db |
Qy 69 MPAPRCRAVRSLLRSYREVLPLATFVRRLLGPOQWRLVQRGDPAAPFALVAQCLVCVPW 128
Db |
Qy 61 DARPPPAAPSFRQVSCLEKELVARVLQRLCERGAKNVLAFGFALLDGGARGGPEAFTTSVR 120
Db |
Qy 129 DARPPPAAPSFRQVSCLEKELVARVLQRLCERGAKNVLAFGFALLDGGARGGPEAFTTSVR 188
Db |
Qy 121 SYLNTVTDALRGSGANGLLRRVDDVLLVHLLARCAALFVLVAPSCAYQVCPPLYQLGA 180
Db |
Qy 189 SYLNTVTDALRGSGANGLLRRVDDVLLVHLLARCAALFVLVAPSCAYQVCPPLYQLGA 248
Db |
Qy 181 ATQARPPPHASGPRRLRCERAMNHSVREAGVPLGLPAPGARRRGGSGASRLPLPKPRR 240
Db |
Qy 249 ATQARPPPHASGPRRLRCERAMNHSVREAGVPLGLPAPGARRRGGSGASRLPLPKPRR 308
Db |
Qy 241 GAAPEPRTVQGSWAHPGTRGSPDRGFCVSPARPAEATSLGALSGTRHSHPSVG 300
Db |
Qy 309 GAAPEPRTVQGSWAHPGTRGSPDRGFCVSPARPAEATSLGALSGTRHSHPSVG 368
Db |
Qy 301 RQHAGPSTSRPPRPMDTPCPVYAEKTHFLYSSGDKQLRPSFLSSLRPSLTGARRL 360
Db |
Qy 369 RQHAGPSTSRPPRPMDTPCPVYAEKTHFLYSSGDKQLRPSFLSSLRPSLTGARRL 428
Db |
Qy 361 VETIFLGRPMWPGTTPRLPLPORYWQMRPLFLELLGNHAQCPYGVLLKTHCPRAAVT 420
Db |
Qy 429 VETIFLGRPMWPGTTPRLPLPORYWQMRPLFLELLGNHAQCPYGVLLKTHCPRAAVT 488
Db |
Qy 421 PAAGVCAREKPGQSVAAPEEDTDPRLLVQLLRHSSPWQYGVFVRACLRLVPPGLWGS 480
Db |
Qy 489 PAAGVCAREKPGQSVAAPEEDTDPRLLVQLLRHSSPWQYGVFVRACLRLVPPGLWGS 548
Db |
Qy 481 RHNERFLRNTKFIISLGKHAQLSLQELTWKMSVRDCAWLRSPGVGCVPAAEHRLREEI 540
Db |
Qy 549 RHNERFLRNTKFIISLGKHAQLSLQELTWKMSVRDCAWLRSPGVGCVPAAEHRLREEI 608
Db |
Qy 541 LAKFLHLMWSVYVVELLRSFPYVTTTFQKNRLEFYKSWKLSQSIGRHLKRVQIRE 600
Db |
Qy 609 LAKFLHLMWSVYVVELLRSFPYVTTTFQKNRLEFYKSWKLSQSIGRHLKRVQIRE 668
Db |
Qy 601 LSEAEVQRHREARPAALLTSRLRFPKPDGLRPIVNDYVVGARTFREKKAERLTSRVKA 660
Db |
Qy 669 LSEAEVQRHREARPAALLTSRLRFPKPDGLRPIVNDYVVGARTFREKKAERLTSRVKA 728
Db |
Qy 661 LFSVLNTERARRPGLGASVLGLDDIHRAWRTFVLVRAQDPPPELYFVKVDVTGAYDTI 720
Db |
Qy 729 LFSVLNTERARRPGLGASVLGLDDIHRAWRTFVLVRAQDPPPELYFVKVDVTGAYDTI 788
Db |
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RESULT 49

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US-10-044-692-314
; Sequence 314, Application US/10044692
; Publication No. US20030096344A1
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; Lingner, Joachim
; Nakamura, Toru
; Chapman, Karen B.
; Morin, Gregg B.
; Harley, Calvin
; Andrews, William H.
;
; TITLE OF INVENTION: HUMAN TELOMERASE CATALYTIC SUBUNIT: DIAGNOSTIC AND
; THERAPEUTIC METHODS
;
; NUMBER OF SEQUENCES: 335
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94111
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/044,692
; FILING DATE: 11-Jan-2002
; CLASSIFICATION: <Unknown>
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/912,951
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US 08/854,050
; FILING DATE: 09-MAY-1997
; APPLICATION NUMBER: US 08/851,843
; FILING DATE: 06-MAY-1997
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; APPLICATION NUMBER: US 08/724,643
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FILING DATE: 01-OCT-1996
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002600US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 314:
SEQUENCE CHARACTERISTICS:
LENGTH: 1285 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 314:
US-10-044-692-314

Query Match 100.0%; Score 5961; DB 14; Length 1285;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPAPRCRAVRSLLRSHYREVLPATFVRRLGQGWRLVORGDPAAFRALVAOCLVCVW 60
Db 154 MPAPRCRAVRSLLRSHYREVLPATFVRRLGQGWRLVORGDPAAFRALVAOCLVCVW 213

QY 61 DARPPPAAPSFROVSCLELVARVLOLRCERGAKNVLAFTGALLDARGGPPFAFTTSVR 120
Db 214 DARPPPAAPSFROVSCLELVARVLOLRCERGAKNVLAFTGALLDARGGPPFAFTTSVR 273

QY 121 SYLPTNTVDALRGSGAWGLLRRVGGDVLVHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180
Db 274 SYLPTNTVDALRGSGAWGLLRRVGGDVLVHLLARCALFVLVAPSCAYQVCGPPLYQLGA 333

QY 181 ATQARPPPHASGRRLGCRANWHSVREAGVPLGLPAGARRRGSASRSPLPKRPRR 240
Db 334 ATQARPPPHASGRRLGCRANWHSVREAGVPLGLPAGARRRGSASRSPLPKRPRR 393

QY 241 GAAPEPERTVPGGSAHAPGRTGPDSDRGFCVSPARPAAEATSLRGALSGTTHSPSVG 300
Db 394 GAAPEPERTVPGGSAHAPGRTGPDSDRGFCVSPARPAAEATSLRGALSGTTHSPSVG 453

QY 301 ROHAGPPSTSRPPMDTPCPVYATKHFLYSSGDKQELRPSFLLSLRPSLTGARLL 360
Db 454 ROHAGPPSTSRPPMDTPCPVYATKHFLYSSGDKQELRPSFLLSLRPSLTGARLL 513

QY 361 VETIFLGSRPWMPGTFRRLPRLPQRYWQMRPLFLELLGNHAQCPYGVLLKTHCPLRAAVT 420
Db 514 VETIFLGSRPWMPGTFRRLPRLPQRYWQMRPLFLELLGNHAQCPYGVLLKTHCPLRAAVT 573

QY 421 PAAGVCAREKPGQSVAAPEEDTDPRLLVOLLRQHSPPMOVYGFVRACLRRLVPPCLWGS 480
Db 574 PAAGVCAREKPGQSVAAPEEDTDPRLLVOLLRQHSPPMOVYGFVRACLRRLVPPCLWGS 633

QY 481 RHNERFLRNTKKFISLGKHAKLSLOELTWKMSVRDCAMLRSPGVGCPVAAEHLRREEI 540
Db 634 RHNERFLRNTKKFISLGKHAKLSLOELTWKMSVRDCAMLRSPGVGCPVAAEHLRREEI 693

QY 541 LAKEFLHLSVYVVELLSRFFYTETTFQKNRLFYRKSWKLSQSIGIRQHLLKRVQLRE 600
Db 694 LAKEFLHLSVYVVELLSRFFYTETTFQKNRLFYRKSWKLSQSIGIRQHLLKRVQLRE 753

QY 601 LSAEVRQREARPAALLTSRLRIPKPDGLRPIVNMDDYVVGARTFRREKRAERLTSRVKA 660
Db 754 LSAEVRQREARPAALLTSRLRIPKPDGLRPIVNMDDYVVGARTFRREKRAERLTSRVKA 813

QY 661 LFSVLNYERARRPCLLGASVLGDDIHRAWRTFVLVRAODPPPELYFVKVDVTGAYDTI 720
Db 814 LFSVLNYERARRPCLLGASVLGDDIHRAWRTFVLVRAODPPPELYFVKVDVTGAYDTI 873

QY 721 PQRLTEVIASIIKPNQTYCVRYAVVQKAAGHVRKAFKSHVSTLTDLPQYMRQFVAHL 780
Db 874 PQRLTEVIASIIKPNQTYCVRYAVVQKAAGHVRKAFKSHVSTLTDLPQYMRQFVAHL 933

QY 781 QETSPLRDAVWIEQSSSLNEASSGLFDVFLRFWCHHAVIRGKSVYQCOGIPGGSILSTL 840
Db 934 QETSPLRDAVWIEQSSSLNEASSGLFDVFLRFWCHHAVIRGKSVYQCOGIPGGSILSTL 993

QY 841 LCSLCYGDMMENKLFAGIRRDGLLLRLVDDFLVTPHLLTHAKTFLRTLVRGVPEYGCVVNL 900
Db 994 LCSLCYGDMMENKLFAGIRRDGLLLRLVDDFLVTPHLLTHAKTFLRTLVRGVPEYGCVVNL 1053

QY 901 RKTVNFVPEDEALGCTAFVQMPAHLFPWCGLLDTRTLEVSQSDYSSVARTSIRASLTF 960
Db 1054 RKTVNFVPEDEALGCTAFVQMPAHLFPWCGLLDTRTLEVSQSDYSSVARTSIRASLTF 1113

QY 961 NRGFKAGRNMRKLFGLRLKCHSLFLDLQVNSLQVCTVNIYKILLQAYRPHACVQLQP 1020
Db 1114 NRGFKAGRNMRKLFGLRLKCHSLFLDLQVNSLQVCTVNIYKILLQAYRPHACVQLQP 1173

QY 1021 FHOQVWKNPTFFLRVISDTASLCYSILKAKNAGMSLGAKGAAGPLPSEAVQWLCHQAFLL 1080
Db 1174 FHOQVWKNPTFFLRVISDTASLCYSILKAKNAGMSLGAKGAAGPLPSEAVQWLCHQAFLL 1233

QY 1081 KLTRHRVTYVPLGLSLRTAQTOLSRKLPCTTLTAAEAANPALPSDFKTILD 1132
Db 1234 KLTRHRVTYVPLGLSLRTAQTOLSRKLPCTTLTAAEAANPALPSDFKTILD 1285

RESULT 50
US-10-044-539-314
; Sequence 314, Application US/10044539
; Publication No. US2003010093A1
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; Lingner, Joachim
; Nakamura, Toru
; Chapman, Karen B.
; Morin, Gregg B.
; Harley, Calvin
; Andrews, William H.
; TITLE OF INVENTION: HUMAN TELOMERASE CATALYTIC SUBUNIT: DIAGNOSTIC AND
; THERAPEUTIC METHODS
; NUMBER OF SEQUENCES: 335
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/044,539
; FILING DATE: 11-Jan-2002
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/912,951
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US 08/854,050
; FILING DATE: 09-MAY-1997
; APPLICATION NUMBER: US 08/851,843
; FILING DATE: 06-MAY-1997
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph T.
; REGISTRATION NUMBER: 36,429

REFERENCE/DOCKET NUMBER: 015389-002600US

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 576-0200

TELEFAX: (415) 576-0300

INFORMATION FOR SEQ ID NO: 314:

SEQUENCE CHARACTERISTICS:

LENGTH: 1285 amino acids

TYPE: amino acid

STRANDEDNESS: <Unknown>

TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 314:

US-10-044-539-314

Query Match	100.0%;	Score	5961;	DB	14;	Length	1285;
Best Local Similarity	100.0%;	Pred. No.	0;				
Matches	1132;	Conservative	0;	Mismatches	0;	Indels	0;
						Gaps	0;
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Db	154	MPRAPRCVAVRSLLRSHYREVLP	PLATFVRR	LGPGQWRLVQRGDPAAF	ALVAQCLVCPV	213	
Qy	61	DARPPAPSPROVSCSKELVARV	LQRLCER	GAKNVLAFA	LLDGGAGGPEAFTTSV	120	
Db	214	DARPPAPSPROVSCSKELVARV	LQRLCER	GAKNVLAFA	LLDGGAGGPEAFTTSV	273	
Qy	121	SYLENTVTDALRGSGANGLL	RRVGGDVLV	HLLARCALFVL	VAPSCAYQVCGPPLYOLGA	180	
Db	274	SYLENTVTDALRGSGANGLL	RRVGGDVLV	HLLARCALFVL	VAPSCAYQVCGPPLYOLGA	333	
Qy	181	ATQARPPHAGSPRRRLGCE	RAMNHSVREAGV	PLGLPAGARRRGSGASRS	SLPLPKPRR	240	
Db	334	ATQARPPHAGSPRRRLGCE	RAMNHSVREAGV	PLGLPAGARRRGSGASRS	SLPLPKPRR	393	
Qy	241	GAAPERTPVQGSWAHPGTR	GPSDRGFCV	SPARPAEATS	LEGALSGTRSHPSVG	300	
Db	394	GAAPERTPVQGSWAHPGTR	GPSDRGFCV	SPARPAEATS	LEGALSGTRSHPSVG	453	
Qy	301	QOHAGPPSTSRPPMDT	PCPPVVAETK	HELYSSGDKQLRPS	FLSSLRPSLTGARRL	360	
Db	454	QOHAGPPSTSRPPMDT	PCPPVVAETK	HELYSSGDKQLRPS	FLSSLRPSLTGARRL	513	
Qy	361	VETIFLGSRRPMPGT	PRRLPQLPQRYQ	WMRPLFLELLGNHAQ	CPYGVLLKTHCPLRAAVT	420	
Db	514	VETIFLGSRRPMPGT	PRRLPQLPQRYQ	WMRPLFLELLGNHAQ	CPYGVLLKTHCPLRAAVT	573	
Qy	421	PAAGVCAREKPGCSVA	APPEEDTPRRLV	OLLROHSSFPWQY	GVGFVACLRRLVPPGLWS	480	
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Qy	481	RHNERRFLRNTKFI	SLGKHAKLSLOEL	TWMSVRDCAWLR	SPGVGCVPAABHRLREI	540	
Db	634	RHNERRFLRNTKFI	SLGKHAKLSLOEL	TWMSVRDCAWLR	SPGVGCVPAABHRLREI	693	
Qy	541	LAKFLHLMSSVYVVEL	LSRFPYVTTT	FQKNRLFYRKS	VMSKLQSIGIRQHLKRVOLRE	600	
Db	694	LAKFLHLMSSVYVVEL	LSRFPYVTTT	FQKNRLFYRKS	VMSKLQSIGIRQHLKRVOLRE	753	
Qy	601	LSEAEVQHRREAR	PALLTSRLRFT	PKDGLRPIVNDY	VVGARTFRREKRAERLTSRVKA	660	
Db	754	LSEAEVQHRREAR	PALLTSRLRFT	PKDGLRPIVNDY	VVGARTFRREKRAERLTSRVKA	813	
Qy	661	LFSVLYNERARR	PGGLGASVLGDD	IHRWRTFVLR	RAODPPPELYFVKVDVTGAYDTI	720	
Db	814	LFSVLYNERARR	PGGLGASVLGDD	IHRWRTFVLR	RAODPPPELYFVKVDVTGAYDTI	873	
Qy	721	PODLTEVIASII	KPQNTYCVRRY	AVVQKAAGHVR	KAFKSHVSTLTDLPYMQFVAHL	780	
Db	874	PODLTEVIASII	KPQNTYCVRRY	AVVQKAAGHVR	KAFKSHVSTLTDLPYMQFVAHL	933	
Qy	781	QETSPLRDADV	IEOSSSINEASS	GLFDVFLR	FMCHHAVIRGKSYVQCQGIPOGSILSTL	840	
Db	934	QETSPLRDADV	IEOSSSINEASS	GLFDVFLR	FMCHHAVIRGKSYVQCQGIPOGSILSTL	993	

Search completed: August 5, 2005, 14:25:39
Job time : 198 secs

Qy	841	LCSLCYGDMENKLFAGIR	RDLRLVDDFLLVTP	HLTHAKTFLRTLVRG	VPYGCVVNL	900	
Db	994	LCSLCYGDMENKLFAGIR	RDLRLVDDFLLVTP	HLTHAKTFLRTLVRG	VPYGCVVNL	1053	
Qy	901	RKTVVNFVEDEALGGT	AFVQMPAHGLFP	WCGLLDTRTLE	VQSDYSYARTSIRASLTP	960	
Db	1054	RKTVVNFVEDEALGGT	AFVQMPAHGLFP	WCGLLDTRTLE	VQSDYSYARTSIRASLTP	1113	
Qy	961	NRGFKAGRNMRRLFG	VLRLKCHSLFLD	LQVNSLQVCTN	IYKILLQAYRFHACVLQLP	1020	
Db	1114	NRGFKAGRNMRRLFG	VLRLKCHSLFLD	LQVNSLQVCTN	IYKILLQAYRFHACVLQLP	1173	
Qy	1021	FHQQVWKNPTFFLR	VISDTASLCYSIL	KAKNAGMSLGAK	GAAGPLPSEAVQWLCHQAFLL	1080	
Db	1174	FHQQVWKNPTFFLR	VISDTASLCYSIL	KAKNAGMSLGAK	GAAGPLPSEAVQWLCHQAFLL	1233	
Qy	1081	KLTRHRVTVYVPL	LGSLRTAQOLSR	KLP	PGTTLTAL	EAANPALPSDFKTILD	1132
Db	1234	KLTRHRVTVYVPL	LGSLRTAQOLSR	KLP	PGTTLTAL	EAANPALPSDFKTILD	1285

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